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(54) Title: BREAST, GASTRIC AND PROSTATE CANCER ASSOCIATED ANTIGENS AND USES THEREFOR

(57) Abstract: Cancer associated antigens have been identified by autologous antibody screening of libraries of nucleic acids expressed in breast, gastric and prostate cancer cells using antisera from cancer patients. The invention relates to nucleic acids and encoded polypeptides which are cancer associated antigens expressed in patients afflicted with cancer. The invention provides, *inter alia*, isolated nucleic acid molecules, expression vectors containing those molecules and host cells transfected with those molecules. The invention also provides isolated proteins and peptides, antibodies to those proteins and peptides and cytotoxic T lymphocytes which recognize the proteins and peptides. Fragments of the foregoing including functional fragments and variants also are provided. Kits containing the foregoing molecules additionally are provided. The molecules provided by the invention can be used in the diagnosis, monitoring, research, or treatment of conditions characterized by the expression of one or more cancer associated antigens.

**BREAST, GASTRIC AND PROSTATE CANCER ASSOCIATED
ANTIGENS AND USES THEREFOR**

Field of the Invention

5 The invention relates to nucleic acids and encoded polypeptides which are cancer associated antigens expressed in patients afflicted with breast, gastric or prostate cancer. The invention also relates to agents which bind the nucleic acids or polypeptides. The nucleic acid molecules, polypeptides coded for by such molecules and peptides derived therefrom, as well as related antibodies and cytolytic T lymphocytes, are useful, *inter alia*, in diagnostic and
10 therapeutic contexts.

Background of the Invention

 The mechanism by which T cells recognize foreign materials has been implicated in cancer. A number of cytolytic T lymphocyte (CTL) clones directed against autologous
15 melanoma antigens, testicular antigens, and melanocyte differentiation antigens have been described. In many instances, the antigens recognized by these clones have been characterized.

 The use of autologous CTLs for identifying tumor antigens requires that the target cells which express the antigens can be cultured *in vitro* and that stable lines of autologous
20 CTL clones which recognize the antigen-expressing cells can be isolated and propagated. While this approach has worked well for melanoma antigens, other tumor types, such as epithelial cancers including breast and colon cancer, have proved refractory to the approach.

 More recently another approach to the problem has been described by Sahin et al. (*Proc. Natl. Acad. Sci. USA* 92:11810-11813, 1995). According to this approach, autologous
25 antisera are used to identify immunogenic protein antigens expressed in cancer cells by screening expression libraries constructed from tumor cell cDNA. Antigen-encoding clones so identified have been found to elicit a high-titer humoral immune response in the patients from which the antisera were obtained. Such a high-titer IgG response implies helper T cell recognition of the detected antigen. These tumor antigens can then be screened for the
30 presence of MHC/HLA class I and class II motifs and reactivity with CTLs.

 Since the individual tumor antigens presently known may be expressed only in a fraction of tumors, the availability of additional tumor antigens would significantly enlarge the

- 2 -

proportion of patients who are potentially eligible for therapeutic interventions. Thus there presently is a need for additional tumor antigens for development of therapeutics and diagnostics applicable to a greater number of cancer patients having various cancers.

The invention is elaborated upon further in the disclosure which follows.

5

Summary of the Invention

Autologous antibody screening has now been applied to breast, gastric and prostate cancer using antisera from cancer patients. Numerous cancer associated antigens have been identified. The invention provides, *inter alia*, isolated nucleic acid molecules, expression
10 vectors containing those molecules and host cells transfected with those molecules. The invention also provides isolated proteins and peptides, antibodies to those proteins and peptides and CTLs which recognize the proteins and peptides. Fragments including functional fragments and variants of the foregoing also are provided. Kits containing the foregoing molecules additionally are provided. The foregoing can be used in the diagnosis,
15 monitoring, research, or treatment of conditions characterized by the expression of one or more cancer associated antigens.

Prior to the present invention, only a handful of cancer associated genes had been identified in the past 20 years. The invention involves the surprising discovery of several genes, some previously known and some previously unknown, which are expressed in
20 individuals who have cancer. These individuals all have serum antibodies against the proteins (or fragments thereof) encoded by these genes. Thus, abnormally expressed genes are recognized by the host's immune system and therefore can form a basis for diagnosis, monitoring and therapy.

The invention involves the use of a single material, a plurality of different materials
25 and even large panels and combinations of materials. For example, a single gene, a single protein encoded by a gene, a single functional fragment thereof, a single antibody thereto, etc. can be used in methods and products of the invention. Likewise, pairs, groups and even panels of these materials and optionally other cancer associated antigen genes and/or gene products can be used for diagnosis, monitoring and therapy. The pairs, groups or panels can
30 involve 2, 3, 4, 5 or more genes, gene products, fragments thereof or agents that recognize such materials. A plurality of such materials are not only useful in monitoring, typing, characterizing and diagnosing cells abnormally expressing such genes, but a plurality of such

materials can be used therapeutically. An example of the use of a plurality of such materials for the prevention, delay of onset, amelioration, etc. of cancer cells, which express or will express such genes prophylactically or acutely. Any and all combinations of the genes, gene products, and materials which recognize the genes and gene products can be tested and identified for use according to the invention. It would be far too lengthy to recite all such combinations; those skilled in the art, particularly in view of the teaching contained herein, will readily be able to determine which combinations are most appropriate for which circumstances.

As will be clear from the following discussion, the invention has *in vivo* and *in vitro* uses, including for therapeutic, diagnostic, monitoring and research purposes. One aspect of the invention is the ability to fingerprint a cell expressing a number of the genes identified according to the invention by, for example, quantifying the expression of such gene products. Such fingerprints will be characteristic, for example, of the stage of the cancer, the type of the cancer, or even the effect in animal models of a therapy on a cancer. Cells also can be screened to determine whether such cells abnormally express the genes identified according to the invention.

The invention, in one aspect, is a method of diagnosing a disorder characterized by expression of a cancer associated antigen precursor coded for by a nucleic acid molecule. The method involves the steps of contacting a biological sample isolated from a subject with an agent that specifically binds to the nucleic acid molecule, an expression product thereof, or a fragment of an expression product thereof complexed with an MHC, preferably an HLA, molecule, wherein the nucleic acid molecule is a NA Group 1 nucleic acid molecule, and determining the interaction between the agent and the nucleic acid molecule, the expression product or fragment of the expression product as a determination of the disorder.

In one embodiment the agent is selected from the group consisting of (a) a nucleic acid molecule comprising NA Group 1 nucleic acid molecules or a fragment thereof, (b) a nucleic acid molecule comprising NA Group 3 nucleic acid molecules or a fragment thereof, (c) a nucleic acid molecule comprising NA Group 5 nucleic acid molecules or a fragment thereof, (d) an antibody that binds to an expression product, or a fragment thereof, of NA group 1 nucleic acids, (e) an antibody that binds to an expression product, or a fragment thereof, of NA group 3 nucleic acids, (f) an antibody that binds to an expression product, or a fragment thereof, of NA group 5 nucleic acids, (g) an agent that binds to a complex of an

MHC, preferably HLA, molecule and a fragment of an expression product of a NA Group 1 nucleic acid, (h) an agent that binds to a complex of an MHC, preferably HLA, molecule and a fragment of an expression product of a NA group 3 nucleic acid, and (i) an agent that binds to a complex of an MHC, preferably HLA, molecule and a fragment of an expression product of a NA Group 5 nucleic acid.

The disorder may be characterized by expression of a plurality of cancer associated antigen precursors. Thus the methods of diagnosis may include use of a plurality of agents, each of which is specific for a different human cancer associated antigen precursor (including at least one of the cancer associated antigen precursors disclosed herein), and wherein said plurality of agents is at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9 or at least 10 such agents. Any of the diagnostic methods disclosed herein can be applied sequentially over time to permit determination of the prognosis or progression (or regression) of the disorder.

In each of the above embodiments the agent may be specific for a human cancer associated antigen precursor, including the breast, gastric and prostate cancer associated antigen precursors disclosed herein.

In another aspect the invention is a method for determining regression, progression or onset of a condition characterized by expression of abnormal levels of a protein encoded by a nucleic acid molecule that is a NA Group 1 molecule. The method involves the steps of monitoring a sample, from a subject who has or is suspected of having the condition, for a parameter selected from the group consisting of (i) the protein, (ii) a peptide derived from the protein, (iii) an antibody which selectively binds the protein or peptide, and (iv) cytolytic T cells specific for a complex of the peptide derived from the protein and an MHC molecule, as a determination of regression, progression or onset of said condition. In one embodiment the sample is a body fluid, a body effusion or a tissue.

In another embodiment the step of monitoring comprises contacting the sample with a detectable agent selected from the group consisting of (a) an antibody which selectively binds the protein of (i), or the peptide of (ii), (b) a protein or peptide which binds the antibody of (iii), and (c) a cell which presents the complex of the peptide and MHC molecule of (iv). In a preferred embodiment the antibody, the protein, the peptide or the cell is labeled with a radioactive label or an enzyme. The sample in a preferred embodiment is assayed for the peptide. Preferably samples are isolated from tissue or bodily fluids of the subject at

sequential time points, and the samples are assayed as a determination of the regression, progression or onset of the condition from a first sequential time point to a second sequential time point.

According to another embodiment the nucleic acid molecule is one of the following: a
5 NA Group 3 molecule or a NA Group 5 molecule. In yet another embodiment the protein is a plurality of proteins, the parameter is a plurality of parameters, each of the plurality of parameters being specific for a different one of the plurality of proteins.

The invention in another aspect is a pharmaceutical preparation for a human subject. The pharmaceutical preparation includes an agent which when administered to the subject
10 enriches selectively the presence of complexes of an HLA molecule and a human cancer associated antigen, and a pharmaceutically acceptable carrier, wherein the human cancer associated antigen is a fragment of a human cancer associated antigen precursor encoded by a nucleic acid molecule which comprises a NA Group 1 molecule. In one embodiment the nucleic acid molecule is a NA Group 3 nucleic acid molecule.

15 The agent in one embodiment comprises a plurality of agents, each of which enriches selectively in the subject complexes of an HLA molecule and a different human cancer associated antigen. Preferably the plurality is at least two, at least three, at least four or at least 5 different such agents.

In another embodiment the agent is selected from the group consisting of (1) an
20 isolated polypeptide comprising the human cancer associated antigen, or a functional variant thereof, (2) an isolated nucleic acid operably linked to a promoter for expressing the isolated polypeptide, or functional variant thereof, (3) a host cell expressing the isolated polypeptide, or functional variant thereof, and (4) isolated complexes of the polypeptide, or functional variants thereof, and an HLA molecule.

25 The agent may be a cell expressing an isolated polypeptide. In one embodiment the agent is a cell expressing an isolated polypeptide comprising the human cancer associated antigen or a functional variant thereof. In another embodiment the agent is a cell expressing an isolated polypeptide comprising the human cancer associated antigen or a functional variant thereof, and wherein the cell expresses an HLA molecule that binds the polypeptide.
30 The cell can express one or both of the polypeptide and HLA molecule recombinantly. In preferred embodiments the cell is nonproliferative. In yet another embodiment the agent is at least two, at least three, at least four or at least five different polypeptides, each representing a

- 6 -

different human cancer associated antigen or functional variant thereof.

The agent in one embodiment is a PP Group 2 polypeptide. In other embodiments the agent is a PP Group 3 polypeptide or a PP Group 4 polypeptide.

In an embodiment each of the pharmaceutical preparations described herein also
5 includes an adjuvant.

According to another aspect the invention, a composition is provided which includes an isolated agent that binds selectively a PP Group 1 polypeptide. In separate embodiments the agent binds selectively to a polypeptide selected from the following: a PP Group 2 polypeptide, a PP Group 3 polypeptide, a PP Group 4 polypeptide, and a PP Group 5
10 polypeptide. In other embodiments, the agent is a plurality of different agents that bind selectively at least two, at least three, at least four, or at least five different such polypeptides. In each of the above described embodiments the agent may be an antibody.

In another aspect the invention is a composition of matter composed of a conjugate of the agent of the above-described compositions of the invention and a therapeutic or diagnostic
15 agent. Preferably the conjugate is of the agent and a therapeutic or diagnostic that is an antineoplastic.

The invention in another aspect is a pharmaceutical composition which includes an isolated nucleic acid molecule selected from the group consisting of: (1) NA Group 1 molecules, and (2) NA Group 2 molecules, and a pharmaceutically acceptable carrier. In one
20 embodiment the isolated nucleic acid molecule comprises a NA Group 3 or NA Group 4 molecule. In another embodiment the isolated nucleic acid molecule comprises at least two isolated nucleic acid molecules coding for two different polypeptides, each polypeptide comprising a different cancer associated antigen.

Preferably the pharmaceutical composition also includes an expression vector with a
25 promoter operably linked to the isolated nucleic acid molecule. In another embodiment the pharmaceutical composition also includes a host cell recombinantly expressing the isolated nucleic acid molecule.

According to another aspect of the invention a pharmaceutical composition is provided. The pharmaceutical composition includes an isolated polypeptide comprising a PP
30 Group 1 or a PP Group 2 polypeptide, and a pharmaceutically acceptable carrier. In one embodiment the isolated polypeptide comprises a PP Group 3 or a PP Group 4 polypeptide.

In another embodiment the isolated polypeptide comprises at least two different

polypeptides, each comprising a different cancer associated antigen at least one of which is encoded by a NA group 1 molecule as disclosed herein. In separate embodiments the isolated polypeptides are selected from the following: breast cancer polypeptides or HLA binding fragments thereof and gastric cancer polypeptides or HLA binding fragments thereof.

5 In an embodiment each of the pharmaceutical compositions described herein also includes an adjuvant.

Another aspect the invention is an isolated nucleic acid molecule comprising a NA Group 3 molecule. Another aspect the invention is an isolated nucleic acid molecule comprising a NA Group 4 molecule.

10 The invention in another aspect is an isolated nucleic acid molecule selected from the group consisting of (a) a fragment of a nucleic acid selected from the group of nucleic acid molecules consisting of SEQ ID Nos:1-593, of sufficient length to represent a sequence unique within the human genome, and identifying a nucleic acid encoding a human cancer associated antigen precursor, (b) complements of (a), provided that the fragment includes a
15 sequence of contiguous nucleotides which is not identical to any sequence selected from the sequence group consisting of (1) sequences having the GenBank accession numbers of Table 1 and other sequences publicly available as of the filing date of this application, (2) complements of (1), and (3) fragments of (1) and (2). Preferably the unique fragments are fragments of a nucleic acid selected from the group of nucleic acid molecules consisting of
20 SEQ ID NOs:12, 15, 34-59, 61, 62, 83-95, 186, 190-205, 297, 327-332, and 335-352.

In one embodiment the sequence of contiguous nucleotides is selected from the group consisting of: (1) at least two contiguous nucleotides nonidentical to the sequences in Table 1, (2) at least three contiguous nucleotides nonidentical to the sequences in Table 1, (3) at least four contiguous nucleotides nonidentical to the sequences in Table 1, (4) at least five
25 contiguous nucleotides nonidentical to the sequences in Table 1, (5) at least six contiguous nucleotides nonidentical to the sequences in Table 1, or (6) at least seven contiguous nucleotides nonidentical to the sequences in Table 1.

In another embodiment the fragment has a size selected from the group consisting of at least: 8 nucleotides, 10 nucleotides, 12 nucleotides, 14 nucleotides, 16 nucleotides, 18
30 nucleotides, 20, nucleotides, 22 nucleotides, 24 nucleotides, 26 nucleotides, 28 nucleotides, 30 nucleotides, 50 nucleotides, 75 nucleotides, 100 nucleotides, 200 nucleotides, 1000 nucleotides and every integer length therebetween.

In yet another embodiment the molecule encodes a polypeptide which, or a fragment of which, binds a human HLA receptor (e.g., class I or class II) or a human antibody.

Another aspect of the invention is an expression vector comprising an isolated nucleic acid molecule of the invention described above operably linked to a promoter.

5 According to one aspect the invention is an expression vector comprising a nucleic acid operably linked to a promoter, wherein the nucleic acid is a NA Group 1 or Group 2 molecule. In another aspect the invention is an expression vector comprising a NA Group 1 or Group 2 molecule and a nucleic acid encoding an MHC, preferably HLA, molecule.

10 In yet another aspect the invention is a host cell transformed or transfected with an expression vector of the invention described above.

In another aspect the invention is a host cell transformed or transfected with an expression vector comprising an isolated nucleic acid molecule of the invention described above operably linked to a promoter, or an expression vector comprising a nucleic acid operably linked to a promoter, wherein the nucleic acid is a NA Group 1 or 2 molecule and
15 further comprising a nucleic acid encoding HLA.

According to another aspect of the invention an isolated polypeptide encoded by the isolated nucleic acid molecules of the invention, described above, is provided. These include PP Group 1-5 polypeptides. The invention also includes a fragment of the polypeptide which is immunogenic. In one embodiment the fragment, or a portion of the fragment, binds HLA
20 or a human antibody.

The invention includes in another aspect an isolated fragment of a human cancer associated antigen precursor which, or a portion of which, binds HLA or a human antibody, wherein the precursor is encoded by a nucleic acid molecule that is a NA Group 1 molecule. In one embodiment the fragment is part of a complex with HLA. In another embodiment the
25 fragment is between 8 and 12 amino acids in length. In another embodiment the invention includes an isolated polypeptide comprising a fragment of the polypeptide of sufficient length to represent a sequence unique within the human genome and identifying a polypeptide that is a human cancer associated antigen precursor.

According to another aspect of the invention a kit for detecting the presence of the
30 expression of a cancer associated antigen precursor is provided. The kit includes a pair of isolated nucleic acid molecules each of which consists essentially of a molecule selected from the group consisting of (a) a 12-32 nucleotide contiguous segment of the nucleotide sequence

any of the NA Group 1 molecules and (b) complements of (a), wherein the contiguous segments are nonoverlapping. In one embodiment the pair of isolated nucleic acid molecules is constructed and arranged to selectively amplify an isolated nucleic acid molecule that is a NA Group 3 molecule. Preferably, the pair amplifies a human NA Group 3 molecule.

5 According to another aspect of the invention a method for treating a subject with a disorder characterized by expression of a human cancer associated antigen precursor is provided. The method includes the step of administering to the subject an amount of an agent, which enriches selectively in the subject the presence of complexes of an HLA molecule and a human cancer associated antigen, effective to ameliorate the disorder, wherein the human
10 cancer associated antigen is a fragment of a human cancer associated antigen precursor encoded by a nucleic acid molecule selected from the group consisting of (a) a nucleic acid molecule comprising NA group 1 nucleic acid molecules, (b) a nucleic acid molecule comprising NA group 3 nucleic acid molecules, (c) a nucleic acid molecule comprising NA group 5 nucleic acid molecules.

15 In one embodiment the disorder is characterized by expression of a plurality of human cancer associated antigen precursors and wherein the agent is a plurality of agents, each of which enriches selectively in the subject the presence of complexes of an HLA molecule and a different human cancer associated antigen. Preferably the plurality is at least 2, at least 3, at least 4, or at least 5 such agents.

20 In another embodiment the agent is an isolated polypeptide selected from the group consisting of PP Group 1, PP Group 2, PP Group 3, PP Group 4, and PP group 5 polypeptides.

In yet another embodiment the disorder is cancer.

According to another aspect the invention is a method for treating a subject having a condition characterized by expression of a cancer associated antigen precursor in cells of the
25 subject. The method includes the steps of (i) removing an immunoreactive cell containing sample from the subject, (ii) contacting the immunoreactive cell containing sample to the host cell under conditions favoring production of cytolytic T cells against a human cancer associated antigen which is a fragment of the precursor, (iii) introducing the cytolytic T cells to the subject in an amount effective to lyse cells which express the human cancer associated
30 antigen, wherein the host cell is transformed or transfected with an expression vector comprising an isolated nucleic acid molecule operably linked to a promoter, the isolated nucleic acid molecule being selected from the group of nucleic acid molecules consisting of

NA Group 1, NA Group 2, NA Group 3, NA Group 4, NA Group 5.

In one embodiment the host cell recombinantly expresses an HLA molecule which binds the human cancer associated antigen. In another embodiment the host cell endogenously expresses an HLA molecule which binds the human cancer associated antigen.

5 The invention includes in another aspect a method for treating a subject having a condition characterized by expression of a cancer associated antigen precursor in cells of the subject. The method includes the steps of (i) identifying a nucleic acid molecule expressed by the cells associated with said condition, wherein said nucleic acid molecule is a NA Group 1 molecule (ii) transfecting a host cell with a nucleic acid molecule selected from the group
10 consisting of (a) the nucleic acid molecule identified, (b) a fragment of the nucleic acid molecule identified which includes a segment coding for a cancer associated antigen, (c) deletions, substitutions or additions to (a) or (b), and (d) degenerates of (a), (b), or (c); (iii) culturing said transfected host cells to express the transfected nucleic acid molecule, and; (iv) introducing an amount of said host cells or an extract thereof to the subject effective to
15 increase an immune response against the cells of the subject associated with the condition. Preferably, the antigen is a human antigen and the subject is a human.

In one embodiment the method also includes the step of (a) identifying an MHC molecule which presents a portion of an expression product of the nucleic acid molecule, wherein the host cell expresses the same MHC molecule as identified in (a) and wherein the
20 host cell presents an MHC binding portion of the expression product of the nucleic acid molecule.

In another embodiment the method also includes the step of treating the host cells to render them non-proliferative.

In yet another embodiment the immune response comprises a B-cell response or a T
25 cell response. Preferably the response is a T-cell response which comprises generation of cytolytic T-cells specific for the host cells presenting the portion of the expression product of the nucleic acid molecule or cells of the subject expressing the human cancer associated antigen.

In another embodiment the nucleic acid molecule is a NA Group 3 molecule.

30 Another aspect of the invention is a method for treating or diagnosing or monitoring a subject having a condition characterized by expression of an abnormal amount of a protein encoded by a nucleic acid molecule that is a NA Group 1 molecule. The method includes the

step of administering to the subject an antibody which specifically binds to the protein or a peptide derived therefrom, the antibody being coupled to a therapeutically useful agent, in an amount effective to treat the condition.

In one embodiment the antibody is a monoclonal antibody. Preferably the monoclonal antibody is a chimeric antibody or a humanized antibody.

In another aspect the invention is a method for treating a condition characterized by expression in a subject of abnormal amounts of a protein encoded by a nucleic acid molecule that is a NA Group 1 nucleic acid molecule. The method involves the step of administering to a subject at least one of the pharmaceutical compositions of the invention described above in an amount effective to prevent, delay the onset of, or inhibit the condition in the subject. In one embodiment the condition is cancer. In another embodiment the method includes the step of first identifying that the subject expresses in a tissue abnormal amounts of the protein.

The invention in another aspect is a method for treating a subject having a condition characterized by expression of abnormal amounts of a protein encoded by a nucleic acid molecule that is a NA Group 1 nucleic acid molecule. The method includes the steps of (i) identifying cells from the subject which express abnormal amounts of the protein; (ii) isolating a sample of the cells; (iii) cultivating the cells, and (iv) introducing the cells to the subject in an amount effective to provoke an immune response against the cells.

In one embodiment the method includes the step of rendering the cells non-proliferative, prior to introducing them to the subject.

In another aspect the invention is a method for treating a pathological cell condition characterized by abnormal expression of a protein encoded by a nucleic acid molecule that is a NA Group 1 nucleic acid molecule. The method includes the step of administering to a subject in need thereof an effective amount of an agent which inhibits the expression or activity of the protein.

In one embodiment the agent is an inhibiting antibody which selectively binds to the protein and wherein the antibody is a monoclonal antibody, a chimeric antibody, a humanized antibody or a fragment thereof. In another embodiment the agent is an antisense nucleic acid molecule which selectively binds to the nucleic acid molecule which encodes the protein. In yet another important embodiment the nucleic acid molecule is a NA Group 3 nucleic acid molecule.

The invention includes in another aspect a composition of matter useful in stimulating

an immune response to a plurality of proteins encoded by nucleic acid molecules that are NA Group 1 molecules. The composition is a plurality of peptides derived from the amino acid sequences of the proteins, wherein the peptides bind to one or more MHC molecules presented on the surface of the cells which express an abnormal amount of the protein.

5 In one embodiment at least a portion of the plurality of peptides bind to MHC molecules and elicit a cytolytic response thereto. In another embodiment the composition of matter includes an adjuvant. In another embodiment the adjuvant is a saponin, GM-CSF, or an interleukin. In still another embodiment, the compositions also includes at least one peptide useful in stimulating an immune response to at least one protein which is not encoded
10 by nucleic acid molecules that are NA Group 1 molecules, wherein the at least one peptide binds to one or more MHC molecules.

According to another aspect the invention is an isolated antibody which selectively binds to a complex of: (i) a peptide derived from a protein encoded by a nucleic acid molecule that is a NA Group 1 molecule and (ii) and an MHC molecule to which binds the peptide to
15 form the complex, wherein the isolated antibody does not bind to (i) or (ii) alone.

In one embodiment the antibody is a monoclonal antibody, a chimeric antibody, a humanized antibody or a fragment thereof.

The invention also involves the use of the genes, gene products, fragments thereof, agents which bind thereto, and so on in the preparation of medicaments. A particular
20 medicament is for treating cancers including, e.g., one or more of cancers of the breast, cervix, ovary, prostate, testis, lung, colon, pancreas, stomach, liver, skin (e.g., melanoma), bladder, head and neck, thyroid, blood cells, bone and kidney. Diagnostics for specific cancers and groups of cancers also are envisioned.

In certain preferred embodimenst, the nucleic acid molecules are selected from the
25 group consisting of SEQ ID NOs:1-18, and the polypeptides are encoded by these preferred nucleic acid molecules.

Still other embodiments and aspects of the invention will become apparent in connection with the description of the invention which follows.

30

Detailed Description of the Inventi n

In the above summary and in the ensuing description, lists of sequences are provided. The lists are meant to embrace each single sequence separately, two or more sequences

together where they form a part of the same gene, any combination of two or more sequences which relate to different genes, including and up to the total number on the list, as if each and every combination were separately and specifically enumerated. Likewise, when mentioning fragment size, it is intended that a range embrace the smallest fragment mentioned to the full-length of the sequence (less one nucleotide or amino acid so that it is a fragment), each and every fragment length intended as if specifically enumerated. Thus, if a fragment could be between 10 and 15 in length, it is explicitly meant to mean 10, 11, 12, 13, 14, or 15 in length.

The summary and the claims mention antigen precursors and antigens. As used in the summary and in the claims, a precursor is substantially the full-length protein encoded by the coding region of the isolated DNA and the antigen is a peptide which complexes with MHC, preferably HLA, and which participates in the immune response as part of that complex. Such antigens are typically 9 amino acids long, although this may vary slightly.

As used herein, a subject is a human, non-human primate, cow, horse, pig, sheep, goat, dog, cat or rodent. In all embodiments human cancer antigens and human subjects are preferred.

The present invention in one aspect involves the cloning of cDNAs encoding human cancer associated antigen precursors using autologous antisera of subjects having breast, gastric or prostate cancer. The sequences of the clones representing genes identified according to the methods described herein are presented in the attached Sequence Listing. Of the foregoing, it can be seen that some of the clones are considered completely novel as no coding regions were found in the databases searched. Other clones are novel but have some nucleotide or amino acid homologies to sequences deposited in databases (mainly EST sequences). Nevertheless, the entire gene sequence was not previously known. In some cases no function was suspected and in other cases, even if a function was suspected, it was not known that the gene was associated with cancer, or with a particular cancer. In all cases, it was not known or suspected that the gene encoded a cancer antigen which reacted with an antibody from autologous sera. Analysis of the clone sequences by comparison to nucleic acid and protein databases determined that still other of the clones surprisingly are closely related to other previously-cloned genes. The sequences of these related genes is also presented in the Sequence Listing. The nature of the foregoing genes as encoding antigens recognized by the immune systems of cancer patients is, of course, unexpected.

The invention thus involves in one aspect cancer associated antigen polypeptides,

genes encoding those polypeptides, functional modifications and variants of the foregoing, useful fragments of the foregoing, as well as diagnostics and therapeutics relating thereto.

Homologs and alleles of the cancer associated antigen nucleic acids of the invention can be identified by conventional techniques. Thus, an aspect of the invention is those nucleic acid sequences which code for cancer associated antigen precursors. Because this application
5 contains so many sequences, the following chart is provided to identify the various groups of sequences discussed in the claims and in the summary:

Nucleic Acid Sequences

10 NA Group 1. (a) nucleic acid molecules which hybridize under stringent conditions to a molecule consisting of a nucleic acid sequence selected from the group consisting of nucleic acid sequences among SEQ ID NOs: 1-593, and which code for a cancer associated antigen precursor,

(b) deletions, additions and substitutions which code for a respective cancer
15 associated antigen precursor,

(c) nucleic acid molecules that differ from the nucleic acid molecules of (a) or (b) in codon sequence due to the degeneracy of the genetic code, and

(d) complements of (a), (b) or (c).

20 NA Group 2. Fragments of NA Group 1, which code for a polypeptide which, or a portion of which, binds an MHC molecule to form a complex recognized by an autologous antibody or lymphocyte.

NA Group 3. The subset of NA Group 1 where the nucleotide sequence is selected from the
25 group consisting of:

(a) previously unknown human nucleic acids coding for a human cancer associated antigen precursor, e.g., SEQ ID NOs: 12, 15, 34-59, 61, 62, 83-95, 186, 190-205, 297, 327-332, and 335-352,

(b) deletions, additions and substitutions which code for a respective human
30 cancer associated antigen precursor,

(c) nucleic acid molecules that differ from the nucleic acid molecules of (a) or (b) in codon sequence due to the degeneracy of the genetic code, and

(d) complements of (a), (b) or (c).

NA Group 4. Fragments of NA Group 3, which code for a polypeptide which, or a portion of which, binds to an MHC molecule to form a complex recognized by an autologous antibody or lymphocyte.

NA Group 5. A subset of NA Group 1, comprising human cancer associated antigens that react with allogeneic cancer antisera.

10

Polypeptide Sequences

PP Group 1. Polypeptides encoded by NA Group 1.

PP Group 2. Polypeptides encoded by NA Group 2.

PP Group 3. Polypeptides encoded by NA Group 3.

PP Group 4. Polypeptides encoded by NA Group 4.

15 PP Group 5. Polypeptides encoded by NA Group 5.

Particularly preferred polypeptides are those recognized by allogeneic sera of cancer patients, but not by non-cancer patient control sera. For example, as shown in the Examples below, polypeptides encoded by SEQ ID NOs:1-18 are recognized only by antibodies in cancer patients antisera.

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The term "stringent conditions" as used herein refers to parameters with which the art is familiar. Nucleic acid hybridization parameters may be found in references which compile such methods, e.g. *Molecular Cloning: A Laboratory Manual*, J. Sambrook, et al., eds., Second Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 1989, or *Current Protocols in Molecular Biology*, F.M. Ausubel, et al., eds., John Wiley & Sons, Inc., New York. More specifically, stringent conditions, as used herein, refers, for example, to hybridization at 65°C in hybridization buffer (3.5 x SSC, 0.02% Ficoll, 0.02% polyvinyl pyrrolidone, 0.02% Bovine Serum Albumin, 2.5 mM NaH₂PO₄(pH7), 0.5% SDS, 2 mM EDTA). SSC is 0.15 M sodium chloride/0.15 M sodium citrate, pH7; SDS is sodium dodecyl sulphate; and EDTA is ethylenediaminetetracetic acid. After hybridization, the membrane upon which the DNA is transferred is washed, for example, in 2 x SSC at room temperature and then at 0.1 - 0.5 x SSC/0.1 x SDS at temperatures up to 68°C.

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- 16 -

There are other conditions, reagents, and s
 similar degree of stringency. The skilled artisan w
 thus they are not given here. It will be understood.
 able to manipulate the conditions in a manner to
 5 and alleles of cancer associated antigen nucleic ac
 stringency conditions). The skilled artisan also is
 cells and libraries for expression of such molecu
 followed by isolation of the pertinent nucleic acid n

In general homologs and alleles typically v.
 10 and/or at least 90% amino acid identity to the seq
 acid and polypeptides, respectively, in some insta
 identity and/or at least 95% amino acid identity and
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 calculated using various, publicly available softwar
 15 Maryland) that can be obtained through the Intern
 tools include the BLAST system available at <http://www.ncbi.nlm.nih.gov/BLAST/>
 default settings. Pairwise and ClustalW alignment
 Kyle-Doolittle hydropathic analysis can be obtaine
 software (Oxford Molecular Group). Watson-Cric
 20 acids also are embraced by the invention.

In screening for cancer associated antigen c
 using the foregoing conditions, together with a rad
 membrane to which the DNA is finally transferred
 film to detect the radioactive signal. In screening
 25 antigen nucleic acids, Northern blot hybridizations
 performed on samples taken from breast, gastric
 suspected of having a condition characterized by ea
 genes disclosed herein. Amplification protocols su
 primers which hybridize to the sequences present
 30 cancer associated antigen genes or expression ther

The breast, gastric and prostate cancer assoc
 593. These sequences represent genes previously a

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SEQ ID Nos:1-
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- 17 -

unknown in humans (e.g., SEQ ID NOs:12, 15, 34-59, 61, 62, 83-95, 186, 190-205, 297, 327-332, and 335-352). Preferred breast, gastric and prostate cancer associated antigens for the methods of diagnosis disclosed herein are those which encode polypeptides that react with allogeneic cancer antisera (i.e. NA Group 5). Encoded polypeptides (e.g., proteins), peptides and antisera thereto are also preferred for diagnosis.

As used herein with respect to nucleic acids, the term "isolated" means: (i) amplified *in vitro* by, for example, polymerase chain reaction (PCR); (ii) recombinantly produced by cloning; (iii) purified, as by cleavage and gel separation; or (iv) synthesized by, for example, chemical synthesis. An isolated nucleic acid is one which is readily manipulable by recombinant DNA techniques well known in the art. Thus, a nucleotide sequence contained in a vector in which 5' and 3' restriction sites are known or for which polymerase chain reaction (PCR) primer sequences have been disclosed is considered isolated but a nucleic acid sequence existing in its native state in its natural host is not. An isolated nucleic acid may be substantially purified, but need not be. For example, a nucleic acid that is isolated within a cloning or expression vector is not pure in that it may comprise only a tiny percentage of the material in the cell in which it resides. Such a nucleic acid is isolated, however, as the term is used herein because it is readily manipulable by standard techniques known to those of ordinary skill in the art. An isolated nucleic acid as used herein is not a naturally occurring chromosome.

As used herein with respect to polypeptides, "isolated" means separated from its native environment and present in sufficient quantity to permit its identification or use. Isolated, when referring to a protein or polypeptide, means, for example: (i) selectively produced by expression cloning or (ii) purified as by chromatography or electrophoresis. Isolated proteins or polypeptides may be, but need not be, substantially pure. The term "substantially pure" means that the proteins or polypeptides are essentially free of other substances with which they may be found in nature or *in vivo* systems to an extent practical and appropriate for their intended use. Substantially pure polypeptides may be produced by techniques well known in the art. Because an isolated protein may be admixed with a pharmaceutically acceptable carrier in a pharmaceutical preparation, the protein may comprise only a small percentage by weight of the preparation. The protein is nonetheless isolated in that it has been separated from the substances with which it may be associated in living systems, i.e. isolated from other proteins.

The invention also includes degenerate nucleic acids which include alternative codons to those present in the native materials. For example, serine residues are encoded by the codons TCA, AGT, TCC, TCG, TCT and AGC. Each of the six codons is equivalent for the purposes of encoding a serine residue. Thus, it will be apparent to one of ordinary skill in the art that any of the serine-encoding nucleotide triplets may be employed to direct the protein synthesis apparatus, *in vitro* or *in vivo*, to incorporate a serine residue into an elongating cancer associated antigen polypeptide. Similarly, nucleotide sequence triplets which encode other amino acid residues include, but are not limited to: CCA, CCC, CCG and CCT (proline codons); CGA, CGC, CGG, CGT, AGA and AGG (arginine codons); ACA, ACC, ACG and ACT (threonine codons); AAC and AAT (asparagine codons); and ATA, ATC and ATT (isoleucine codons). Other amino acid residues may be encoded similarly by multiple nucleotide sequences. Thus, the invention embraces degenerate nucleic acids that differ from the biologically isolated nucleic acids in codon sequence due to the degeneracy of the genetic code.

The invention also provides modified nucleic acid molecules which include additions, substitutions and deletions of one or more nucleotides. In preferred embodiments, these modified nucleic acid molecules and/or the polypeptides they encode retain at least one activity or function of the unmodified nucleic acid molecule and/or the polypeptides, such as antigenicity, enzymatic activity, receptor binding, formation of complexes by binding of peptides by MHC class I and class II molecules, etc. In certain embodiments, the modified nucleic acid molecules encode modified polypeptides, preferably polypeptides having conservative amino acid substitutions as are described elsewhere herein. The modified nucleic acid molecules are structurally related to the unmodified nucleic acid molecules and in preferred embodiments are sufficiently structurally related to the unmodified nucleic acid molecules so that the modified and unmodified nucleic acid molecules hybridize under stringent conditions known to one of skill in the art.

For example, modified nucleic acid molecules which encode polypeptides having single amino acid changes can be prepared. Each of these nucleic acid molecules can have one, two or three nucleotide substitutions exclusive of nucleotide changes corresponding to the degeneracy of the genetic code as described herein. Likewise, modified nucleic acid molecules which encode polypeptides having two amino acid changes can be prepared which have, e.g., 2-6 nucleotide changes. Numerous modified nucleic acid molecules like these will

- 19 -

be readily envisioned by one of skill in the art, including for example, substitutions of nucleotides in codons encoding amino acids 2 and 3, 2 and 4, 2 and 5, 2 and 6, and so on. In the foregoing example, each combination of two amino acids is included in the set of modified nucleic acid molecules, as well as all nucleotide substitutions which code for the amino acid substitutions. Additional nucleic acid molecules that encode polypeptides having additional substitutions (i.e., 3 or more), additions or deletions (e.g., by introduction of a stop codon or a splice site(s)) also can be prepared and are embraced by the invention as readily envisioned by one of ordinary skill in the art. Any of the foregoing nucleic acids or polypeptides can be tested by routine experimentation for retention of structural relation or activity to the nucleic acids and/or polypeptides disclosed herein.

The invention also provides isolated unique fragments of cancer associated antigen nucleic acid sequences or complements thereof. A unique fragment is one that is a 'signature' for the larger nucleic acid. It, for example, is long enough to assure that its precise sequence is not found in molecules within the human genome outside of the cancer associated antigen nucleic acids defined above (and human alleles). Those of ordinary skill in the art may apply no more than routine procedures to determine if a fragment is unique within the human genome. Unique fragments, however, exclude fragments completely composed of the nucleotide sequences of any of the GenBank accession numbers listed in Table 1 or other previously published sequences as of the filing date of the priority documents for sequences listed in a respective priority document or the filing date of this application for sequences listed for the first time in this application which overlap the sequences of the invention.

A fragment which is completely composed of the sequence described in the foregoing GenBank deposits is one which does not include any of the nucleotides unique to the sequences of the invention. Thus, a unique fragment must contain a nucleotide sequence other than the exact sequence of those in GenBank or fragments thereof. The difference may be an addition, deletion or substitution with respect to the GenBank sequence or it may be a sequence wholly separate from the GenBank sequence.

Unique fragments can be used as probes in Southern and Northern blot assays to identify such nucleic acids, or can be used in amplification assays such as those employing PCR. As known to those skilled in the art, large probes such as 200, 250, 300 or more nucleotides are preferred for certain uses such as Southern and Northern blots, while smaller fragments will be preferred for uses such as PCR. Unique fragments also can be used to

- 20 -

produce fusion proteins for generating antibodies or determining binding of the polypeptide fragments, or for generating immunoassay components. Likewise, unique fragments can be employed to produce nonfused fragments of the cancer associated antigen polypeptides, useful, for example, in the preparation of antibodies, and in immunoassays. Unique fragments
5 further can be used as antisense molecules to inhibit the expression of cancer associated antigen nucleic acids and polypeptides, particularly for therapeutic purposes as described in greater detail below. Unique fragments also can be used to create chimeric nucleic acid molecule or polypeptide molecules by, for example, joining all or part of the unique fragment to another nucleic acid or polypeptide molecule (homologous or not). For example, the
10 unique fragment may be similar or identical in large part to a known molecule but may have a portion which is nonidentical to the known molecule; the known molecule and the unique fragment can be used to construct a molecule containing in large part the known molecule with the portion unique to the unique fragment added. Other chimeric molecules will be known to one of ordinary skill in the art and can be prepared using standard molecular biology
15 techniques.

As will be recognized by those skilled in the art, the size of the unique fragment will depend upon its conservancy in the genetic code. Thus, some regions of cancer associated antigen sequences and complements thereof will require longer segments to be unique while others will require only short segments, typically between 12 and 32 nucleotides (e.g. 12, 13,
20 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 and 32 or more bases long), up to the entire length of the disclosed sequence. As mentioned above, this disclosure intends to embrace each and every fragment of each sequence, beginning at the first nucleotide, the second nucleotide and so on, up to 8 nucleotides short of the end, and ending anywhere from nucleotide number 8, 9, 10 and so on for each sequence, up to the very last
25 nucleotide (provided the sequence is unique as described above).

Virtually any segment of the polypeptide coding region of novel cancer associated antigen nucleic acids, or complements thereof, that is 25 or more nucleotides in length will be unique. Those skilled in the art are well versed in methods for selecting such sequences, typically on the basis of the ability of the unique fragment to selectively distinguish the
30 sequence of interest from other sequences in the human genome of the fragment to those on known databases typically is all that is necessary, although *in vitro* confirmatory hybridization and sequencing analysis may be performed.

Especially preferred include nucleic acids encoding a series of epitopes, known as "polytopes". The epitopes can be arranged in sequential or overlapping fashion (*see, e.g., Thomson et al., Proc. Natl. Acad. Sci. USA 92:5845-5849, 1995; Gilbert et al., Nature Biotechnol. 15:1280-1284, 1997*), with or without the natural flanking sequences, and can be separated by unrelated linker sequences if desired. The polytope is processed to generate individual epitopes which are recognized by the immune system for generation of immune responses.

Thus, for example, peptides derived from a polypeptide having an amino acid sequence encoded by one of the nucleic acid disclosed herein, and which are presented by MHC molecules and recognized by CTL or T helper lymphocytes, can be combined with peptides from one or more other cancer associated antigens (e.g. by preparation of hybrid nucleic acids or polypeptides) to form "polytopes". The two or more peptides (or nucleic acids encoding the peptides) can be selected from those described herein, or they can include one or more peptides of previously known cancer associated antigens. Exemplary cancer associated peptide antigens that can be administered to induce or enhance an immune response are derived from tumor associated genes and encoded proteins including MAGE-A1, MAGE-A2, MAGE-A3, MAGE-A4, MAGE-A5, MAGE-A6, MAGE-A7, MAGE-A8, MAGE-A9, MAGE-A10, MAGE-A11, MAGE-A12, GAGE-1, GAGE-2, GAGE-3, GAGE-4, GAGE-5, GAGE-6, GAGE-7, GAGE-8, GAGE-9, BAGE-1, RAGE-1, LB33/MUM-1, PRAME, NAG, MAGE-B2, MAGE-B3, MAGE-B4, tyrosinase, brain glycogen phosphorylase, Melan-A, MAGE-C1, MAGE-C2, MAGE-C3, MAGE-C4, MAGE-C5, NY-ESO-1, LAGE-1, SSX-1, SSX-2 (HOM-MEL-40), SSX-4, SSX-5, SCP-1 and CT-7. See, for example, PCT application publication no. WO96/10577. Other examples will be known to one of ordinary skill in the art (for example, see Coulie, *Stem Cells* 13:393-403, 1995), and can be used in the invention in a like manner as those disclosed herein. One of ordinary skill in the art can prepare polypeptides comprising one or more peptides and one or more of the foregoing cancer associated peptides, or nucleic acids encoding such polypeptides, according to standard procedures of molecular biology.

Thus polytopes are groups of two or more potentially immunogenic or immune response stimulating peptides which can be joined together in various arrangements (e.g. concatenated, overlapping). The polytope (or nucleic acid encoding the polytope) can be administered in a standard immunization protocol, e.g. to animals, to test the effectiveness of

the polytope in stimulating, enhancing and/or provoking an immune response.

The peptides can be joined together directly or via the use of flanking sequences to form polytopes, and the use of polytopes as vaccines is well known in the art (see, e.g., Thomson et al., *Proc. Acad. Natl. Acad. Sci USA* 92(13):5845-5849, 1995; Gilbert et al.,
5 *Nature Biotechnol.* 15(12):1280-1284, 1997; Thomson et al., *J. Immunol.* 157(2):822-826, 1996; Tam et al., *J. Exp. Med.* 171(1):299-306, 1990). For example, Tam showed that polytopes consisting of both MHC class I and class II binding epitopes successfully generated antibody and protective immunity in a mouse model. Tam also demonstrated that polytopes comprising "strings" of epitopes are processed to yield individual epitopes which are
10 presented by MHC molecules and recognized by CTLs. Thus polytopes containing various numbers and combinations of epitopes can be prepared and tested for recognition by CTLs and for efficacy in increasing an immune response.

It is known that tumors express a set of tumor antigens, of which only certain subsets may be expressed in the tumor of any given patient. Polytopes can be prepared which
15 correspond to the different combination of epitopes representing the subset of tumor rejection antigens expressed in a particular patient. Polytopes also can be prepared to reflect a broader spectrum of tumor rejection antigens known to be expressed by a tumor type. Polytopes can be introduced to a patient in need of such treatment as polypeptide structures, or via the use of nucleic acid delivery systems known in the art (see, e.g., Allsopp et al., *Eur. J. Immunol.*
20 26(8):1951-1959, 1996). Adenovirus, pox virus, Ty-virus like particles, adeno-associated virus, plasmids, bacteria, etc. can be used in such delivery. One can test the polytope delivery systems in mouse models to determine efficacy of the delivery system. The systems also can be tested in human clinical trials.

In instances in which a human HLA class I molecule presents tumor rejection antigens
25 derived from cancer associated nucleic acids, the expression vector may also include a nucleic acid sequence coding for the HLA molecule that presents any particular tumor rejection antigen derived from these nucleic acids and polypeptides. Alternatively, the nucleic acid sequence coding for such a HLA molecule can be contained within a separate expression vector. In a situation where the vector contains both coding sequences, the single vector can
30 be used to transfect a cell which does not normally express either one. Where the coding sequences for a cancer associated antigen precursor and the HLA molecule which presents it are contained on separate expression vectors, the expression vectors can be cotransfected.

The cancer associated antigen precursor coding sequence may be used alone, when, e.g. the host cell already expresses a HLA molecule which presents a cancer associated antigen derived from precursor molecules. Of course, there is no limit on the particular host cell which can be used. As the vectors which contain the two coding sequences may be used in
5 any antigen-presenting cells if desired, and the gene for cancer associated antigen precursor can be used in host cells which do not express a HLA molecule which presents a cancer associated antigen. Further, cell-free transcription systems may be used in lieu of cells.

As mentioned above, the invention embraces antisense oligonucleotides that selectively bind to a nucleic acid molecule encoding a cancer associated antigen polypeptide,
10 to reduce the expression of cancer associated antigens. This is desirable in virtually any medical condition wherein a reduction of expression of cancer associated antigens is desirable, e.g., in the treatment of cancer. This is also useful for *in vitro* or *in vivo* testing of the effects of a reduction of expression of one or more cancer associated antigens.

As used herein, the term "antisense oligonucleotide" or "antisense" describes an
15 oligonucleotide that is an oligoribonucleotide, oligodeoxyribonucleotide, modified oligoribonucleotide, or modified oligodeoxyribonucleotide which hybridizes under physiological conditions to DNA comprising a particular gene or to an mRNA transcript of that gene and, thereby, inhibits the transcription of that gene and/or the translation of that mRNA. The antisense molecules are designed so as to interfere with transcription or
20 translation of a target gene upon hybridization with the target gene or transcript. Those skilled in the art will recognize that the exact length of the antisense oligonucleotide and its degree of complementarity with its target will depend upon the specific target selected, including the sequence of the target and the particular bases which comprise that sequence. It is preferred that the antisense oligonucleotide be constructed and arranged so as to bind selectively with
25 the target under physiological conditions, i.e., to hybridize substantially more to the target sequence than to any other sequence in the target cell under physiological conditions. Based upon the sequences of nucleic acids encoding breast, gastric or prostate cancer associated antigens, or upon allelic or homologous genomic and/or cDNA sequences, one of skill in the art can easily choose and synthesize any of a number of appropriate antisense molecules for
30 use in accordance with the present invention. For example, a "gene walk" comprising a series of oligonucleotides of 15-30 nucleotides spanning the length of a cancer associated antigen can be prepared, followed by testing for inhibition of cancer associated antigen expression.

Optionally, gaps of 5-10 nucleotides can be left between the ligonucleotides to reduce the number of ligonucleotides synthesized and tested.

In order to be sufficiently selective and potent for inhibition, such antisense oligonucleotides should comprise at least 10 and, more preferably, at least 15 consecutive bases which are complementary to the target, although in certain cases modified oligonucleotides as short as 7 bases in length have been used successfully as antisense oligonucleotides (Wagner et al., *Nature Biotechnol.* 14:840-844, 1996). Most preferably, the antisense oligonucleotides comprise a complementary sequence of 20-30 bases. Although oligonucleotides may be chosen which are antisense to any region of the gene or mRNA transcripts, in preferred embodiments the antisense oligonucleotides correspond to N-terminal or 5' upstream sites such as translation initiation, transcription initiation or promoter sites. In addition, 3'-untranslated regions may be targeted. Targeting to mRNA splicing sites has also been used in the art but may be less preferred if alternative mRNA splicing occurs. In addition, the antisense is targeted, preferably, to sites in which mRNA secondary structure is not expected (see, e.g., Sainio et al., *Cell Mol. Neurobiol.* 14(5):439-457, 1994) and at which proteins are not expected to bind. Finally, although the listed sequences are cDNA sequences, one of ordinary skill in the art may easily derive the genomic DNA corresponding to the cDNA of a cancer associated antigen. Thus, the present invention also provides for antisense oligonucleotides which are complementary to the genomic DNA corresponding to nucleic acids encoding cancer associated antigens. Similarly, antisense to allelic or homologous cDNAs and genomic DNAs are enabled without undue experimentation.

In one set of embodiments, the antisense oligonucleotides of the invention may be composed of "natural" deoxyribonucleotides, ribonucleotides, or any combination thereof. That is, the 5' end of one native nucleotide and the 3' end of another native nucleotide may be covalently linked, as in natural systems, via a phosphodiester internucleoside linkage. These oligonucleotides may be prepared by art recognized methods which may be carried out manually or by an automated synthesizer. They also may be produced recombinantly by vectors.

In preferred embodiments, however, the antisense oligonucleotides of the invention also may include "modified" oligonucleotides. That is, the oligonucleotides may be modified in a number of ways which do not prevent them from hybridizing to their target but which enhance their stability or targeting or which otherwise enhance their therapeutic effectiveness.

The term "modified oligonucleotide" as used herein describes an oligonucleotide in which (1) at least two of its nucleotides are covalently linked via a synthetic internucleoside linkage (i.e., a linkage other than a phosphodiester linkage between the 5' end of one
5 nucleotide and the 3' end of another nucleotide) and/or (2) a chemical group not normally associated with nucleic acids has been covalently attached to the oligonucleotide. Preferred synthetic internucleoside linkages are phosphorothioates, alkylphosphonates, phosphorodithioates, phosphate esters, alkylphosphonothioates, phosphoramidates, carbamates, carbonates, phosphate triesters, acetamides, carboxymethyl esters and peptides.

10 The term "modified oligonucleotide" also encompasses oligonucleotides with a covalently modified base and/or sugar. For example, modified oligonucleotides include oligonucleotides having backbone sugars which are covalently attached to low molecular weight organic groups other than a hydroxyl group at the 3' position and other than a phosphate group at the 5' position. Thus modified oligonucleotides may include a 2'-O-
15 alkylated ribose group. In addition, modified oligonucleotides may include sugars such as arabinose instead of ribose. The present invention, thus, contemplates pharmaceutical preparations containing modified antisense molecules that are complementary to and hybridizable with, under physiological conditions, nucleic acids encoding breast, gastric or prostate cancer associated antigen polypeptides, together with pharmaceutically acceptable
20 carriers.

Antisense oligonucleotides may be administered as part of a pharmaceutical composition. Such a pharmaceutical composition may include the antisense oligonucleotides in combination with any standard physiologically and/or pharmaceutically acceptable carriers which are known in the art. The compositions should be sterile and contain a therapeutically
25 effective amount of the antisense oligonucleotides in a unit of weight or volume suitable for administration to a patient. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredients. The term "physiologically acceptable" refers to a non-toxic material that is compatible with a biological system such as a cell, cell culture, tissue, or organism. The
30 characteristics of the carrier will depend on the route of administration. Physiologically and pharmaceutically acceptable carriers include diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials which are well known in the art, as further described below.

- 26 -

As used herein, a "vector" may be any of a number of nucleic acids into which a desired sequence may be inserted by restriction and ligation for transport between different genetic environments or for expression in a host cell. Vectors are typically composed of DNA although RNA vectors are also available. Vectors include, but are not limited to, plasmids, phagemids and virus genomes. A cloning vector is one which is able to replicate autonomously or integrated in the genome in a host cell, and which is further characterized by one or more endonuclease restriction sites at which the vector may be cut in a determinable fashion and into which a desired DNA sequence may be ligated such that the new recombinant vector retains its ability to replicate in the host cell. In the case of plasmids, replication of the desired sequence may occur many times as the plasmid increases in copy number within the host bacterium or just a single time per host before the host reproduces by mitosis. In the case of phage, replication may occur actively during a lytic phase or passively during a lysogenic phase. An expression vector is one into which a desired DNA sequence may be inserted by restriction and ligation such that it is operably joined to regulatory sequences and may be expressed as an RNA transcript. Vectors may further contain one or more marker sequences suitable for use in the identification of cells which have or have not been transformed or transfected with the vector. Markers include, for example, genes encoding proteins which increase or decrease either resistance or sensitivity to antibiotics or other compounds, genes which encode enzymes whose activities are detectable by standard assays known in the art (e.g., β -galactosidase, luciferase or alkaline phosphatase), and genes which visibly affect the phenotype of transformed or transfected cells, hosts, colonies or plaques (e.g., green fluorescent protein). Preferred vectors are those capable of autonomous replication and expression of the structural gene products present in the DNA segments to which they are operably joined.

As used herein, a coding sequence and regulatory sequences are said to be "operably" joined when they are covalently linked in such a way as to place the expression or transcription of the coding sequence under the influence or control of the regulatory sequences. If it is desired that the coding sequences be translated into a functional protein, two DNA sequences are said to be operably joined if induction of a promoter in the 5' regulatory sequences results in the transcription of the coding sequence and if the nature of the linkage between the two DNA sequences does not (1) result in the introduction of a frame-shift mutation, (2) interfere with the ability of the promoter region to direct the transcription

of the coding sequences, or (3) interfere with the ability of the corresponding RNA transcript to be translated into a protein. Thus, a promoter region would be operably joined to a coding sequence if the promoter region were capable of effecting transcription of that DNA sequence such that the resulting transcript might be translated into the desired protein or polypeptide.

5 The precise nature of the regulatory sequences needed for gene expression may vary between species or cell types, but shall in general include, as necessary, 5' non-transcribed and 5' non-translated sequences involved with the initiation of transcription and translation respectively, such as a TATA box, capping sequence, CAAT sequence, and the like. Especially, such 5' non-transcribed regulatory sequences will include a promoter region
10 which includes a promoter sequence for transcriptional control of the operably joined gene. Regulatory sequences may also include enhancer sequences or upstream activator sequences as desired. The vectors of the invention may optionally include 5' leader or signal sequences. The choice and design of an appropriate vector is within the ability and discretion of one of ordinary skill in the art.

15 Expression vectors containing all the necessary elements for expression are commercially available and known to those skilled in the art. See, e.g., Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor Laboratory Press, 1989. Cells are genetically engineered by the introduction into the cells of heterologous DNA (RNA) encoding a cancer associated antigen polypeptide or fragment or variant thereof.
20 That heterologous DNA (RNA) is placed under operable control of transcriptional elements to permit the expression of the heterologous DNA in the host cell.

Preferred systems for mRNA expression in mammalian cells are those such as pRc/CMV (available from Invitrogen, Carlsbad, CA) that contain a selectable marker such as a gene that confers G418 resistance (which facilitates the selection of stably transfected cell
25 lines) and the human cytomegalovirus (CMV) enhancer-promoter sequences. Additionally, suitable for expression in primate or canine cell lines is the pCEP4 vector (Invitrogen), which contains an Epstein Barr Virus (EBV) origin of replication, facilitating the maintenance of plasmid as a multicopy extrachromosomal element. Another expression vector is the pEF-BOS plasmid containing the promoter of polypeptide Elongation Factor 1 α , which stimulates
30 efficiently transcription *in vitro*. The plasmid is described by Mishizuma and Nagata (*Nuc. Acids Res.* 18:5322, 1990), and its use in transfection experiments is disclosed by, for example, Demoulin (*Mol. Cell. Biol.* 16:4710-4716, 1996). Still another preferred expression

- 28 -

vector is an adenovirus, described by Stratford-Perricaudet, which is defective for E1 and E3 proteins (*J. Clin. Invest.* 90:626-630, 1992). The use of the adenovirus as an Adeno.P1A recombinant for the expression of an antigen is disclosed by Warnier et al., in intradermal injection in mice for immunization against P1A (*Int. J. Cancer*, 67:303-310, 1996).

5 Additional vectors for delivery of nucleic acid are provided below.

The invention also embraces so-called expression kits, which allow the artisan to prepare a desired expression vector or vectors. Such expression kits include at least separate portions of a vector and one or more of the previously discussed cancer associated antigen nucleic acid molecules. Other components may be added, as desired, as long as the previously
10 mentioned nucleic acid molecules, which are required, are included. The invention also includes kits for amplification of a cancer associated antigen nucleic acid, including at least one pair of amplification primers which hybridize to a cancer associated antigen nucleic acid. The primers preferably are 12-32 nucleotides in length and are non-overlapping to prevent formation of "primer-dimers". One of the primers will hybridize to one strand of the cancer
15 associated antigen nucleic acid and the second primer will hybridize to the complementary strand of the cancer associated antigen nucleic acid, in an arrangement which permits amplification of the cancer associated antigen nucleic acid. Selection of appropriate primer pairs is standard in the art. For example, the selection can be made with assistance of a computer program designed for such a purpose, optionally followed by testing the primers for
20 amplification specificity and efficiency.

The invention also permits the construction of cancer associated antigen gene "knock-outs" and transgenic overexpression in cells and in animals, providing materials for studying certain aspects of cancer and immune system responses to cancer.

The invention also provides isolated polypeptides (including whole proteins and
25 partial proteins) encoded by the foregoing cancer associated antigen nucleic acids. Such polypeptides are useful, for example, alone or as fusion proteins to generate antibodies, as components of an immunoassay or diagnostic assay or as therapeutics. Cancer associated antigen polypeptides can be isolated from biological samples including tissue or cell homogenates, and can also be expressed recombinantly in a variety of prokaryotic and
30 eukaryotic expression systems by constructing an expression vector appropriate to the expression system, introducing the expression vector into the expression system, and isolating the recombinantly expressed protein. Short polypeptides, including antigenic peptides (such

as are presented by MHC molecules on the surface of a cell for immune recognition) also can be synthesized chemically using well-established methods of peptide synthesis.

A unique fragment of a cancer associated antigen polypeptide, in general, has the features and characteristics of unique fragments as discussed above in connection with nucleic acids. As will be recognized by those skilled in the art, the size of the unique fragment will depend upon factors such as whether the fragment constitutes a portion of a conserved protein domain. Thus, some regions of cancer associated antigens will require longer segments to be unique while others will require only short segments, typically between 5 and 12 amino acids (e.g. 5, 6, 7, 8, 9, 10, 11 or 12 or more amino acids including each integer up to the full length).

Unique fragments of a polypeptide preferably are those fragments which retain a distinct functional capability of the polypeptide. Functional capabilities which can be retained in a unique fragment of a polypeptide include interaction with antibodies, interaction with other polypeptides or fragments thereof, selective binding of nucleic acids or proteins, and enzymatic activity. One important activity is the ability to act as a signature for identifying the polypeptide. Another is the ability to complex with HLA and to provoke in a human an immune response. Those skilled in the art are well versed in methods for selecting unique amino acid sequences, typically on the basis of the ability of the unique fragment to selectively distinguish the sequence of interest from non-family members. A comparison of the sequence of the fragment to those on known databases typically is all that is necessary.

The invention embraces variants of the cancer associated antigen polypeptides described above. As used herein, a "variant" of a cancer associated antigen polypeptide is a polypeptide which contains one or more modifications to the primary amino acid sequence of a cancer associated antigen polypeptide. Modifications which create a cancer associated antigen variant can be made to a cancer associated antigen polypeptide 1) to reduce or eliminate an activity of a cancer associated antigen polypeptide; 2) to enhance a property of a cancer associated antigen polypeptide, such as protein stability in an expression system or the stability of protein-protein binding; 3) to provide a novel activity or property to a cancer associated antigen polypeptide, such as addition of an antigenic epitope or addition of a detectable moiety; or 4) to provide equivalent or better binding to an HLA molecule. Modifications to a cancer associated antigen polypeptide are typically made to the nucleic acid which encodes the cancer associated antigen polypeptide, and can include deletions, point

mutations, truncations, amino acid substitutions and additions of amino acids or non-amino acid moieties. Alternatively, modifications can be made directly to the polypeptide, such as by cleavage, addition of a linker molecule, addition of a detectable moiety, such as biotin, addition of a fatty acid, substitution of L-amino acids with D-amino acids, and the like.

5 Modifications also embrace fusion proteins comprising all or part of the cancer associated antigen amino acid sequence. One of skill in the art will be familiar with methods for predicting the effect on protein conformation of a change in protein sequence, and can thus "design" a variant cancer associated antigen polypeptide according to known methods. One example of such a method is described by Dahiyat and Mayo in *Science* 278:82-87, 1997, whereby proteins can be designed *de novo*. The method can be applied to a known protein to vary only a portion of the polypeptide sequence. By applying the computational methods of Dahiyat and Mayo, specific variants of a cancer associated antigen polypeptide can be proposed and tested to determine whether the variant retains a desired conformation. Other computational and computer modeling methods for designing polypeptide mimetics which retain activity of the polypeptides described herein, as well as selection methods such as phage display of peptide libraries are known in the art.

In general, variants include cancer associated antigen polypeptides which are modified specifically to alter a feature of the polypeptide unrelated to its desired physiological activity. For example, cysteine residues can be substituted or deleted to prevent unwanted disulfide linkages. Similarly, certain amino acids can be changed to enhance expression of a cancer associated antigen polypeptide by eliminating proteolysis by proteases in an expression system (e.g., dibasic amino acid residues in yeast expression systems in which KEX2 protease activity is present).

25 Mutations of a nucleic acid which encode a cancer associated antigen polypeptide preferably preserve the amino acid reading frame of the coding sequence, and preferably do not create regions in the nucleic acid which are likely to hybridize to form secondary structures, such as hairpins or loops, which can be deleterious to expression of the variant polypeptide.

30 Mutations can be made by selecting an amino acid substitution, or by random mutagenesis of a selected site in a nucleic acid which encodes the polypeptide. Variant polypeptides are then expressed and tested for one or more activities to determine which mutation provides a variant polypeptide with the desired properties. Further mutations can be

- 31 -

made to variants (or to non-variant cancer associated antigen polypeptides) which are silent as to the amino acid sequence of the polypeptide, but which provide preferred codons for translation in a particular host. The preferred codons for translation of a nucleic acid in, e.g., *E. coli*, are well known to those of ordinary skill in the art. Still other mutations can be made to the noncoding sequences of a cancer associated antigen gene or cDNA clone to enhance expression of the polypeptide. The activity of variants of cancer associated antigen polypeptides can be tested by cloning the gene encoding the variant cancer associated antigen polypeptide into a bacterial or mammalian expression vector, introducing the vector into an appropriate host cell, expressing the variant cancer associated antigen polypeptide, and testing for a functional capability of the cancer associated antigen polypeptides as disclosed herein. For example, the variant cancer associated antigen polypeptide can be tested for reaction with autologous or allogeneic sera as disclosed in the Examples. Preparation of other variant polypeptides may favor testing of other activities, as will be known to one of ordinary skill in the art.

The skilled artisan will also realize that conservative amino acid substitutions may be made in cancer associated antigen polypeptides to provide functionally equivalent variants of the foregoing polypeptides, i.e., the variants retain the functional capabilities of the cancer associated antigen polypeptides. As used herein, a "conservative amino acid substitution" refers to an amino acid substitution which does not alter the relative charge or size characteristics of the protein in which the amino acid substitution is made. Variants can be prepared according to methods for altering polypeptide sequence known to one of ordinary skill in the art such as are found in references which compile such methods, e.g. *Molecular Cloning: A Laboratory Manual*, J. Sambrook, et al., eds., Second Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 1989, or *Current Protocols in Molecular Biology*, F.M. Ausubel, et al., eds., John Wiley & Sons, Inc., New York. Exemplary functionally equivalent variants of the cancer associated antigen polypeptides include conservative amino acid substitutions of in the amino acid sequences of proteins disclosed herein. Conservative substitutions of amino acids include substitutions made amongst amino acids within the following groups: (a) M, I, L, V; (b) F, Y, W; (c) K, R, H; (d) A, G; (e) S, T; (f) Q, N; and (g) E, D.

For example, upon determining that a peptide derived from a cancer associated antigen polypeptide is presented by an MHC molecule and recognized by CTLs, one can make

conservative amino acid substitutions to the amino acid sequence of the peptide, particularly at residues which are thought not to be direct contact points with the MHC molecule. For example, methods for identifying functional variants of HLA class II binding peptides are provided in a published PCT application of Strominger and Wucherpfennig

- 5 (PCT/US96/03182). Peptides bearing one or more amino acid substitutions also can be tested for concordance with known HLA/MHC motifs prior to synthesis using, e.g. the computer program described by D'Amaro and Drijfhout (D'Amaro et al., *Human Immunol.* 43:13-18, 1995; Drijfhout et al., *Human Immunol.* 43:1-12, 1995). The substituted peptides can then be tested for binding to the MHC molecule and recognition by CTLs when bound to MHC.
- 10 These variants can be tested for improved stability and are useful, *inter alia*, in vaccine compositions.

- Conservative amino-acid substitutions in the amino acid sequence of cancer associated antigen polypeptides to produce functionally equivalent variants of cancer associated antigen polypeptides typically are made by alteration of a nucleic acid encoding a cancer associated
- 15 antigen polypeptide. Such substitutions can be made by a variety of methods known to one of ordinary skill in the art. For example, amino acid substitutions may be made by PCR-directed mutation, site-directed mutagenesis according to the method of Kunkel (Kunkel, *Proc. Nat. Acad. Sci. U.S.A.* 82: 488-492, 1985), or by chemical synthesis of a gene encoding a cancer associated antigen polypeptide. Where amino acid substitutions are made to a small unique
- 20 fragment of a cancer associated antigen polypeptide, such as an antigenic epitope recognized by autologous or allogeneic sera or cytolytic T lymphocytes, the substitutions can be made by directly synthesizing the peptide. The activity of functionally equivalent fragments of cancer associated antigen polypeptides can be tested by cloning the gene encoding the altered cancer associated antigen polypeptide into a bacterial or mammalian expression vector, introducing
- 25 the vector into an appropriate host cell, expressing the altered cancer associated antigen polypeptide, and testing for a functional capability of the cancer associated antigen polypeptides as disclosed herein. Peptides which are chemically synthesized can be tested directly for function, e.g., for binding to antisera recognizing associated antigens.

- The invention as described herein has a number of uses, some of which are described
- 30 elsewhere herein. First, the invention permits production and/or isolation of the cancer associated antigen protein molecules. A variety of methodologies well-known to the skilled practitioner can be utilized to obtain isolated cancer associated antigen molecules. The

polypeptide may be purified from cells which naturally produce the polypeptide by chromatographic means or immunological recognition. Alternatively, an expression vector may be introduced into cells to cause production of the polypeptide. In another method, mRNA transcripts may be microinjected or otherwise introduced into cells to cause
5 production of the encoded polypeptide. Translation of mRNA in cell-free extracts such as the reticulocyte lysate system also may be used to produce polypeptide. Those skilled in the art also can readily follow known methods for isolating cancer associated antigen polypeptides. These include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography and immune-affinity chromatography.

10 The isolation and identification of cancer associated antigen genes also makes it possible for the artisan to diagnose a disorder characterized by expression of cancer associated antigens. These methods involve determining expression of one or more cancer associated antigen nucleic acids, and/or encoded cancer associated antigen polypeptides and/or peptides derived therefrom. In the former situation, such determinations can be carried out via any
15 standard nucleic acid determination assay, including the polymerase chain reaction, or assaying with labeled hybridization probes. In the latter situation, such determinations can be carried out by screening patient antisera for recognition of the polypeptide.

The invention also makes it possible isolate proteins which bind to cancer associated antigens as disclosed herein, including antibodies and cellular binding partners of the cancer
20 associated antigens. Additional uses are described further herein.

The invention also provides, in certain embodiments, "dominant negative" polypeptides derived from cancer associated antigen polypeptides. A dominant negative polypeptide is an inactive variant of a protein, which, by interacting with the cellular machinery, displaces an active protein from its interaction with the cellular machinery or
25 competes with the active protein, thereby reducing the effect of the active protein. For example, a dominant negative receptor which binds a ligand but does not transmit a signal in response to binding of the ligand can reduce the biological effect of expression of the ligand. Likewise, a dominant negative catalytically-inactive kinase which interacts normally with target proteins but does not phosphorylate the target proteins can reduce phosphorylation of
30 the target proteins in response to a cellular signal. Similarly, a dominant negative transcription factor which binds to a promoter site in the control region of a gene but does not increase gene transcription can reduce the effect of a normal transcription factor by occupying

- 34 -

promoter binding sites without increasing transcription.

The end result of the expression of a dominant negative polypeptide in a cell is a reduction in function of active proteins. One of ordinary skill in the art can assess the potential for a dominant negative variant of a protein, and using standard mutagenesis techniques to create one or more dominant negative variant polypeptides. For example, given the teachings contained herein of breast, gastric and prostate cancer associated antigens, especially those which are similar to known proteins which have known activities, one of ordinary skill in the art can modify the sequence of the cancer associated antigens by site-specific mutagenesis, scanning mutagenesis, partial gene deletion or truncation, and the like.

See, e.g., U.S. Patent No. 5,580,723 and Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor Laboratory Press, 1989. The skilled artisan then can test the population of mutagenized polypeptides for diminution in a selected and/or for retention of such an activity. Other similar methods for creating and testing dominant negative variants of a protein will be apparent to one of ordinary skill in the art.

The invention also involves agents such as polypeptides which bind to cancer associated antigen polypeptides. Such binding agents can be used, for example, in screening assays to detect the presence or absence of cancer associated antigen polypeptides and complexes of cancer associated antigen polypeptides and their binding partners and in purification protocols to isolated cancer associated antigen polypeptides and complexes of cancer associated antigen polypeptides and their binding partners. Such agents also can be used to inhibit the native activity of the cancer associated antigen polypeptides, for example, by binding to such polypeptides.

The invention, therefore, embraces peptide binding agents which, for example, can be antibodies or fragments of antibodies having the ability to selectively bind to cancer associated antigen polypeptides. Antibodies include polyclonal and monoclonal antibodies, prepared according to conventional methodology.

Significantly, as is well-known in the art, only a small portion of an antibody molecule, the paratope, is involved in the binding of the antibody to its epitope (see, in general, Clark, W.R. (1986) The Experimental Foundations of Modern Immunology Wiley & Sons, Inc., New York; Ritt, I. (1991) Essential Immunology, 7th Ed., Blackwell Scientific Publications, Oxford). The pFc' and Fc regions, for example, are effectors of the complement cascade but are not involved in antigen binding. An antibody from which the pFc' region has

- 35 -

been enzymatically cleaved, r which has been produced without the pFc' region, designated an F(ab')₂ fragment, retains both of the antigen binding sites of an intact antibody. Similarly, an antibody from which the Fc region has been enzymatically cleaved, or which has been produced without the Fc region, designated an Fab fragment, retains one of the antigen
5 binding sites of an intact antibody molecule. Proceeding further, Fab fragments consist of a covalently bound antibody light chain and a portion of the antibody heavy chain denoted Fd. The Fd fragments are the major determinant of antibody specificity (a single Fd fragment may be associated with up to ten different light chains without altering antibody specificity) and Fd fragments retain epitope-binding ability in isolation.

10 Within the antigen-binding portion of an antibody, as is well-known in the art, there are complementarity determining regions (CDRs), which directly interact with the epitope of the antigen, and framework regions (FRs), which maintain the tertiary structure of the paratope (see, in general, Clark, 1986; Roitt, 1991). In both the heavy chain Fd fragment and the light chain of IgG immunoglobulins, there are four framework regions (FR1 through FR4)
15 separated respectively by three complementarity determining regions (CDR1 through CDR3). The CDRs, and in particular the CDR3 regions, and more particularly the heavy chain CDR3, are largely responsible for antibody specificity.

It is now well-established in the art that the non-CDR regions of a mammalian antibody may be replaced with similar regions of conspecific or heterospecific antibodies
20 while retaining the epitopic specificity of the original antibody. This is most clearly manifested in the development and use of "humanized" antibodies in which non-human CDRs are covalently joined to human FR and/or Fc/pFc' regions to produce a functional antibody. See, e.g., U.S. patents 4,816,567, 5,225,539, 5,585,089, 5,693,762 and 5,859,205.

Thus, for example, PCT International Publication Number WO 92/04381 teaches the
25 production and use of humanized murine RSV antibodies in which at least a portion of the murine FR regions have been replaced by FR regions of human origin. Such antibodies, including fragments of intact antibodies with antigen-binding ability, are often referred to as "chimeric" antibodies.

Thus, as will be apparent to one of ordinary skill in the art, the present invention also
30 provides f r F(ab')₂, Fab, Fv and Fd fragments; chimeric antibodies in which the Fc and/or FR and/or CDR1 and/or CDR2 and/or light chain CDR3 regions have been replaced by homologous human or non-human sequences; chimeric F(ab')₂ fragment antibodies in which

- 36 -

the FR and/or CDR1 and/or CDR2 and/or light chain CDR3 regions have been replaced by homologous human or non-human sequences; chimeric Fab fragment antibodies in which the FR and/or CDR1 and/or CDR2 and/or light chain CDR3 regions have been replaced by homologous human or non-human sequences; and chimeric Fd fragment antibodies in which the FR and/or CDR1 and/or CDR2 regions have been replaced by homologous human or non-human sequences. The present invention also includes so-called single chain antibodies.

Thus, the invention involves polypeptides of numerous size and type that bind specifically to cancer associated antigen polypeptides, and complexes of both cancer associated antigen polypeptides and their binding partners. These polypeptides may be derived also from sources other than antibody technology. For example, such polypeptide binding agents can be provided by degenerate peptide libraries which can be readily prepared in solution, in immobilized form or as phage display libraries. Combinatorial libraries also can be synthesized of peptides containing one or more amino acids. Libraries further can be synthesized of peptoids and non-peptide synthetic moieties.

Phage display can be particularly effective in identifying binding peptides useful according to the invention. Briefly, one prepares a phage library (using e.g. m13, fd, or lambda phage), displaying inserts from 4 to about 80 amino acid residues using conventional procedures. The inserts may represent, for example, a completely degenerate or biased array. One then can select phage-bearing inserts which bind to the cancer associated antigen polypeptide. This process can be repeated through several cycles of reselection of phage that bind to the cancer associated antigen polypeptide. Repeated rounds lead to enrichment of phage bearing particular sequences. DNA sequence analysis can be conducted to identify the sequences of the expressed polypeptides. The minimal linear portion of the sequence that binds to the cancer associated antigen polypeptide can be determined. One can repeat the procedure using a biased library containing inserts containing part or all of the minimal linear portion plus one or more additional degenerate residues upstream or downstream thereof. Yeast two-hybrid screening methods also may be used to identify polypeptides that bind to the cancer associated antigen polypeptides. Thus, the cancer associated antigen polypeptides of the invention, or a fragment thereof, can be used to screen peptide libraries, including phage display libraries, to identify and select peptide binding partners of the cancer associated antigen polypeptides of the invention. Such molecules can be used, as described, for screening assays, for purification protocols, for interfering directly with the functioning of

cancer associated antigen and for other purposes that will be apparent to those of ordinary skill in the art.

As detailed herein, the foregoing antibodies and other binding molecules may be used for example to identify tissues expressing protein or to purify protein. Antibodies also may be
5 coupled to specific diagnostic labeling agents for imaging of cells and tissues that express cancer associated antigens or to therapeutically useful agents according to standard coupling procedures. Diagnostic agents include, but are not limited to, barium sulfate, iocetamic acid, iopanoic acid, ipodate calcium, diatrizoate sodium, diatrizoate meglumine, metrizamide, tyropanoate sodium and radiodiagnostics including positron emitters such as fluorine-18 and
10 carbon-11, gamma emitters such as iodine-123, technetium-99m, iodine-131 and indium-111, and nuclides for nuclear magnetic resonance such as fluorine and gadolinium. Other diagnostic agents useful in the invention will be apparent to one of ordinary skill in the art. As used herein, "therapeutically useful agents" include any therapeutic molecule which desirably is targeted selectively to a cell expressing one of the cancer antigens disclosed
15 herein, including antineoplastic agents, radioiodinated compounds, toxins, other cytostatic or cytolytic drugs, and so forth. Antineoplastic therapeutics are well known and include: aminoglutethimide, azathioprine, bleomycin sulfate, busulfan, carmustine, chlorambucil, cisplatin, cyclophosphamide, cyclosporine, cytarabidine, dacarbazine, dactinomycin, daunorubicin, doxorubicin, taxol, etoposide, fluorouracil, interferon- α , lomustine,
20 mercaptopurine, methotrexate, mitotane, procarbazine HCl, thioguanine, vinblastine sulfate and vincristine sulfate. Additional antineoplastic agents include those disclosed in Chapter 52, Antineoplastic Agents (Paul Calabresi and Bruce A. Chabner), and the introduction thereto, 1202-1263, of Goodman and Gilman's "The Pharmacological Basis of Therapeutics", Eighth Edition, 1990, McGraw-Hill, Inc. (Health Professions Division). Toxins can be
25 proteins such as, for example, pokeweed anti-viral protein, cholera toxin, pertussis toxin, ricin, gelonin, abrin, diphtheria exotoxin, or *Pseudomonas* exotoxin. Toxin moieties can also be high energy-emitting radionuclides such as cobalt-60.

In the foregoing methods and compositions, antibodies prepared according to the invention also preferably are specific for the cancer associated antigen/MHC complexes
30 described herein.

When "disorder" is used herein, it refers to any pathological condition where the cancer associated antigens are expressed. An example of such a disorder is cancer, including

breast, gastric and prostate cancer as particular examples.

Samples of tissue and/or cells for use in the various methods described herein can be obtained through standard methods such as tissue biopsy, including punch biopsy and cell scraping, and collection of blood or other bodily fluids by aspiration or other methods.

5 In certain embodiments of the invention, an immunoreactive cell sample is removed from a subject. By "immunoreactive cell" is meant a cell which can mature into an immune cell (such as a B cell, a helper T cell, or a cytolytic T cell) upon appropriate stimulation. Thus immunoreactive cells include CD34⁺ hematopoietic stem cells, immature T cells and
10 immature B cells. When it is desired to produce cytolytic T cells which recognize a cancer associated antigen, the immunoreactive cell is contacted with a cell which expresses a cancer associated antigen under conditions favoring production, differentiation and/or selection of cytolytic T cells; the differentiation of the T cell precursor into a cytolytic T cell upon exposure to antigen is similar to clonal selection of the immune system.

Some therapeutic approaches based upon the disclosure are premised on a response by
15 a subject's immune system, leading to lysis of antigen presenting cells, such as breast, gastric or prostate cancer cells which present one or more cancer associated antigens. One such approach is the administration of autologous CTLs specific to a cancer associated antigen/MHC complex to a subject with abnormal cells of the phenotype at issue. It is within the ability of one of ordinary skill in the art to develop such CTLs *in vitro*. An example of a
20 method for T cell differentiation is presented in International Application number PCT/US96/05607. Generally, a sample of cells taken from a subject, such as blood cells, are contacted with a cell presenting the complex and capable of provoking CTLs to proliferate. The target cell can be a transfectant, such as a COS cell. These transfectants present the desired complex at their surface and, when combined with a CTL of interest, stimulate its
25 proliferation. COS cells are widely available, as are other suitable host cells. Specific production of CTL clones is well known in the art. The clonally expanded autologous CTLs then are administered to the subject.

CTL proliferation can be increased by increasing the level of tryptophan in T cell cultures, by inhibiting enzymes which catabolize tryptophan, such as indoleamine 2,3-
30 dioxygenase (IDO), or by adding tryptophan to the culture. Proliferation of T cells is enhanced by increasing the rate of proliferation and/or extending the number of divisions of the T cells in culture. In addition, increasing tryptophan in T cell cultures also enhances the

lytic activity of the T cells grown in culture.

Another method for selecting antigen-specific CTL clones has recently been described (Altman et al., *Science* 274:94-96, 1996; Dunbar et al., *Curr. Biol.* 8:413-416, 1998), in which fluorogenic tetramers of MHC class I molecule/peptide complexes are used to detect specific CTL clones. Briefly, soluble MHC class I molecules are folded *in vitro* in the presence of β_2 -microglobulin and a peptide antigen which binds the class I molecule. After purification, the MHC/peptide complex is purified and labeled with biotin. Tetramers are formed by mixing the biotinylated peptide-MHC complex with labeled avidin (e.g. phycoerythrin) at a molar ratio of 4:1. Tetramers are then contacted with a source of CTLs such as peripheral blood or lymph node. The tetramers bind CTLs which recognize the peptide antigen/MHC class I complex. Cells bound by the tetramers can be sorted by fluorescence activated cell sorting to isolate the reactive CTLs. The isolated CTLs then can be expanded *in vitro* for use as described herein.

To detail a therapeutic methodology, referred to as adoptive transfer (Greenberg, *J. Immunol.* 136(5): 1917, 1986; Riddell et al., *Science* 257: 238, 1992; Lynch et al, *Eur. J. Immunol.* 21: 1403-1410, 1991; Kast et al., *Cell* 59: 603-614, 1989), cells presenting the desired complex (e.g., dendritic cells) are combined with CTLs leading to proliferation of the CTLs specific thereto. The proliferated CTLs are then administered to a subject with a cellular abnormality which is characterized by certain of the abnormal cells presenting the particular complex. The CTLs then lyse the abnormal cells, thereby achieving the desired therapeutic goal.

The foregoing therapy assumes that at least some of the subject's abnormal cells present the relevant HLA/cancer associated antigen complex. This can be determined very easily, as the art is very familiar with methods for identifying cells which present a particular HLA molecule, as well as how to identify cells expressing DNA of the pertinent sequences, in this case a cancer associated antigen sequence. Once cells presenting the relevant complex are identified via the foregoing screening methodology, they can be combined with a sample from a patient, where the sample contains CTLs. If the complex presenting cells are lysed by the mixed CTL sample, then it can be assumed that a cancer associated antigen is being presented, and the subject is an appropriate candidate for the therapeutic approaches set forth *supra*.

Adoptive transfer is not the only form of therapy that is available in accordance with the invention. CTLs can also be provoked *in vivo*, using a number of approaches. One

- 40 -

approach is the use of non-proliferative cells expressing the complex. The cells used in this approach may be those that normally express the complex, such as irradiated tumor cells or cells transfected with one or both of the genes necessary for presentation of the complex (i.e. the antigenic peptide and the presenting HLA molecule). Chen et al. (*Proc. Natl. Acad. Sci. USA* 88: 110-114, 1991) exemplifies this approach, showing the use of transfected cells expressing HPV-E7 peptides in a therapeutic regime. Various cell types may be used. Similarly, vectors carrying one or both of the genes of interest may be used. Viral or bacterial vectors are especially preferred. For example, nucleic acids which encode a cancer associated antigen polypeptide or peptide may be operably linked to promoter and enhancer sequences which direct expression of the cancer associated antigen polypeptide or peptide in certain tissues or cell types. The nucleic acid may be incorporated into an expression vector. Expression vectors may be unmodified extrachromosomal nucleic acids, plasmids or viral genomes constructed or modified to enable insertion of exogenous nucleic acids, such as those encoding cancer associated antigens, as described elsewhere herein. Nucleic acids encoding one or more cancer associated antigens also may be inserted into a retroviral genome, thereby facilitating integration of the nucleic acid into the genome of the target tissue or cell type. In these systems, the gene of interest is carried by a microorganism, e.g., a *Vaccinia* virus, pox virus, herpes simplex virus, retrovirus or adenovirus, and the materials de facto "infect" host cells. The cells which result present the complex of interest, and are recognized by autologous CTLs, which then proliferate.

A similar effect can be achieved by combining the cancer associated antigen or a stimulatory fragment thereof with an adjuvant to facilitate incorporation into antigen presenting cells *in vivo*. The cancer associated antigen polypeptide is processed to yield the peptide partner of the HLA molecule while a cancer associated antigen peptide may be presented without the need for further processing. Generally, subjects can receive an intradermal injection of an effective amount of the cancer associated antigen. Initial doses can be followed by booster doses, following immunization protocols standard in the art. Preferred cancer associated antigens include those found to react with allogeneic cancer antisera, shown in the examples below.

The invention involves the use of various materials disclosed herein to "immunize" subjects or as "vaccines". As used herein, "immunization" or "vaccination" means increasing or activating an immune response against an antigen. It does not require elimination or

eradication of a condition but rather contemplates the clinically favorable enhancement of an immune response toward an antigen. Generally accepted animal models can be used for testing of immunization against cancer using a cancer associated antigen nucleic acid. For example, human cancer cells can be introduced into a mouse to create a tumor, and one or
5 more cancer associated antigen nucleic acids can be delivered by the methods described herein. The effect on the cancer cells (e.g., reduction of tumor size) can be assessed as a measure of the effectiveness of the cancer associated antigen nucleic acid immunization. Of course, testing of the foregoing animal model using more conventional methods for immunization can include the administration of one or more cancer associated antigen
10 polypeptides or peptides derived therefrom, optionally combined with one or more adjuvants and/or cytokines to boost the immune response. Methods for immunization, including formulation of a vaccine composition and selection of doses, route of administration and the schedule of administration (e.g. primary and one or more booster doses), are well known in the art. The tests also can be performed in humans, where the end point is to test for the
15 presence of enhanced levels of circulating CTLs against cells bearing the antigen, to test for levels of circulating antibodies against the antigen, to test for the presence of cells expressing the antigen and so forth.

As part of the immunization compositions, one or more cancer associated antigens or stimulatory fragments thereof are administered with one or more adjuvants to induce an
20 immune response or to increase an immune response. An adjuvant is a substance incorporated into or administered with antigen which potentiates the immune response. Adjuvants may enhance the immunological response by providing a reservoir of antigen (extracellularly or within macrophages), activating macrophages and stimulating specific sets of lymphocytes. Adjuvants of many kinds are well known in the art. Specific examples of adjuvants include
25 monophosphoryl lipid A (MPL, SmithKline Beecham), a congener obtained after purification and acid hydrolysis of *Salmonella minnesota* Re 595 lipopolysaccharide; saponins including QS21 (SmithKline Beecham), a pure QA-21 saponin purified from *Quillja saponaria* extract; DQS21, described in PCT application WO96/33739 (SmithKline Beecham); QS-7, QS-17, QS-18, and QS-L1 (So et al., *Mol. Cells* 7:178-186, 1997); incomplete Freund's adjuvant;
30 complete Freund's adjuvant; montanide; alum; CpG ligonucleotides (see e.g. Kreig et al., *Nature* 374:546-9, 1995); and various water-in-oil emulsions prepared from biodegradable oils such as squalene and/or tocopherol. Preferably, the peptides are administered mixed with

- 42 -

a combination of DQS21/MPL. The ratio of DQS21 to MPL typically will be about 1:10 to 10:1, preferably about 1:5 to 5:1 and more preferably about 1:1. Typically for human administration, DQS21 and MPL will be present in a vaccine formulation in the range of about 1 µg to about 100 µg. Other adjuvants are known in the art and can be used in the invention (see, e.g. Goding, *Monoclonal Antibodies: Principles and Practice*, 2nd Ed., 1986). Methods for the preparation of mixtures or emulsions of peptide and adjuvant are well known to those of skill in the art of vaccination.

Other agents which stimulate the immune response of the subject can also be administered to the subject. For example, other cytokines are also useful in vaccination protocols as a result of their lymphocyte regulatory properties. Many other cytokines useful for such purposes will be known to one of ordinary skill in the art, including interleukin-12 (IL-12) which has been shown to enhance the protective effects of vaccines (see, e.g., *Science* 268: 1432-1434, 1995), GM-CSF and IL-18. Thus cytokines can be administered in conjunction with antigens and adjuvants to increase the immune response to the antigens.

There are a number of immune response potentiating compounds that can be used in vaccination protocols. These include costimulatory molecules provided in either protein or nucleic acid form. Such costimulatory molecules include the B7-1 and B7-2 (CD80 and CD86 respectively) molecules which are expressed on dendritic cells (DC) and interact with the CD28 molecule expressed on the T cell. This interaction provides costimulation (signal 2) to an antigen/MHC/TCR stimulated (signal 1) T cell, increasing T cell proliferation and effector function. B7 also interacts with CTLA4 (CD152) on T cells and studies involving CTLA4 and B7 ligands indicate that the B7-CTLA4 interaction can enhance antitumor immunity and CTL proliferation (Zheng P., et al. *Proc. Natl. Acad. Sci. USA* 95 (11):6284-6289 (1998)).

B7 typically is not expressed on tumor cells so they are not efficient antigen presenting cells (APCs) for T cells. Induction of B7 expression would enable the tumor cells to stimulate more efficiently CTL proliferation and effector function. A combination of B7/IL-6/IL-12 costimulation has been shown to induce IFN-gamma and a Th1 cytokine profile in the T cell population leading to further enhanced T cell activity (Gajewski et al., *J. Immunol.* 154:5637-5648 (1995)). Tumor cell transfection with B7 has been discussed in relation to *in vitro* CTL expansion for adoptive transfer immunotherapy by Wang et al., (*J. Immunol.*, 19:1-8 (1986)). Other delivery mechanisms for the B7 molecule would include nucleic acid (naked DNA) immunization (Kim J., et al. *Nat Biotechnol.*, 15:7:641-646 (1997)) and recombinant viruses

such as adeno and pox (Wendtner et al., *Gene Ther.*, 4:7:726-735 (1997)). These systems are all amenable to the construction and use of expression cassettes for the coexpression of B7 with other molecules of choice such as the antigens or fragment(s) of antigens discussed herein (including polytopes) or cytokines. These delivery systems can be used for induction of the appropriate molecules *in vitro* and for *in vivo* vaccination situations. The use of anti-CD28 antibodies to directly stimulate T cells *in vitro* and *in vivo* could also be considered. Similarly, the inducible co-stimulatory molecule ICOS which induces T cell responses to foreign antigen could be modulated, for example, by use of anti-ICOS antibodies (Hutloff et al., *Nature* 397:263-266, 1999).

Lymphocyte function associated antigen-3 (LFA-3) is expressed on APCs and some tumor cells and interacts with CD2 expressed on T cells. This interaction induces T cell IL-2 and IFN-gamma production and can thus complement but not substitute, the B7/CD28 costimulatory interaction (Parra et al., *J. Immunol.*, 158:637-642 (1997), Fenton et al., *J. Immunother.*, 21:2:95-108 (1998)).

Lymphocyte function associated antigen-1 (LFA-1) is expressed on leukocytes and interacts with ICAM-1 expressed on APCs and some tumor cells. This interaction induces T cell IL-2 and IFN-gamma production and can thus complement but not substitute, the B7/CD28 costimulatory interaction (Fenton et al., *J. Immunother.*, 21:2:95-108 (1998)). LFA-1 is thus a further example of a costimulatory molecule that could be provided in a vaccination protocol in the various ways discussed above for B7.

Complete CTL activation and effector function requires Th cell help through the interaction between the Th cell CD40L (CD40 ligand) molecule and the CD40 molecule expressed by DCs (Ridge et al., *Nature*, 393:474 (1998), Bennett et al., *Nature*, 393:478 (1998), Schoenberger et al., *Nature*, 393:480 (1998)). This mechanism of this costimulatory signal is likely to involve upregulation of B7 and associated IL-6/IL-12 production by the DC (APC). The CD40-CD40L interaction thus complements the signal 1 (antigen/MHC-TCR) and signal 2 (B7-CD28) interactions.

The use of anti-CD40 antibodies to stimulate DC cells directly, would be expected to enhance a response to tumor antigens which are normally encountered outside of an inflammatory context or are presented by non-professional APCs (tumor cells). In these situations Th help and B7 costimulation signals are not provided. This mechanism might be used in the context of antigen pulsed DC based therapies or in situations where Th epitopes

have not been defined within known cancer antigen precursors.

A cancer associated antigen polypeptide, or a fragment thereof, also can be used to isolate their native binding partners. Isolation of such binding partners may be performed according to well-known methods. For example, isolated cancer associated antigen polypeptides can be attached to a substrate (e.g., chromatographic media, such as polystyrene beads, or a filter), and then a solution suspected of containing the binding partner may be applied to the substrate. If a binding partner which can interact with cancer associated antigen polypeptides is present in the solution, then it will bind to the substrate-bound cancer associated antigen polypeptide. The binding partner then may be isolated.

It will also be recognized that the invention embraces the use of the cancer associated antigen cDNA sequences in expression vectors, as well as to transfect host cells and cell lines, be these prokaryotic (e.g., *E. coli*), or eukaryotic (e.g., dendritic cells, B cells, CHO cells, COS cells, yeast expression systems and recombinant baculovirus expression in insect cells).

Especially useful are mammalian cells such as human, mouse, hamster, pig, goat, primate, etc.

They may be of a wide variety of tissue types, and include primary cells and cell lines. Specific examples include keratinocytes, peripheral blood leukocytes, bone marrow stem cells and embryonic stem cells. The expression vectors require that the pertinent sequence, i.e., those nucleic acids described *supra*, be operably linked to a promoter.

The invention also contemplates delivery of nucleic acids, polypeptides or peptides for vaccination. Delivery of polypeptides and peptides can be accomplished according to standard vaccination protocols which are well known in the art. In another embodiment, the delivery of nucleic acid is accomplished by *ex vivo* methods, i.e. by removing a cell from a subject, genetically engineering the cell to include a cancer associated antigen, and reintroducing the engineered cell into the subject. One example of such a procedure is outlined in U.S. Patent 5,399,346 and in exhibits submitted in the file history of that patent, all of which are publicly available documents. In general, it involves introduction *in vitro* of a functional copy of a gene into a cell(s) of a subject, and returning the genetically engineered cell(s) to the subject. The functional copy of the gene is under operable control of regulatory elements which permit expression of the gene in the genetically engineered cell(s). Numerous transfection and transduction techniques as well as appropriate expression vectors are well known to those of ordinary skill in the art, some of which are described in PCT application WO95/00654. *In vivo* nucleic acid delivery using vectors such as viruses and targeted

lip some also is contemplated according to the invention.

In preferred embodiments, a virus vector for delivering a nucleic acid encoding a cancer associated antigen is selected from the group consisting of adenoviruses, adeno-associated viruses, poxviruses including vaccinia viruses and attenuated poxviruses, Semliki Forest virus, Venezuelan equine encephalitis virus, retroviruses, Sindbis virus, and Ty virus-like particle. Examples of viruses and virus-like particles which have been used to deliver exogenous nucleic acids include: replication-defective adenoviruses (e.g., Xiang et al., *Virology* 219:220-227, 1996; Eloit et al., *J. Virol.* 71:5375-5381, 1997; Chengalvala et al., *Vaccine* 15:335-339, 1997), a modified retrovirus (Townsend et al., *J. Virol.* 71:3365-3374, 1997), a nonreplicating retrovirus (Irwin et al., *J. Virol.* 68:5036-5044, 1994), a replication defective Semliki Forest virus (Zhao et al., *Proc. Natl. Acad. Sci. USA* 92:3009-3013, 1995), canarypox virus and highly attenuated vaccinia virus derivative (Paoletti, *Proc. Natl. Acad. Sci. USA* 93:11349-11353, 1996), non-replicative vaccinia virus (Moss, *Proc. Natl. Acad. Sci. USA* 93:11341-11348, 1996), replicative vaccinia virus (Moss, *Dev. Biol. Stand.* 82:55-63, 1994), Venezuelan equine encephalitis virus (Davis et al., *J. Virol.* 70:3781-3787, 1996), Sindbis virus (Pugachev et al., *Virology* 212:587-594, 1995), and Ty virus-like particle (Allsopp et al., *Eur. J. Immunol* 26:1951-1959, 1996). In preferred embodiments, the virus vector is an adenovirus.

Another preferred virus for certain applications is the adeno-associated virus, a double-stranded DNA virus. The adeno-associated virus is capable of infecting a wide range of cell types and species and can be engineered to be replication-deficient. It further has advantages, such as heat and lipid solvent stability, high transduction frequencies in cells of diverse lineages, including hematopoietic cells, and lack of superinfection inhibition thus allowing multiple series of transductions. The adeno-associated virus can integrate into human cellular DNA in a site-specific manner, thereby minimizing the possibility of insertional mutagenesis and variability of inserted gene expression. In addition, wild-type adeno-associated virus infections have been followed in tissue culture for greater than 100 passages in the absence of selective pressure, implying that the adeno-associated virus genomic integration is a relatively stable event. The adeno-associated virus can also function in an extrachromosomal fashion.

In general, other preferred viral vectors are based on non-cytopathic eukaryotic viruses in which non-essential genes have been replaced with the gene of interest. Non-cytopathic

viruses include retroviruses, the life cycle of which involves reverse transcription of genomic viral RNA into DNA with subsequent proviral integration into host cellular DNA.

Adenoviruses and retroviruses have been approved for human gene therapy trials. In general, the retroviruses are replication-deficient (i.e., capable of directing synthesis of the desired
5 proteins, but incapable of manufacturing an infectious particle). Such genetically altered retroviral expression vectors have general utility for the high-efficiency transduction of genes *in vivo*. Standard protocols for producing replication-deficient retroviruses (including the steps of incorporation of exogenous genetic material into a plasmid, transfection of a packaging cell lined with plasmid, production of recombinant retroviruses by the packaging
10 cell line, collection of viral particles from tissue culture media, and infection of the target cells with viral particles) are provided in Kriegler, M., "Gene Transfer and Expression, A Laboratory Manual," W.H. Freeman Co., New York (1990) and Murry, E.J. Ed. "Methods in Molecular Biology," vol. 7, Humana Press, Inc., Clifton, New Jersey (1991).

Preferably the foregoing nucleic acid delivery vectors: (1) contain exogenous genetic
15 material that can be transcribed and translated in a mammalian cell and that can induce an immune response in a host, and (2) contain on a surface a ligand that selectively binds to a receptor on the surface of a target cell, such as a mammalian cell, and thereby gains entry to the target cell.

Various techniques may be employed for introducing nucleic acids of the invention
20 into cells, depending on whether the nucleic acids are introduced *in vitro* or *in vivo* in a host. Such techniques include transfection of nucleic acid-CaPO₄ precipitates, transfection of nucleic acids associated with DEAE, transfection or infection with the foregoing viruses including the nucleic acid of interest, liposome mediated transfection, and the like. For certain uses, it is preferred to target the nucleic acid to particular cells. In such instances, a
25 vehicle used for delivering a nucleic acid of the invention into a cell (e.g., a retrovirus, or other virus; a liposome) can have a targeting molecule attached thereto. For example, a molecule such as an antibody specific for a surface membrane protein on the target cell or a ligand for a receptor on the target cell can be bound to or incorporated within the nucleic acid delivery vehicle. Preferred antibodies include antibodies which selectively bind a cancer
30 associated antigen, alone or as a complex with a MHC molecule. Especially preferred are monoclonal antibodies. Where liposomes are employed to deliver the nucleic acids of the invention, proteins which bind to a surface membrane protein associated with endocytosis

- 47 -

may be incorporated into the liposome formulation for targeting and/or to facilitate uptake. Such proteins include capsid proteins or fragments thereof tropic for a particular cell type, antibodies for proteins which undergo internalization in cycling, proteins that target intracellular localization and enhance intracellular half life, and the like. Polymeric delivery systems also have been used successfully to deliver nucleic acids into cells, as is known by those skilled in the art. Such systems even permit oral delivery of nucleic acids.

The therapeutics of the invention can be administered by any conventional route, including injection or by gradual infusion over time. The administration may, for example, be oral, intravenous, intraperitoneal, intramuscular, intracavity, subcutaneous, or transdermal.

When cancer associated antigen peptides are used for vaccination, modes of administration which effectively deliver the cancer associated antigen and adjuvant, such that an immune response to the antigen is increased, can be used. For administration of a cancer associated antigen peptide in adjuvant, preferred methods include intradermal, intravenous, intramuscular and subcutaneous administration. Although these are preferred embodiments, the invention is not limited by the particular modes of administration disclosed herein.

Standard references in the art (e.g., *Remington's Pharmaceutical Sciences*, 18th edition, 1990) provide modes of administration and formulations for delivery of immunogens with adjuvant or in a non-adjuvant carrier. When antibodies are used therapeutically, a preferred route of administration is by pulmonary aerosol. Techniques for preparing aerosol delivery systems containing antibodies are well known to those of skill in the art. Generally, such systems should utilize components which will not significantly impair the biological properties of the antibodies, such as the paratope binding capacity (see, for example, Sciarra and Cutie, "Aerosols," in *Remington's Pharmaceutical Sciences*, 18th edition, 1990, pp 1694-1712; incorporated by reference). Those of skill in the art can readily determine the various parameters and conditions for producing antibody aerosols without resort to undue experimentation. When using antisense preparations of the invention, slow intravenous administration is preferred.

The compositions of the invention are administered in effective amounts. An "effective amount" is that amount of a cancer associated antigen composition that alone, or together with further doses, produces the desired response, e.g. increases an immune response to the cancer associated antigen. In the case of treating a particular disease or condition characterized by expression of one or more cancer associated antigens, such as breast, gastric

or prostate cancers, the desired response is inhibiting the progression of the disease. This may involve only slowing the progression of the disease temporarily, although more preferably, it involves halting the progression of the disease permanently. This can be monitored by routine methods or can be monitored according to diagnostic methods of the invention discussed
5 herein. The desired response to treatment of the disease or condition also can be delaying the onset or even preventing the onset of the disease or condition.

Such amounts will depend, of course, on the particular condition being treated, the severity of the condition, the individual patient parameters including age, physical condition, size and weight, the duration of the treatment, the nature of concurrent therapy (if any), the
10 specific route of administration and like factors within the knowledge and expertise of the health practitioner. These factors are well known to those of ordinary skill in the art and can be addressed with no more than routine experimentation. It is generally preferred that a maximum dose of the individual components or combinations thereof be used, that is, the highest safe dose according to sound medical judgment. It will be understood by those of
15 ordinary skill in the art, however, that a patient may insist upon a lower dose or tolerable dose for medical reasons, psychological reasons or for virtually any other reasons.

The pharmaceutical compositions used in the foregoing methods preferably are sterile and contain an effective amount of cancer associated antigen or nucleic acid encoding cancer associated antigen for producing the desired response in a unit of weight or volume suitable
20 for administration to a patient. The response can, for example, be measured by determining the immune response following administration of the cancer associated antigen composition via a reporter system by measuring downstream effects such as gene expression, or by measuring the physiological effects of the cancer associated antigen composition, such as regression of a tumor or decrease of disease symptoms. Other assays will be known to one of
25 ordinary skill in the art and can be employed for measuring the level of the response.

The doses of cancer associated antigen compositions (e.g., polypeptide, peptide, antibody, cell or nucleic acid) administered to a subject can be chosen in accordance with different parameters, in particular in accordance with the mode of administration used and the state of the subject. Other factors include the desired period of treatment. In the event that a
30 response in a subject is insufficient at the initial doses applied, higher doses (or effectively higher doses by a different, more localized delivery route) may be employed to the extent that patient tolerance permits.

In general, for treatments for eliciting or increasing an immune response, doses of cancer associated antigen are formulated and administered in doses between 1 ng and 1 mg, and preferably between 10 ng and 100 μ g, according to any standard procedure in the art. Where nucleic acids encoding cancer associated antigen or variants thereof are employed, 5 doses of between 1 ng and 0.1 mg generally will be formulated and administered according to standard procedures. Other protocols for the administration of cancer associated antigen compositions will be known to one of ordinary skill in the art, in which the dose amount, schedule of injections, sites of injections, mode of administration (e.g., intra-tumoral) and the like vary from the foregoing. Administration of cancer associated antigen compositions to 10 mammals other than humans, e.g. for testing purposes or veterinary therapeutic purposes, is carried out under substantially the same conditions as described above.

When administered, the pharmaceutical compositions of the invention are applied in pharmaceutically-acceptable amounts and in pharmaceutically-acceptable preparations. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with 15 the effectiveness of the biological activity of the active ingredients. Such preparations may routinely contain salts, buffering agents, preservatives, compatible carriers, and optionally other therapeutic agents. When used in medicine, the salts should be pharmaceutically acceptable, but non-pharmaceutically acceptable salts may conveniently be used to prepare pharmaceutically-acceptable salts thereof and are not excluded from the scope of the 20 invention. Such pharmacologically and pharmaceutically-acceptable salts include, but are not limited to, those prepared from the following acids: hydrochloric, hydrobromic, sulfuric, nitric, phosphoric, maleic, acetic, salicylic, citric, formic, malonic, succinic, and the like. Also, pharmaceutically-acceptable salts can be prepared as alkaline metal or alkaline earth salts, such as sodium, potassium or calcium salts.

25 A cancer associated antigen composition may be combined, if desired, with a pharmaceutically-acceptable carrier. The term "pharmaceutically-acceptable carrier" as used herein means one or more compatible solid or liquid fillers, diluents or encapsulating substances which are suitable for administration into a human. The term "carrier" denotes an organic or inorganic ingredient, natural or synthetic, with which the active ingredient is 30 combined to facilitate the application. The components of the pharmaceutical compositions also are capable of being co-mingled with the molecules of the present invention, and with each other, in a manner such that there is no interaction which would substantially impair the

desired pharmaceutical efficacy.

The pharmaceutical compositions may contain suitable buffering agents, including: acetic acid in a salt; citric acid in a salt; boric acid in a salt; and phosphoric acid in a salt.

The pharmaceutical compositions also may contain, optionally, suitable preservatives,
5 such as: benzalkonium chloride; chlorobutanol; parabens and thimerosal.

The pharmaceutical compositions may conveniently be presented in unit dosage form and may be prepared by any of the methods well-known in the art of pharmacy. All methods include the step of bringing the active agent into association with a carrier which constitutes one or more accessory ingredients. In general, the compositions are prepared by uniformly
10 and intimately bringing the active compound into association with a liquid carrier, a finely divided solid carrier, or both, and then, if necessary, shaping the product.

Compositions suitable for oral administration may be presented as discrete units, such as capsules, tablets, lozenges, each containing a predetermined amount of the active compound. Other compositions include suspensions in aqueous liquids or non-aqueous
15 liquids such as a syrup, elixir or an emulsion.

Compositions suitable for parenteral administration conveniently comprise a sterile aqueous or non-aqueous preparation of cancer associated antigen polypeptides or nucleic acids, which is preferably isotonic with the blood of the recipient. This preparation may be formulated according to known methods using suitable dispersing or wetting agents and
20 suspending agents. The sterile injectable preparation also may be a sterile injectable solution or suspension in a non-toxic parenterally-acceptable diluent or solvent, for example, as a solution in 1,3-butane diol. Among the acceptable vehicles and solvents that may be employed are water, Ringer's solution, and isotonic sodium chloride solution. In addition, sterile, fixed oils are conventionally employed as a solvent or suspending medium. For this
25 purpose any bland fixed oil may be employed including synthetic mono- or di-glycerides. In addition, fatty acids such as oleic acid may be used in the preparation of injectables. Carrier formulation suitable for oral, subcutaneous, intravenous, intramuscular, etc. administrations can be found in *Remington's Pharmaceutical Sciences*, Mack Publishing Co., Easton, PA.

30

Examples

Example 1: SEREX screening of breast, gastric and prostate cancer cells

Breast, gastric and prostate cancer cDNA libraries were established, using standard

techniques, and the libraries were screened, using the SEREX methodology described by Sahin et al., *Proc. Natl. Acad. Sci. USA* 92: 11810 (1995), and by Chen et al., *Proc. Natl. Acad. Sci. USA* 94: 1914 (1997), each of which is incorporated by reference in its entirety.

To be specific, total RNA was isolated by homogenizing tumor samples in 4M
5 guanidinium thiocyanate/0.5% sodium N-lauryl sarcosine/25 mM EDTA followed by
centrifugation in 5.7 M CsCl/25 mM sodium acetate/10 μ M EDTA at 32,000 rpm. Total
mRNA was removed by passing the sample over an oligo-dT cellulose column. The cDNA
libraries were then constructed by taking 5 μ g of mRNA, using standard methodologies to
reverse transcribe the material. Breast cancer libraries were prepared from two different
10 breast cancer patients, referred to as "MT" and "MK". Gastric cancer libraries were prepared
from a gastric cancer patient, referred to as "YS".

The cDNA was used to construct a lambda phage library, and 500 phages were plated
onto XL1-Blue MRF *E. coli*, and incubated for eight hours at 37°C. A nitrocellulose
membrane was then placed on the plate, followed by overnight incubation. The membrane
15 was then washed, four times, with Tris buffered saline (TBS) which contained 0.05% Tween,
and was then immersed in TBS containing 5% non-fat dried milk. After one hour, the
membrane was incubated with conjugates of peroxidase-goat anti human IgG specific for Fc
portions of human antibodies (1:2000, diluted in TBS with 1% BSA). The incubation was
carried out for one hour, at room temperature, and the membrane was then washed three times
20 with TBS. Those clones which produced antibodies were visualized with 0.06%
3,3'-diaminobenzidine tetrachloride and 0.015% H₂O₂, in 50 mM Tris (pH 7.5). Any clones
which produced immunoglobulin were marked, and then the membrane was washed, two
further times, with TBS that contained 0.05% Tween, and then twice with "neat" TBS.

The membranes were then incubated in 1:100 diluted patient serum, overnight, at 4°C.
25 The patient serum had been pretreated. Specifically, 5 ml samples were diluted to 10 ml with
TBS containing 1% bovine serum albumin, and 0.02% Na₃N. The serum had been treated to
remove antibodies to bacteriophage, by passing it through a 5 ml Sepharose column, to which
a lysate of *E. coli* Y1090 had been attached, followed by passage over a second column which
had *E. coli* lysate and lysate of *E. coli* infected with lambda bacteriophage. The screening was
30 carried out five times. The samples were then diluted to 50 ml, and kept at -80°C, until used
as described herein.

Following the overnight incubation with the membrane, the membrane was washed

twice with TBS/0.05% Tween 20, and then once with TBS. A further incubation was carried out, using the protocols discussed supra, for the peroxidase labeled antibodies.

The positive clones were then sequenced, using standard techniques. Following comparison of the sequences to information available in data banks, clones were resolved into
5 known and unknown genes. Some clones corresponded to previously identified human proteins and nucleotide sequences, and other clones have not been identified in humans previously, although there were related molecules found in other species. Still other clones represent molecules for which no related sequences were found (most clones contained very short sections (e.g. 25 or fewer nucleotides) that corresponded to portions of unrelated
10 sequences). Some GenBank accession numbers representative of sequences having homology to the cancer associated antigen nucleotide sequences of the invention are presented in Table 1. All of the homologous sequences are accessible in publicly-available databases by reference to the sequences' accession numbers provided in Table 1.

15 Breast cancer clones:

The nucleotide sequences of clones derived from breast cancer patients "MT" and "MK" are presented as SEQ ID NOs:1-205. Polypeptides encoded by open reading frames of the nucleic acid clones are presented as SEQ ID Nos: 594-829; the correspondence between nucleic acid molecules and encoded polypeptides is shown in Table 2.

20

Gastric cancer clones:

The nucleotide sequences of clones derived from gastric cancer patient "YS" are presented as SEQ ID NOs:206-352 (clones beginning with "YS"). Polypeptides encoded by open reading frames of the YS nucleic acid clones are presented as SEQ ID Nos:830-1083;
25 the correspondence between nucleic acid molecules and encoded polypeptides is shown in Table 2.

Prostate cancer clones

The nucleotide sequences of clones derived from prostate cancer patient "ZH" are
30 presented as SEQ ID NOs:353-593(clones beginning with "ZH"). Polypeptides encoded by open reading frames of the ZH nucleic acid clones are presented as SEQ ID Nos:1084-1332; the correspondence between nucleic acid molecules and encoded polypeptides is shown in

Table 2.

Table 1: Sequence homologies (GenBank Accession Numbers)

5	SEQ ID NO. 1
	NGO-Br-38 combined
	NM_006644.1, AF039695.1, AB003334.1, AB003333.1, D86956.1, D67017.1, D67016.1, Z47807.1, NM_013559.1, L40406.1, AB005282.1, AB005281.1, AB005280.1, AB023420.1, X67643.1, NM_008300.1, D85904.1, AC011661.5, AE003611.1, AL109620.4, AC007049.8, AC005992.15, AC007066.4, AC006080.1, AC009155.3, AF222716.1, AC009223.2, AC004251.1, AC002367.1, AL161553.2, AL161539.2, AL117202.1, AL009183.10, Z97336.1, AB006696.1, AI658961.1, AW571648.1, AW474070.1, AA843693.1, AW608075.1, AW470142.1, AW572452.1, AA543054.1, AW385582.1, AI742981.1, AW612980.1, AW612983.1, AI582881.1, AI751853.1, AI378269.1, AI920808.1, AI654608.1, AI819251.1, AI831339.1, AI753470.1, AI312753.1, AI803588.1, AI563996.1, AA232636.1, AW015796.1, AW117974.1, AI668853.1, AA535277.1, AA993280.1, AA632202.1, AA912023.1, AW627645.1, AW027050.1, AI337175.1, AI123280.1, AA761750.1, AW316651.1, AI223412.1, AW771160.1, AA219263.1, AW068948.1, AA482770.1, AA166716.1, AW236067.1, AA166806.1, AA485151.1, AI369932.1, AI250881.1, AA933881.1, AI262020.1, AI751852.1, AI050716.1, H52653.1, AI651186.1, AA678506.1, AA582157.1, AW628153.1, AI493255.1, AW340810.1, AI223825.1, AW837156.1, AA136424.1, AA953645.1, AI582484.1, AI673134.1, AW820299.1, AA394027.1, T58153.1, T36072.1, AW390368.1, F22410.1, AA417317.1, AW020035.1, AA278231.1, AI361237.1, AI288972.1, AA810686.1, AW103624.1, AW604836.1, AA730742.1, AA082043.1, Z20100.1, D58216.1, AI799265.1, D29622.1, AA435594.1, AA233888.1, AA485036.1, AI612928.1, AI630481.1, F07487.1, AA731716.1, AA417255.1, AA804371.1, AA571359.1, AA465183.1, F08794.1, T34783.1, Z41841.1, F03714.1, AL137142.8, AC012569.3, AP001563.1, AC022671.2, AC020999.4, AC011743.3, AP000635.1, AP000610.2, AC008070.3, AC022797.3, AC005506.6, AL096782.3,
25	SEQ ID NO. 2
	NGO-Br-39
	MK262/T3 5'
	AF039695.1, AB003334.1, D86956.1, NM_006644.1, AB003333.1, NM_013559.1, D67016.1, L40406.1, Z47807.1, D67017.1, AB005277.1, AB005278.1, NM_011020.1, U23921.1, D49482.1, AB001926.1, NM_014278.1, AB023421.1, L12723.1, AB005279.1, X67643.1, AB005280.1, AF077354.1, NM_008300.1, AB023420.1, D85904.1, AB005281.1, AC024830.1, L08605.1, AC011294.3, AC009424.2, AC022520.2, NM_013393.1, AC019018.7, AF093415.1, AF161311.1, AF136711.1, AE001434.1, AE001433.1, Z49769.1, AC024813.1, AE003645.1, AC011609.9, AC004150.8, AC004801.1, AL163244.2, AP001699.1, AP001605.1, L16771.1, AW820299.1, AW859988.1, AW859943.1, AW604836.1, AW820234.1, AW206874.1, AI094015.1, AA885873.1, AW820232.1, AI702970.1, AW390368.1, AA777564.1, AA580595.1, H91160.1, AA777031.1, AW608075.1, H54657.1, H64019.1, AI658961.1, H63551.1, AA811573.1, AW628153.1, AA749004.1, AI800379.1, W45471.1, AI751852.1, AW385582.1, AI290252.1, AW389335.1, AA953645.1, AW238563.1, AA805016.1, F08794.1, F07487.1, AW631423.1, T63090.1, N84915.1, AW630933.1, AW474070.1, AA166806.1, N84914.1, AI758907.1, AW103624.1, AW571648.1, AA394027.1, AI002886.1, AA094644.1, AW391561.1, AW362751.1, H63595.1, AW609781.1, H54656.1, AW572452.1, W86085.1, AW577563.1, AW820231.1, AW362766.1, AA555929.1, AA555921.1, AA485036.1, AW820224.1, AW391572.1, H91211.1, AW316651.1, AI838486.1, AA571359.1, AJ397361.1, AA334479.1, AW754210.1, AW583074.1, AI760838.1, AW578928.1, AA212025.1, C81194.1, AA645750.1, AW819755.1, AW125594.1, AU080443.1, AA919208.1, AA755774.1, AA615363.1, AA445826.1, AA117945.1, AI337175.1, AW819997.1, AW470142.1, AA626524.1, AA079853.1, W22433.1, T29047.1, AI626242.1, AW839103.1, AU035998.1, AA624532.1, AA572403.1, AA431598.1, AA370218.1, AA571473.1, AW754207.1, AW366794.1, AL137142.8, AC015501.3, AC021286.3, AC006882.2, AC068895.1, AC055115.2, AC013660.4, AL354918.3, AL138763.2, AC010646.4, AC010267.5, AC008642.3, AC008484.3, AC006279.6, AC006278.6, AC016522.4, AC019327.4, AC021435.2, AC011301.4, AF216669.1, AL159973.2, AL034557.7,
50	SEQ ID NO. 3
	NGO-Br-39
	MK494/T3 5'
	AF039695.1, AB003334.1, D86956.1, Z47807.1, NM_006644.1, AB003333.1, NM_013559.1, D67016.1, L40406.1, D67017.1, AB005277.1, AB005278.1, AB005276.1, NM_011020.1, U23921.1, D49482.1, AB001926.1, NM_014278.1, AB023421.1, L12723.1, AB005279.1, X67643.1, AF077354.1, NM_008300.1, AB005275.1, AB023420.1, D85904.1, AC009424.2, NM_013393.1, AF093415.1, AC010852.5, AF161311.1, AF136711.1, AC005516.1, AE001434.1, AE001433.1, AC003099.1, Z49769.1, AP001821.1, AC007678.3, AC006403.3, AC024813.1, AE003684.1, AC004668.1, AC004879.1, AC006354.2, AC010183.6, AC005049.2, AC004150.8, AC004801.1, AF049895.1, AF068862.1, AF004739.1, AL162911.1, Z68341.1, AL032629.1, AL023578.1, U41009.1, L16771.1, AI094015.1, AW206874.1, AA777564.1, AA885873.1, AI702970.1, AI800379.1, AA580595.1, AA805016.1, AW631423.1, AA811573.1,
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- AW630933.1, H91160.1, AI290252.1, H54657.1, H64019.1, AI002886.1, N84915.1, W45471.1, H63551.1, H63595.1, AW238563.1, H54656.1, AW577563.1, N84914.1, AA094644.1, AA749004.1, H91211.1, AI758907.1, AA777031.1, AA334479.1, AW604836.1, AW820299.1, AA580712.1, AW859988.1, AW859943.1, AW820232.1, AW820234.1, AL042714.2, AW390368.1, AW391561.1, H64073.1, AW362751.1, W86141.1, W86085.1, AA105012.1, AW608075.1, 5 AW389335.1, AW820231.1, AW362766.1, AA555929.1, AA555921.1, AI658961.1, AW820224.1, AW391572.1, AA714219.1, AA108277.1, AA580845.1, AJ397361.1, AW210124.1, AW754210.1, AW583074.1, AI760838.1, AW578928.1, AA212025.1, AI656127.1, AW385582.1, AA645750.1, AW819755.1, AW125594.1, AU080443.1, AA919208.1, AA755774.1, AA615363.1, AA445826.1, AA117945.1, AI633338.1, AI203278.1, AW819997.1, AW628153.1, AA626524.1, W22433.1, AI751852.1, AA953645.1, F08794.1, F07487.1, T63090.1, T29047.1, C81194.1, 10 AW839103.1, AU035998.1, AA370218.1, AW754207.1, AI314009.1, AW366794.1, AV162858.1, AI792084.1, AA909261.1, AL137142.8, AC015501.3, AC021286.3, AC069062.1, AC024112.9, AC008876.3, AL138763.2, AC010646.4, AC006278.6, AC016522.4, AC023956.2, AC005282.1, AP001863.1, AL034557.7, AC023855.3, AC026995.2, AC018688.4, AC022758.3, AC013294.3, AC006876.1, AL117373.6, AL117335.19, AL157821.1,
- 15 SEQ ID NO. 4
NGO-Br-55
MK225/T3 5'
- NM_005716.1, AF089816.1, AF022120.1, AF089818.1, AF089817.1, AF104358.1, AF061263.1, AL050318.12, AC007678.3, AC012099.4, NM_004364.1, AC006019.2, AC007397.21, AC007535.3, U51244.1, U34070.1, U94788.1, 20 U92845.1, Z69303.1, Z95127.1, Z31375.1, X54156.1, X87248.1, Y11525.1, AP000559.1, M93344.1, AW732338.1, AW409923.1, T25830.1, W06974.1, AW258706.1, AA396587.1, AA300306.1, AA839164.1, AF143339.1, AW416823.1, AI645842.1, AA702414.1, AA259652.1, AA158704.1, AW316813.1, AW293608.1, AI989542.1, AI971171.1, AI903437.1, AI903333.1, AI903269.1, AI903268.1, AI810739.1, AI696771.1, AI669881.1, AU056473.1, AI508747.1, AI462731.1, AI424712.1, AI418022.1, AI369600.1, AI335709.1, AI193578.1, AA974969.1, AA565967.1, AA513461.1, AA468577.1, 25 AA396061.1, AA367767.1, W87364.1, N39553.1, H49150.1, H25130.1, R10174.1, T52003.1, AW795860.1, AW594540.1, AW514789.1, AW472932.1, AW359396.1, AW293828.1, AW149413.1, AW064723.1, AW016496.1, AW008028.1, AI955331.1, AI697357.1, AI660572.1, AI565813.1, AI540768.1, AI538719.1, AI360009.1, AI126655.1, AI033638.1, AA515831.1, AA503485.1, AA496487.1, AA428815.1, AA280408.1, AA036554.1, N67732.1, N25184.1, H03122.1, T35597.1, T16741.1, AC008569.5, AC022478.3, AL355872.2, AL162371.5, AL137781.3, AC010442.4, AC031984.2, 30 AC060234.2, AC015958.3, AP000898.2, AP000919.2, AL121920.11, AL353195.1,
- SEQ ID NO. 5
NGO-Br-55
MK225/T7 3'
- 35 AF028824.1, NM_005716.1, AF089816.1, AE001104.1, AL096829.17, AJ007636.1, L38482.1, AC012467.9, AC007252.2, AC005757.1, AL049759.10, AB033031.1, AL033502.1, AF155065.1, AL138995.3, Z82214.23, AL031680.17, AJ222796.1, AW409924.1, AI720167.1, AI660895.1, AI755163.1, AI472081.1, AA781474.1, AI073909.1, W73036.1, AI697434.1, AI887371.1, AI032395.1, AA581812.1, AA149940.1, AA535595.1, AI085734.1, AI951003.1, AA666165.1, AI869948.1, AA579893.1, AI624402.1, R32110.1, AI241188.1, N64621.1, AA740666.1, AI589363.1, AW079516.1, 40 AA677956.1, AW166984.1, AI343472.1, AI831080.1, AW613269.1, AA878576.1, AI634734.1, AI955436.1, AI423229.1, AI683679.1, R50716.1, AA705739.1, AI690685.1, AW050771.1, H64249.1, AI867388.1, AW131086.1, AI654473.1, AI272198.1, AA325291.1, AI672928.1, AW193998.1, R40181.1, AI886660.1, AA612759.1, AI867293.1, AI499113.1, AA404606.1, AI270050.1, AI056166.1, AA995431.1, AW664356.1, AI695629.1, AI289585.1, AI218312.1, T54484.1, AA918644.1, AI709119.1, R33590.1, AI889242.1, R32109.1, AI804816.1, T30333.1, R09164.1, R77191.1, AA404222.1, 45 AA304135.1, AW664565.1, AW664371.1, R33694.1, AA160211.1, AW439960.1, AA320369.1, AA135772.1, AA135729.1, AI392813.1, AW190218.1, AI370449.1, W73301.1, AI298917.1, AA160212.1, AA434159.1, T16203.1, AW752314.1, AI769156.1, AW338853.1, N78888.1, AA295659.1, T48755.1, AI933841.1, AA887316.1, AW470194.1, N55776.1, AW007413.1, AC008569.5, AC010765.2, AL157781.1, AC007819.7, AL355350.2, AL161646.5, AL162454.2, AC051621.1, AC026055.3, AC013570.3, AC020565.4, AC023193.3, AC011286.4, AP000846.1, AC053465.3, 50 AC024715.3, AC023914.1, AC010729.3, AC010147.4, AL139253.1, AL031301.1,
- SEQ ID NO. 6
NGO-Br-61
MK751/T3 5'
- 55 AK001824.1, AK001625.1, AB020657.1, AK000931.1, AL137640.1, NM_016389.1, AF161553.1, AK001273.1, NM_006469.1, AJ012449.1, AL031674.1, AC006928.15, AC006581.16, AC007436.1, AL049861.18, AC009303.2, AE003772.1, AC004843.1, AF003141.1, U88180.1, AL034350.2, AP000606.1, AC006068.3, AC006031.2, AC006996.2, AC013417.4, AC005319.1, AC003050.1, AJ009736.1, AC002065.1, Z69383.1, L14324.1, AP000185.1, AP000283.1, AP000109.1, AI887429.1, Z42725.1, AA486796.1, AI697765.1, AI300924.1, W31762.1, AA516054.1, H47565.1, 60 AI625041.1, AI498683.1, AA962704.1, AA581961.1, Z28830.1, AI621215.1, AI560075.1, AA603342.1, AA211203.1, AI453000.1, AA505767.1, H29506.1, AI493165.1, AW338106.1, AW271945.1, AI561182.1, AI357213.1, AA888065.1, AI950251.1, AA182641.1, AI750267.1, AW536810.1, AI893732.1, AA881079.1, AA833428.1, AA759435.1, AA274870.1, AA260237.1, AI564193.1, AI72740.1, AA837350.1, AA572435.1, AA290546.1, AA563475.1, AA622090.1, AW681468.1, AW261744.1, AA638984.1, AW107357.1, AW261646.1, AA170526.1, AA848235.1, AI873826.1,

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- AI157598.1, AI750915.1, AI596266.1, AI929865.1, AI790736.1, AI649320.1, AI043196.1, AL023060.1, AW630831.1, AI314622.1, AI314243.1, AI098095.1, AI043182.1, AA511211.1, AA434721.1, AA140498.1, AA098508.1, R74754.1, AW532477.1, AI408553.1, AW750607.1, AV218438.1, AI048358.1, AA458054.1, AI763491.1, AV311575.1, AV005809.1, AA091451.1, D58165.1, AI911938.1, AI548180.1, AA086929.1, AI581089.1, AW822437.1, AW208414.1, AW145984.1, AV159067.1, AI607800.1, AW535768.1, AW822436.1, AI182297.1, AA313132.1, AA799539.1, AI971805.1, AV209231.1, AV207950.1, AV154324.1, AV118302.1, AV175071.1, AC016552.5, AC008499.4, AP001803.1, AP000479.2, AC027649.4, AC012429.4, AL353692.3, AC069214.1, AC024096.7, AC008670.3, AC067813.1, AC021601.3, AC023659.2, AC023818.2, AC009009.2, Z97201.7, AP001815.1,
- 10 SEQ ID NO. 7
NGO-Br-61
MK751/T7 3'
AK001824.1, AK001625.1, AB020657.1, AK000931.1, AL137640.1, NM_016389.1, AF161553.1, AK001273.1, NM_006469.1, AJ012449.1, AL031674.1, AC006928.15, AC006581.16, AC007436.1, AL049861.18, AC009303.2, AE003772.1, AC004843.1, AF003141.1, U88180.1, AL034350.2, AP000606.1, AC006068.3, AC006031.2, AC006996.2, AC013417.4, AC005319.1, AC003050.1, AJ009736.1, AC002065.1, Z69383.1, L14324.1, AP000185.1, AP000283.1, AP000109.1, AI887429.1, Z42725.1, AA486796.1, AI697765.1, AI300924.1, W31762.1, AA516054.1, H47565.1, AI625041.1, AI498683.1, AA962704.1, AA581961.1, Z28830.1, AI621215.1, AI560075.1, AA603342.1, AA211203.1, AI453000.1, AA505767.1, H29506.1, AI493165.1, AW338106.1, AW271945.1, AI561182.1, AI357213.1, AA888065.1, AI950251.1, AA182641.1, AI750267.1, AW536810.1, AI893732.1, AA881079.1, AA833428.1, AA759435.1, AA274870.1, AA260237.1, AI564193.1, AA172740.1, AA837350.1, AA572435.1, AA290546.1, AA563475.1, AA622090.1, AW681468.1, AW261744.1, AA638984.1, AW107357.1, AW261646.1, AA170526.1, AA848235.1, AI873826.1, AI157598.1, AI750915.1, AI596266.1, AI929865.1, AI790736.1, AI649320.1, AI043196.1, AL023060.1, AW630831.1, AI314622.1, AI314243.1, AI098095.1, AI043182.1, AA511211.1, AA434721.1, AA140498.1, AA098508.1, R74754.1, AW532477.1, AI408553.1, AW750607.1, AV218438.1, AI048358.1, AA458054.1, AI763491.1, AV311575.1, AV005809.1, AA091451.1, D58165.1, AI911938.1, AI548180.1, AA086929.1, AI581089.1, AW822437.1, AW208414.1, AW145984.1, AV159067.1, AI607800.1, AW535768.1, AW822436.1, AI182297.1, AA313132.1, AA799539.1, AI971805.1, AV209231.1, AV207950.1, AV154324.1, AV118302.1, AV175071.1, AC016552.5, AC008499.4, AP001803.1, AP000479.2, AC027649.4, AC012429.4, AL353692.3, AC069214.1, AC024096.7, AC008670.3, AC067813.1, AC021601.3, AC023659.2, AC023818.2, AC009009.2, Z97201.7, AP001815.1,
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- SEQ ID NO. 8
NGO-Br-57 combined;
AF025438.1, AL050353.1, AL121924.12, U42838.1, AL031055.1, AE003680.1, AC005539.1, AL121931.10, AL139076.2, AL024458.1, AC004680.2, AC010889.2, NM_007050.2, AF043644.4, AE003844.1, AE003787.1, AE003676.1, AE003533.1, AE003519.1, AE003480.1, AE003422.1, AE003217.1, AE002799.1, AC004455.1, AC009320.7, AC007478.1, AC007123.1, AC005966.1, AC005548.1, AL163232.2, AC000389.1, AL035633.18, AL032654.1, Z68335.1, AL024473.1, Z92844.1, AL110503.1, Y18930.1, AP001687.1, AP001297.1, AP000459.3, AB005234.1, D17799.1, D17798.1, D17797.1, X79080.1, AB009052.1, AB006621.1, AA701988.1, AI337332.1, AI765742.1, AI964006.1, AI828070.1, AI304319.1, AI760923.1, AA236789.1, AW161742.1, AI765022.1, AI935340.1, AW592648.1, AA865602.1, AI765999.1, N66532.1, AI631687.1, AA916723.1, AW161135.1, W58718.1, AA236836.1, N32746.1, AW051324.1, AA024685.1, AW152251.1, AW772254.1, AA916358.1, AA313566.1, AI336121.1, AA024784.1, AW614505.1, AI888263.1, N23163.1, AA007455.1, AW272790.1, AI167263.1, AI283104.1, AA451907.1, AA995467.1, AI753758.1, AA505618.1, AI073755.1, AA913049.1, AI538205.1, AA670386.1, AA007319.1, AI352390.1, AA680352.1, AW151295.1, AA720562.1, AI090162.1, AW466965.1, AA723980.1, AI808237.1, R72404.1, AI081040.1, AA992256.1, AI267913.1, AA541923.1, AA532854.1, R41738.1, AA236656.1, AA928158.1, AW117185.1, AI630438.1, AA016221.1, AA345744.1, AA137279.1, R72405.1, AI140745.1, AI084344.1, AI079153.1, AA852227.1, AA852226.1, H89982.1, AA000683.1, AI539552.1, AA385531.1, AW427494.1, AW557853.1, N50079.1, AI461713.1, AA858049.1, AW536613.1, AI599140.1, W10638.1, AI678339.1, AA637410.1, H30501.1, AW172462.1, R17187.1, AI630424.1, AI678340.1, R77800.1, W43974.1, AI198148.1, N56244.1, AW433804.1, AI841918.1, H25699.1, AA003291.1, AL136131.7, AL355349.1, AL138706.1, AL050335.24, AC016073.2, AC023651.2, AL354992.1, AC026285.4, AC055116.2, AC012133.3, AC006756.1, AC012031.7, AC007953.7, AC027502.3, AC026747.3, AC008821.4, AC016635.4, AC008926.5, AC008924.3, AC008592.3, AC009679.3, AC011639.6, AC016824.4, AC013237.1, AL356427.1, AL138899.6, AL160276.2, AP000841.1, AP000783.1,
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- SEQ ID NO:9
D26077, AJ009839, U00996, AF035621, AJ002223, AF013116, X57435, AF134401.1, AC004653, AL024473, AC004741, AC004453, AL023806, U36562, U64849, AF016450, AC003689, Z77652, AJ223630, AF026029, M76713, AC006525, Z70687, AL034351, Z94054, AC005955, U91325, AF051917, D90054, AF039047, AC003024, U23168, X89969, U21317, W88219, AI390662, AA107502, AA959827, AA562519, AA139695, AI505854, C80964, AI646091.1, AA217408, AU017533, W44823, AA381672, AI492198, AI185648, AI630930.1, T86437, AA558491, AA216567, AA368001, AA827488, AA425663, N84321, AA040741, AA084287, AA339843, AI524007.1, N73729, N75454, AA025609, AI244351, AA489142, AI283076, W05252, T98110, AI244357, AA659485, AI266380, AA972439, AI659137.1, D36418, AI065185, C67420, AA116198, AU000875, N98152, C56081, AU039284.1, AU039994.1,
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SEQ ID NO. 14

NGO-Br-60

MK746/T3 5'

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10 MK746/T7 3'

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SEQ ID NO.16

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MK442/T3 5'

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SEQ ID NO:21

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SEQ ID NO:28

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50

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60

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- 77 -

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SEQ ID NO:91

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SEQ ID NO:92

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SEQ ID NO:93

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SEQ ID NO:94

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- 79 -

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SEQ ID NO. 96

NGO-Br-37 combined

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SEQ ID NO. 97

NGO-Br-37

MK136/T7 3'

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SEQ ID NO. 98

NGO-Br-37

MK151/T7 3'

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SEQ ID NO. 99

NGO-Br-37

MK212/T3 5'

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35 SEQ ID NO. 100

NGO-Br-37

MK212/T7 3'

40 NM_006644.1, AF039695.1, AB003334.1, AB003333.1, D86956.1, D67017.1, D67016.1, NM_013559.1, L40406.1, Z47807.1, AB005282.1, AB005281.1, AC005215.1, AL163279.2, AF193508.1, AC006080.1, AC009223.2, AF016672.2, U22892.1, AL161539.2, Z98981.2, X04465.1, Z92838.1, Z83109.1, AL035258.10, AB042297.1, Z97336.1, L08612.1, X01647.1, AI658961.1, AW571648.1, AW474070.1, AW572452.1, AW608075.1, AW385582.1, AW470142.1, AW316651.1, AA232636.1, AA166806.1, AI751852.1, AW771160.1, AW628153.1, AW820299.1, AA953645.1, AI337175.1, AI651186.1, AA394027.1, AW390368.1, AA136424.1, AI223825.1, AW604836.1, AA435594.1, AI582484.1, AI103624.1, AA485036.1, AI288972.1, AA624532.1, AA571359.1, F07487.1, AW859988.1, AW859943.1, Z20100.1, 45 F08794.1, AW820234.1, AW085874.1, AI799265.1, T63090.1, AA572403.1, AW609781.1, AI838486.1, AA571473.1, AW820232.1, C81194.1, AA417317.1, AW020035.1, AW389335.1, AA079853.1, T34627.1, AA777031.1, Z21220.1, AW491178.1, AI842560.1, AA843693.1, AV275994.1, AA278231.1, AA967441.1, AA856248.1, Z41841.1, AA238818.1, AI115351.1, AV347805.1, AW147250.1, AV348434.1, AV200611.1, AV181186.1, AV178670.1, AV059415.1, AU055867.1, AI365340.1, AI341168.1, AA882330.1, C78586.1, C56104.1, C55163.1, C54236.1, C54007.1, C34122.1, 50 C31088.1, AA522360.1, CI2303.1, D64277.1, R98128.1, T26732.1, D33807.1, AL137142.8, AC012569.3, AP001895.1, AP001563.1, AC027128.3, AC023471.2, AF129408.1, AC021710.4, AC020725.3, AC009039.5, AC007337.2, AC008361.7, AC014468.1, AC026863.3, AC032034.2, AC008902.3, AC027359.2, AC026650.3, AC019267.3, AC024681.2, AC022776.2, AC018519.3, AL109916.3, AL162264.4, AL138705.3, AL158817.2,

55 SEQ ID NO. 101

NGO-Br-37

MK379/T7 3'

60 NM_006644.1, AF039695.1, AB003334.1, AB003333.1, D86956.1, D67017.1, D67016.1, NM_013559.1, L40406.1, Z47807.1, AB005281.1, AB005282.1, AC005371.1, AB005280.1, AC009223.2, AC005951.1, Z79754.1, AL009183.10, Z74617.1, AL035258.10, AW571648.1, AI658961.1, AW572452.1, AW474070.1, AW385582.1, AW608075.1, AW470142.1, AW316651.1, AA232636.1, AA166806.1, AI751852.1, AW771160.1, AW628153.1, AA394027.1, AA953645.1, AI651186.1, AA136424.1, AW103624.1, AW820299.1, AI223825.1, AI582484.1, AI337175.1, AW390368.1, AA435594.1, AA485036.1, AI288972.1, AW604836.1, Z20100.1, AI799265.1, AW609781.1, F08794.1, F07487.1, AW859988.1, AW859943.1, AW085874.1, T63090.1, AW820234.1, AA624532.1, AA571359.1, AA417317.1,

AA572403.1, AW020035.1, AI838486.1, AA571473.1, T34627.1, Z21220.1, C81194.1, AW820232.1, AA079853.1, AA278231.1, AA843693.1, AW491178.1, AI842560.1, AA967441.1, AA856248.1, AV275994.1, Z41841.1, AW389335.1, AA238818.1, AA524050.1, AW670042.1, AW467587.1, AW440906.1, AW301952.1, AV347805.1, AW148805.1, AW080765.1, AW073417.1, AW021546.1, AW006027.1, AI870113.1, AI766462.1, AI699756.1, AI680535.1, AI563975.1, AI510837.1, AI378898.1, AI378423.1, AI290741.1, AI288939.1, AI092211.1, AA987850.1, AA877634.1, AA806917.1, AA745943.1, AA725830.1, AA682373.1, AA506124.1, AA465237.1, AA232282.1, AA129977.1, AA035579.1, W58443.1, N91182.1, T63600.1, AL137142.8, AC012569.3, AP001895.1, AP001563.1, AC008689.4, AC027117.2, AC022671.2, AC021710.4, AC020725.3, AC009039.5, AC007337.2, AC023309.1, AF176680.1, AL132989.1, AC034128.2, AC027057.2, AC025225.2, AC024681.2, AC023557.1, AL356059.1, AL139800.1, AP000780.1,

SEQ ID NO. 102

NGO-Br-37

MK394/T7 3'

NM_006644.1, AF039695.1, AB003334.1, AB003333.1, D86956.1, D67017.1, D67016.1, NM_013559.1, L40406.1, Z47807.1, AB005281.1, AB005282.1, AB023420.1, X67643.1, NM_008300.1, AC005371.1, D85904.1, AC005215.1, AC011294.3, AE003589.1, AF241729.1, AC005762.1, AC007161.1, AC005539.1, AC005951.1, Z71259.1, Z99289.1, AL035258.10, Z74739.1, AI658961.1, AW571648.1, AW474070.1, AW608075.1, AW572452.1, AW385582.1, AW470142.1, AI751852.1, AW316651.1, AA166806.1, AW628153.1, AA232636.1, AA953645.1, AW820299.1, AW390368.1, AW604836.1, AW771160.1, AA394027.1, AW103624.1, AI651186.1, AA136424.1, AI223825.1, AI337175.1, AW820234.1, F07487.1, AA485036.1, AW859988.1, AW859943.1, F08794.1, AI582484.1, AA435594.1, T63090.1, AI288972.1, AW820232.1, AW609781.1, AI799265.1, Z20100.1, AA624532.1, AA571359.1, AW085874.1, AW389335.1, AI838486.1, AA572403.1, C81194.1, AA571473.1, AA417317.1, AW020035.1, AA777031.1, T34627.1, AA079853.1, Z21220.1, AA278231.1, AA843693.1, AW491178.1, AI842560.1, Z41841.1, AV275994.1, AA967441.1, AA856248.1, AW861588.1, AW819997.1, AW819755.1, AW604699.1, AW366794.1, AW085727.1, AI925201.1, AI754819.1, AI567970.1, AA703912.1, AA493400.1, AA173193.1, R54223.1, AW754207.1, AW545353.1, AW545094.1, AW542227.1, AW537735.1, AW060626.1, AI956869.1, AA823019.1, AA799083.1, AA445826.1, AA238818.1, AA205597.1, AW604696.1, AW583074.1, AW578928.1, AI626242.1, AA542420.1, AV347805.1, AW619786.1, AW391561.1, AI806597.1, AV059415.1, AI115351.1, R98128.1, AL137142.8, AC008689.4, AC027399.2, AC026927.2, AC022212.3, AC023574.2, AC012569.3, AC020725.3, AC009039.5, AC007337.2, AC017242.1, AF176680.1, AL353894.3, AL353753.1, AL158817.2, AP001895.1, AP001563.1, AC034128.2, AC016926.4, AC024909.8, AC012135.2, AC017024.4, AC025673.2, AC027057.2, AC022537.3, AC025971.2, AC009925.3, AC024681.2, AC021571.3, AC021903.5, AC012434.3, AC009969.4, AC021326.1, AC013759.2, AC013493.1, AL121927.18, AL354749.2, AL136220.2, AL133350.7, AL139800.1, AL031745.7,

SEQ ID NO 103

NGO-Br-37

MK401/T3 5'

NM_006644.1, AF039695.1, AB003334.1, AB003333.1, D86956.1, Z47807.1, D67017.1, D67016.1, NM_013559.1, L40406.1, NM_011020.1, U23921.1, D49482.1, AB001926.1, NM_014278.1, AB023421.1, L12723.1, AB005279.1, AB005280.1, X67643.1, AF077354.1, NM_008300.1, AB023420.1, D85904.1, AB005281.1, AL109620.4, L08605.1, AE003589.1, AF161311.1, AF136711.1, AE001434.1, AE001433.1, AC005762.1, AC004045.1, AC006403.3, AE003657.1, AE003645.1, AE003411.1, AC011609.9, AC011662.1, AC006288.1, X94582.1, X94581.1, AB020374.1, AB020372.1, AB020370.1, AB020368.1, AB020366.1, AB020364.1, AB020362.1, AB020360.1, AB020356.1, AB020350.1, AB020347.1, AB020345.1, AB020343.1, AC010722.2, AC011299.3, AF169288.1, AC005161.1, AF198095.1, AF128525.1, Z95559.1, AL109865.36, AL034488.1, AL110490.1, AL117205.2, Z35595.1, AB020876.1, AW820299.1, AW390368.1, AW859988.1, AW859943.1, AW820234.1, AW604836.1, AW608075.1, AI658961.1, AW820232.1, AW628153.1, AI751852.1, AW385582.1, F07487.1, AA777031.1, F08794.1, AA953645.1, AW389335.1, T63090.1, AA166806.1, AW474070.1, AW571648.1, AA394027.1, AW103624.1, AW609781.1, AA485036.1, AW572452.1, AW391561.1, AI838486.1, AA571359.1, AW316651.1, AW362751.1, C81194.1, AW470142.1, AJ397361.1, AA624532.1, AW754210.1, AW583074.1, AI760838.1, AI337175.1, AW819755.1, AW578928.1, AA212025.1, AU080443.1, AW206874.1, AW125594.1, AA919208.1, AA755774.1, AA645750.1, AA615363.1, AA445826.1, AA117945.1, AW819997.1, AI626242.1, AI094015.1, W86085.1, AA885873.1, AA626524.1, W22433.1, H63551.1, T29047.1, AW861588.1, AW604699.1, AW366794.1, AW085727.1, AI925201.1, AI754819.1, AI567970.1, AU035998.1, AA703912.1, AA493400.1, AA431598.1, AA173193.1, H64019.1, R54223.1, AI758907.1, AW754207.1, AW545353.1, AW545094.1, AW542227.1, AW537735.1, AW060626.1, AI956869.1, AI702970.1, AA823019.1, AA799083.1, AA777564.1, AW839103.1, AA555929.1, AA370218.1, AA205597.1, AW604696.1, AA580595.1, AA542420.1, AW861596.1, AI314009.1, C76500.1, AA549968.1, H91160.1, AL137142.8, AC015501.3, AC021286.3, AC008642.3, AC006278.6, AC019327.4, AC017242.1, AL034557.7, AC025358.3, AC011333.4, AC027429.2, AC025673.2, AC027054.2, AC024968.2, AC016459.2, AC021997.2, AC017097.2, AL139034.3, AL157821.1,

SEQ ID NO. 104

NGO-Br-37

MK401/T7 3'

NM_006644.1, AF039695.1, AB003334.1, AB003333.1, D86956.1, D67017.1, D67016.1, NM_013559.1, L40406.1,

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- SEQ ID NO. 105
NGO-Br-37
MK508/T3 5'
NM_006644.1, AF039695.1, AB003334.1, AB003333.1, D86956.1, D67017.1, D67016.1, NM_013559.1, L40406.1, Z47807.1, AB005282.1, AB005281.1, AB005280.1, AB023420.1, X67643.1, NM_008300.1, D85904.1, AF262041.1, AC011661.5, AL163279.2, AL109620.4, AC004684.2, AE003720.1, AE003522.1, AF222716.1, AC009223.2, AC004251.1, AC002367.1, AL163234.2, AL161553.2, AL161539.2, X04465.1, AL139077.2, AL009183.10, AP001689.1, Z97336.1, AI658961.1, AW571648.1, AW474070.1, AW572452.1, AW470142.1, AW608075.1, AW385582.1, AA232636.1, AW316651.1, AW771160.1, AA166806.1, AI751852.1, AI651186.1, AI223825.1, AW628153.1, AA136424.1, AA953645.1, AI582484.1, AA394027.1, AW820299.1, AW390368.1, AW103624.1, AI288972.1, AI337175.1, AW604836.1, Z20100.1, AI799265.1, AA435594.1, AA485036.1, AA571359.1, F07487.1, F08794.1, T63090.1, AA624532.1, AW859988.1, AW859943.1, AW609781.1, AI838486.1, AW020035.1, AW820234.1, T34627.1, Z21220.1, C81194.1, AA843693.1, AA278231.1, AA079853.1, AW491178.1, AI842560.1, AV275994.1, AW837156.1, AA967441.1, AA856248.1, AA777031.1, AW068948.1, F03714.1, AA238818.1, AV146133.1, AI528497.1, AI115351.1, AA462732.1, AW861588.1, AW819997.1, AW819755.1, AW604699.1, AW366794.1, AW085727.1, AI925201.1, AV149067.1, AI754819.1, AI567970.1, AA703912.1, AA493400.1, AA173193.1, R54223.1, AW545353.1, AW545094.1, AW542227.1, AW537735.1, AW060626.1, AI956869.1, AA823019.1, AA799083.1, AA445826.1, AV160311.1, AI600071.1, AI236601.1, AA205597.1, AW604696.1, AW700938.1, AI790491.1, AA681295.1, AU053616.1, AL137142.8, AC012569.3, AP001895.1, AP001563.1, AC023471.2, AC021531.3, AC005506.6, AC021722.4, AC009039.5, AC007337.2, AC008361.7, AC014468.1, AL162502.2, AC027149.2, AC009634.3, AC019267.3, AC024681.2, AC006281.6, AC022461.3, AL109916.3, AL138705.3, AL161449.2, Z98863.1,
- SEQ ID NO. 106
NGO-Br-37
MK612/T3 5'
NM_006644.1, AF039695.1, AB003334.1, AB003333.1, D86956.1, Z47807.1, D67017.1, D67016.1, NM_013559.1, L40406.1, AB005281.1, NM_011020.1, U23921.1, D49482.1, AB001926.1, NM_014278.1, AB023421.1, L12723.1, AB005279.1, X67643.1, AF077354.1, NM_008300.1, AB023420.1, D85904.1, AB005280.1, L08605.1, AE003589.1, AF161311.1, AF136711.1, AE001434.1, AE001433.1, AC005762.1, AC004045.1, AC006403.3, AC011609.9, AF049895.1, AC006288.1, AC005951.1, AE001393.1, AF068862.1, L04162.1, AB026651.1, L08135.1, L22219.1, AW820299.1, AW608075.1, AW604836.1, AW390368.1, AI658961.1, AW628153.1, AW859988.1, AW859943.1, AI751852.1, AW820234.1, AW385582.1, AW820232.1, AA953645.1, AA166806.1, AW571648.1, AA394027.1, AW474070.1, AA777031.1, AW103624.1, F07487.1, AW572452.1, F08794.1, AW389335.1, AA485036.1, T63090.1, AW316651.1, AW609781.1, AW470142.1, AW391561.1, AI838486.1, AI337175.1, AA571359.1, AW362751.1, C81194.1, AA624532.1, AA079853.1, AA232636.1, AA572403.1, AJ397361.1, AA571473.1, AW771160.1, AW754210.1, AW583074.1, AW206874.1, AI760838.1, AW578928.1, AA212025.1, AI094015.1, AA645750.1, W86085.1, AW819755.1, AA885873.1, AW125594.1, AU080443.1, AA919208.1, AA755774.1, AA615363.1, AA445826.1, AA117945.1, H63551.1, H64019.1, AI758907.1, AI702970.1, AA777564.1, AW819997.1, AA626524.1, AA580595.1, W22433.1, H91160.1, T29047.1, AW861588.1, AW839103.1, AW604699.1, AW366794.1, AW085727.1, AI925201.1, AI754819.1, AI626242.1, AI567970.1, AU035998.1, AA703912.1, AA493400.1, AA370218.1, AA173193.1, H54657.1, R54223.1, AW754207.1, AW545353.1, AW545094.1, AW542227.1, AW537735.1, AW060626.1, AI956869.1, AI314009.1, AA823019.1, AA799083.1, AA555929.1, AA205597.1, AW604696.1, AA542420.1, AL137142.8, AC015501.3, AC021286.3, AC008642.3, AC023574.2, AC006279.6, AC006278.6, AC019327.4, AC009039.5, AC007337.2, AC017242.1, AL353894.3, AL353753.1, AL034557.7, AC055800.2, AC037481.2, AC024891.8, AC026825.2, AC025358.3, AC011333.4, AC008714.2, AC034128.2, AC024909.8, AC015533.4, AC027429.2,

AC016805.3, AC009786.2, AC027057.2, AC027054.2, AC025538.3, AC024968.2, AC024681.2, AC016459.2, AC020712.4, AC021903.5, AC022758.3, AC021997.2, AC017097.2, AC022725.1, AC009728.2, AL353714.2, AL138705.3, AL355483.1, AL355135.1, AL353630.1, AC002421.1, AL157821.1, AL138920.2, AL137247.3,

5 SEQ ID NO. 107

NGO-Br-37

MK661/T3 5'

NM_006644.1, AF039695.1, AB003334.1, AB003333.1, D86956.1, NM_013559.1, D67017.1, D67016.1, L40406.1, Z47807.1, AB005282.1, AB005281.1, AL163279.2, AF193508.1, AE003720.1, AC009223.2, AC004251.1, AL163234.2, 10 AL161553.2, AL161539.2, AL139077.2, AP001689.1, Z97336.1, AP000477.2, AE003728.1, AE003686.1, AE003627.1, AE003520.1, AF065404.1, AC000104.1, AC005771.1, AF069291.1, U67495.1, AL163285.2, Z68004.1, AW571648.1, AW572452.1, AW474070.1, AW470142.1, AA232636.1, AI658961.1, AW771160.1, AW316651.1, AW608075.1, AW385582.1, AI651186.1, AA136424.1, AI223825.1, AA435594.1, AI582484.1, AI337175.1, AI288972.1, AA166806.1, Z20100.1, AI799265.1, AW085874.1, AA624532.1, AA571473.1, AA571359.1, AA572403.1, AA417317.1, AI751852.1, 15 AA394027.1, AW020035.1, AI838486.1, C81194.1, T34627.1, Z21220.1, AW628153.1, AW103624.1, AW491178.1, AI842560.1, AA843693.1, AV275994.1, AW604836.1, AA278231.1, AW820299.1, AA485036.1, AA953645.1, AA967441.1, AA856248.1, AA079853.1, Z41841.1, AA238818.1, AW390368.1, AI115351.1, AV347805.1, AW147250.1, AV348434.1, AV200611.1, AV181186.1, AV178670.1, AU055867.1, AI365340.1, AI341168.1, AA882330.1, AA834218.1, C56104.1, C55163.1, C54236.1, C54007.1, C34122.1, C31088.1, C12303.1, D64277.1, T26732.1, D33807.1, 20 AW383218.1, AV272251.1, AV269906.1, AW037622.1, AI807000.1, AI804139.1, AA893644.1, AL137142.8, AC012569.3, AP001895.1, AP001563.1, AC027117.2, AC022671.2, AC027128.3, AC023471.2, AC018818.3, AF129408.1, AC021531.3, AC005506.6, AC021722.4, AC008361.7, AC018789.2, AC014468.1, AC044830.2, AC008902.3, AC027359.2, AC009634.3, AC022530.4, AC026650.3, AC025973.2, AC019267.3, AC009925.3, AC018717.5, AC015974.4, AC013110.1, Z98863.1,

25 SEQ ID NO. 108

NGO-Br-38

MK015/T3 5'

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SEQ ID NO. 109

50 NGO-Br-38

MK015/T7 3'

AF039695.1, D86956.1, NM_006644.1, AB003334.1, AB003333.1, D67017.1, D67016.1, AB005282.1, NM_013559.1, L40406.1, Z47807.1, AE003611.1, AL035259.1, AC007677.3, AE003628.1, AE003571.1, AE003567.1, AC007066.4, 55 AL022164.1, AF218257.1, AC016752.2, AC006413.3, AE003477.1, AC005927.2, AC007061.5, U71249.1, AC003078.1, U95740.1, AF104919.1, AC005324.1, AL133419.15, AL034556.3, AL138995.3, AL161492.2, AL035706.10, AL049188.3, AJ010316.1, AB004275.1, AB006696.1, AP000555.1, Z11695.1, AB006689.1, AA843693.1, AA543054.1, AI742981.1, AW612980.1, AW612983.1, AI582881.1, AI751853.1, AI378269.1, AI920808.1, AI654608.1, AI819251.1, AI337175.1, AI753470.1, AI831339.1, AI312753.1, AI803588.1, AI563996.1, AW015796.1, AW117974.1, AI668853.1, AA993280.1, AA912023.1, AA535277.1, AI123280.1, AA632202.1, AW027050.1, AW627645.1, AA761750.1, AI223412.1, 60 AA219263.1, AW068948.1, AA166716.1, AA482770.1, AW236067.1, AA485151.1, AI369932.1, AI250881.1, AA933881.1, AI262020.1, AI050716.1, H52653.1, AA678506.1, AA582157.1, AW340810.1, AI493255.1, AW837156.1, AI673134.1, TS8153.1, T36072.1, F22410.1, AA417317.1, AW020035.1, AI361237.1, AA278231.1, AA810686.1, AA730742.1, AA082043.1, D58216.1, D29622.1, AA233888.1, AI630481.1, AI612928.1, D29371.1, AA731716.1, AA417255.1, AA804371.1, AA465183.1, AA780104.1, AA491870.1, T34783.1, Z41841.1, AW771160.1, AI357434.1,

- AI799265.1, AI582484.1, AI288972.1, F03714.1, AW381433.1, AW381418.1, TI0428.1, AW163535.1, AW059721.1, AA773435.1, AI651186.1, AW824279.1, AW544862.1, AW061135.1, AL117974.1, AW049097.1, AW011890.1, AI845946.1, AU019569.1, AU019107.1, C78223.1, C78213.1, C77722.1, AA048547.1, AA986561.1, AI154454.1, AW700938.1, AL137142.8, AC011966.3, AC027326.2, AC027323.2, AC010622.3, AC020999.4, AC018938.3, AC018104.1, AC004390.1, AL161779.7, AP001547.1, AP000635.1, AP000610.2, AC022101.3, AC010093.3, AC011799.5, AC023003.2, AC018466.3, AC020183.1, AC014557.1, AC015076.1, AC009849.6, AC011758.5, AC025391.3, AC022516.3, AC044816.2, AC026911.2, AC022462.3, AC015684.3, AC009835.5, AC015714.4, AC011227.3, AC010018.4, AL355575.2, AL133344.21, AL157687.2, AL034359.4
- 10 SEQ ID NO. 110
NGO-Br-38
MK249/T7 3'
- 15 AF039695.1, D86956.1, NM_006644.1, AB003334.1, AB003333.1, Z47807.1, D67017.1, D67016.1, AB005282.1, NM_013559.1, L40406.1, AC011661.5, AE003611.1, AL035259.1, AC004684.2, AE003571.1, AE003567.1, AC010168.6, AF140273.1, U32370.1, U30930.1, AC002367.1, AE000823.1, AC002292.1, AL158059.2, AJ006409.1, AB026658.1, AF218257.1, AC016752.2, AC009155.3, AC006413.3, U09675.1, AC005927.2, AC007061.5, AF030694.2, AF222716.1, U95740.1, AC009501.3, AC005083.1, AC007590.1, AF104919.1, AF074946.1, AF030693.1, AF030692.1, AC005324.1, AL133419.15, AL034556.3, AL034560.3, AL110502.1, AL049779.4, AL049188.3, U27707.1, U40933.1, U41018.1, AB004275.1, AP000069.1, AB006696.1, Z18921.1, AB006689.1, AA543054.1, AA843693.1, AW612980.1, AI582881.1, AW612983.1, AI378269.1, AI920808.1, AI654608.1, AI742981.1, AI312753.1, AI753470.1, AI831339.1, AI819251.1, AI803588.1, AI751853.1, AI563996.1, AW117974.1, AI668853.1, AA993280.1, AA632202.1, AA219263.1, AW627645.1, AW015796.1, AI337175.1, AI123280.1, AA912023.1, AA761750.1, AW027050.1, AI223412.1, AA535277.1, AA485151.1, AA166716.1, AW236067.1, AI369932.1, AI250881.1, AA482770.1, AA933881.1, AI262020.1, AI050716.1, AI493255.1, AA678506.1, AA582157.1, AW340810.1, AI673134.1, H52653.1, T58153.1, AW068948.1, AI361237.1, AA810686.1, T36072.1, F22410.1, AW837156.1, AA417317.1, AA082043.1, D58216.1, D29622.1, AA278231.1, AW020035.1, AI612928.1, AI630481.1, AA730742.1, D29371.1, AA731716.1, AA417255.1, AA804371.1, AA465183.1, AA233888.1, AA780104.1, AA491870.1, AI357434.1, AW381433.1, AW163535.1, T34783.1, TI0428.1, AW381418.1, Z41841.1, AW771160.1, F03714.1, AI799265.1, AI582484.1, AI288972.1, AW059721.1, AA773435.1, AW470142.1, AI651186.1, AI223825.1, AA232636.1, T34627.1, Z20100.1, Z21220.1, AI658961.1, AA136424.1, AW824279.1, AL117974.1, AU049097.1, AI845946.1, C78213.1, AA048547.1, AA986561.1, AW700938.1, AL137142.8, AC011966.3, AC018938.3, AC019338.4, AC018104.1, AP001547.1, AP000635.1, AP000610.2, AC022101.3, AC067877.1, AC018700.3, AC010093.3, AC008107.2, AC022636.3, AC011799.5, AC009919.2, AC014557.1, AC015336.1, AC015076.1, AL354655.3, AL353639.2, AL161449.2, AC025440.3, AC022516.3, AC008395.5, AC027149.2, AC019075.6, AC067945.1, AC026911.2, AC023461.2, AC025246.5, AC055117.1, AC027646.3, AC015714.4, AC026641.1, AC006281.6, AC018934.2, AC009015.2, AC002043.1, AC023302.2, AC006763.1, AC006187.1, AL139318.2, AL132640.1, AL138776.2, AL136303.3, AL049183.5, AL034359.4, AP000840.1,
- SEQ ID NO. 111
NGO-Br-38
MK4110/T3 5'
- 40 NM_006644.1, AB003334.1, AB003333.1, D86956.1, AF039695.1, D67017.1, D67016.1, Z47807.1, NM_013559.1, L40406.1, AB005267.1, AB023420.1, L12723.1, X67643.1, NM_008300.1, AC011013.17, D85904.1, AF077354.1, NM_014278.1, NM_011020.1, U23921.1, AB023421.1, D49482.1, AB005268.1, NM_004455.1, U67191.1, AC006661.2, AE003724.1, U95739.1, AW137489.1, AW665093.1, AL120219.1, AI052062.1, AI023309.1, AU077146.1, AI052577.1, AI219339.1, AI003212.1, AA078767.1, AL043449.1, AW475538.1, AW227137.1, AW105834.1, AI931227.1, AI787816.1, AI746652.1, AI006526.1, AW209689.1, AU066691.1, AA168224.1, AA081692.1, AW069322.1, AW318627.1, AI956324.1, AI956249.1, AI316935.1, AA408320.1, AW227160.1, AA407914.1, AL044212.1, AA226851.1, AW141567.1, AA840049.1, AA726333.1, AW416815.1, AI087282.1, AI510184.1, AA799078.1, AA038974.1, AW281373.1, AW249190.1, AW174950.1, AW140856.1, AI777243.1, AI717978.1, AI667993.1, AI593889.1, AI564662.1, AI548407.1, AI132100.1, AA798531.1, AA657153.1, AA309538.1, AA010464.1, W52045.1, W39574.1, N77720.1, AL137142.8, AL138965.3, AC046137.3, AC020834.2, AC015501.3, AC021286.3, AC068888.1, AC008686.5, AC023175.1, AC027676.2, AC044785.1, AC015810.3, AC009972.4, AC006091.9, AC017374.1, AC006802.1, AL354832.2, AL354813.2,
- 55 SEQ ID NO. 112
NGO-Br-38
MK447/T3 5'
- 60 AC004079.1, AL023812.1, AF116671.1, AC010739.3, NM_000146.1, AF147331.1, AL031670.6, Z94054.1, L37679.1, M12938.1, M11147.1, X03743.1, M10119.1, AW516833.1, AW300978.1, AW162231.1, AV257466.1, AW157374.1, AW079316.1, AW009956.1, AW004961.1, AI962098.1, AI815894.1, AI755008.1, AI748966.1, AI718110.1, AI709101.1, AI672960.1, F19164.2, AI589785.1, AI583347.1, AI479061.1, AI420287.1, AI361309.1, AI354529.1, AI292111.1, AI219615.1, AI219349.1, AI214612.1, AI200269.1, AI193445.1, AI189444.1, AI184382.1, AI143808.1, AI127965.1, AI127854.1, AI093293.1, AI089317.1, AI015377.1, AA989142.1, AA970214.1, AA946915.1, AA928899.1, AA918624.1, AA876284.1, AA861967.1, AA857441.1, AA854288.1, AA845736.1, AA838065.1, AA838024.1, AA775012.1,

AA757403.1, AA658536.1, AA654568.1, AA618051.1, AA604054.1, AA600804.1, AA588452.1, AA587371.1, AA587071.1, AA582703.1, AA582484.1, AA582386.1, AA568291.1, AA564050.1, AA555249.1, AA541585.1, AA533130.1, AA531161.1, AA515081.1, AA494515.1, AA486095.1, AA468679.1, AA399366.1, AA373996.1, AA342114.1, AA223994.1, AA206785.1, AA192374.1, AA187220.1, AA152396.1, AA085100.1, AA083345.1, AA057726.1, AA039420.1, AA028129.1, AA011234.1, W40483.1, W40152.1, N79615.1, N53835.1, N42345.1, N25279.1, H66026.1, R97999.1, D51234.1, H22588.1, R28740.1, T60144.1, T19029.1, AC023169.3, AC021399.3, AC022015.2, AC016474.2, AC018910.4, AC024270.1, AC016185.1, AC021886.4, AC068615.2, AC068712.1, AC040169.2, AC026803.2, AC008749.4, AC022916.2, AC021554.4, AC027626.2, AC024616.1, AC009867.1, AL139824.12, AC003117.1, AL139158.1, AP001939.1, AP001374.1

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SEQ ID NO.113

NGO-Br-38

MK447/T7 3'

15

AF039695.1, D86956.1, NM_006644.1, AB003334.1, AB003333.1, D67017.1, D67016.1, AB005282.1, NM_013559.1, L40406.1, Z47807.1, AF262041.1, AC000065.1, AC011661.5, AL034560.3, AL035259.1, AC004684.2, AE003567.1, AC007049.8, AC005992.15, AC016752.2, AC006586.9, AC004165.2, AL133419.15, AL034556.3, AL117202.1, Z68116.1, AL049188.3, U27707.1, AJ010316.1, AP000555.1, AA843693.1, AA543054.1, AI742981.1, AW612980.1, AW612983.1, AI582881.1, AI378269.1, AI920808.1, AI751853.1, AI654608.1, AI819251.1, AI831339.1, AI753470.1, AI312753.1, AI803588.1, AI563996.1, AW015796.1, AW117974.1, AI668853.1, AA535277.1, AA993280.1, AA632202.1, AA912023.1, AW627645.1, AW027050.1, AI337175.1, AI123280.1, AA761750.1, AI223412.1, AA219263.1, AW068948.1, AA482770.1, AA166716.1, AW236067.1, AA485151.1, AI369932.1, AI250881.1, AA933881.1, AI262020.1, AI050716.1, H52653.1, AA678506.1, AA582157.1, AI493255.1, AW340810.1, AW837156.1, AI673134.1, T58153.1, T36072.1, F22410.1, AA417317.1, AW020035.1, AI361237.1, AA278231.1, AA810686.1, AA730742.1, AA082043.1, D58216.1, D29622.1, AA233888.1, AI612928.1, D29371.1, AI630481.1, AA731716.1, AA417255.1, AA804371.1, AA465183.1, AA780104.1, AA491870.1, T34783.1, Z41841.1, AW771160.1, AI357434.1, AI799265.1, AI582484.1, AI288972.1, F03714.1, AW381433.1, AW381418.1, T10428.1, AW163535.1, Z21220.1, AW470142.1, AI651186.1, AI223825.1, AA232636.1, Z20100.1, T34627.1, AI658961.1, AA136424.1, AW059721.1, AW571648.1, AA773435.1, AW544862.1, AI790491.1, AU019107.1, C78223.1, AI115351.1, AW700938.1, AA238818.1, AL137142.8, AC010034.5, AC011966.3, AC027326.2, AC018938.3, AC018104.1, AC004390.1, AP000635.1, AP000610.2, AC068643.5, AC022101.3, AC020183.1, AC009849.6, AC018934.2, AL354895.3, AL353639.2, AL133344.21, AL157687.2, Z98865.1, Z92818.1,

SEQ ID NO.114

NGO-Br-38

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MK633/T3 5'

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NM_006644.1, AF039695.1, AB003334.1, AB003333.1, D86956.1, D67017.1, D67016.1, Z47807.1, NM_013559.1, L40406.1, AB005282.1, AB005281.1, AB005280.1, AB023420.1, X67643.1, NM_008300.1, D85904.1, AE003525.1, AL163279.2, AL109620.4, AF193508.1, AE003720.1, AE003589.1, AE003522.1, AC009223.2, AC004251.1, AC002367.1, AL163234.2, AL161553.2, AL161539.2, AL139077.2, AL009183.10, AP001689.1, Z97336.1, AP000477.2, AI658961.1, AW571648.1, AW474070.1, AW608075.1, AW572452.1, AW385582.1, AW470142.1, AA232636.1, AW316651.1, AA166806.1, AI751852.1, AW771160.1, AW628153.1, AI651186.1, AA953645.1, AW820299.1, AA394027.1, AI223825.1, AA136424.1, AW390368.1, AI582484.1, AW103624.1, AW604836.1, AI337175.1, AI288972.1, AA435594.1, AA485036.1, F07487.1, AA571359.1, Z20100.1, F08794.1, AI799265.1, T63090.1, AW859988.1, AW859943.1, AA624532.1, AW820234.1, AI838486.1, AW609781.1, C81194.1, AW085874.1, AW820232.1, AA572403.1, AW020035.1, AA571473.1, T34627.1, Z21220.1, AA417317.1, AA278231.1, AA843693.1, AW389335.1, Z41841.1, AA079853.1, AW491178.1, AI842560.1, AV275994.1, AA777031.1, AA967441.1, AA856248.1, AW837156.1, AA238818.1, H52653.1, T34783.1, AI751853.1, F03714.1, AW861588.1, AW819997.1, AW819755.1, AW604699.1, AW366794.1, AW085727.1, AW068948.1, AI925201.1, AI754819.1, AI567970.1, AA703912.1, AA493400.1, AA173193.1, R54223.1, AI115351.1, AW545353.1, AW545094.1, AW542227.1, AW537735.1, AW060626.1, AI956869.1, AV146133.1, AI528497.1, AA823019.1, AA799083.1, AA462732.1, AA445826.1, AW754207.1, AA205597.1, AW604696.1, AV279553.1, AV149067.1, AI600071.1, AL137142.8, AC012569.3, AP001895.1, AP001563.1, AC023471.2, AC018495.3, AC010070.5, AC010069.6, AC015410.1, AF129408.1, AC022797.3, AC021531.3, AC005506.6, AC021722.4, AC009039.5, AC007337.2, AC008361.7, AC014468.1, AL162502.2, AC034128.2, AC018700.3, AC022530.4, AC019267.3, AC009925.3, AC024681.2, AC022461.3, AL109916.3, AL138705.3, AL161449.2, Z98863.1,

SEQ ID NO.115

NGO-Br-40 combined

60

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AI830004.1, AW058212.1, AA876142.1, AI983562.1, AI439472.1, AW820994.1, AW468007.1, AI969542.1, AI760378.1, AW078537.1, AW614912.1, AW577433.1, AA075477.1, W37973.1, AI870195.1, AW804484.1, AI906045.1, AI859339.1, AA622193.1, AW341927.1, W37755.1, AI500511.1, AA642656.1, AI492530.1, AI902944.1, AI500507.1, AA837842.1, AI865686.1, AA075671.1, AA131850.1, AA635989.1, AA587444.1, AW297239.1, AI285460.1, AW804456.1, AW821048.1, AI862178.1, AW793466.1, AI922648.1, AA937007.1, AA903286.1, AW373870.1, AI289455.1, AI251115.1, AA533156.1, AI084027.1, AW368079.1, AA627607.1, AW362711.1, AA532369.1, AA579973.1, AW815880.1, AA586545.1, AA917383.1, AW026936.1, AI138455.1, W72748.1, T29528.1, AI962517.1, AI795779.1, AI073859.1, AW797814.1, AW578905.1, AI371522.1, AA044192.1, AW861558.1, AW609821.1, AW797815.1, AI702366.1, AA471169.1, AI683358.1, AI528561.1, AW320458.1, AA424070.1, AA164464.1, AI989871.1, AW474440.1, AI683206.1, AA122936.1, W01896.1, AA880099.1, AA100063.1, AW211765.1, AI905784.1, AI905719.1, AA305909.1, AI811907.1, AW797793.1, AW629741.1, AA354725.1, H05350.1, AW817431.1, AA486849.1, F06345.1, AW239153.1, AA174655.1, AA347633.1, AA315174.1, AA487747.1, AL161639.4, AL160008.1, AL139416.1, AL138786.3, AC021689.2, AL355818.2, AC060233.1, AC021626.3, AC009729.4, AC026091.3, AC010872.4, AL138889.2, AP000831.1, AC013475.4, AC024551.3, AC024150.5, AC060776.2, AC063963.3, AC008373.6, AC010630.3, AC034166.2, AC025799.2, AC021399.3, AC025482.2, AC027133.1, AC022015.2, AC024303.2, AC018807.4, AC016720.4, AC016696.4, AC011210.3, AC016474.2, AC019071.2, AC010118.5, AC010743.4, AC017393.1, U82205.1, AL158849.7, AL356126.1, AL158070.2, AP001809.1,

SEQ ID NO. 116

20 NGO-Br-40

MK121/T3 5'

NM_004120.2, M55543.1, NM_002053.1, M55542.1, AK001823.1, NM_010259.1, M63961.1, M55544.1, M80367.1, NM_010260.1, AF109168.1, AF077007.1, AJ007970.1, U44731.1, NM_008620.1, M81128.1, X77129.1, Z95388.1, Z78546.1, AE003629.1, AE003472.1, AF085699.1, AC007980.1, AC005557.1, AL133283.9, AL008639.15, X92112.1, AL117265.1, AB015429.1, AF257304.1, AF257303.1, AE003459.1, AC007177.1, U69633.1, AL117319.1, AL031587.3, AW297239.1, AI962517.1, AI795779.1, AW320458.1, AI528561.1, AW368079.1, AA424070.1, AA122936.1, AA880099.1, AA100063.1, AW211765.1, AA305909.1, AW362711.1, AW629741.1, AA354725.1, AW815880.1, AW239153.1, AA347633.1, AA296543.1, AA709608.1, AA337079.1, AA911189.1, AA873192.1, F14838.1, AU076892.1, AA576498.1, AW106727.1, AA878690.1, W77927.1, AW428394.1, AA296485.1, AI906045.1, AA131850.1, AW820809.1, T83604.1, F14828.1, AA487747.1, AW669464.1, AW817439.1, AW609764.1, AA158924.1, AU076806.1, T75545.1, AW817360.1, AI980812.1, AI626652.1, AA848004.1, W13273.1, AI979397.1, AI529783.1, AI194988.1, AA889865.1, C05965.1, R54285.1, R54280.1, F06574.1, T34309.1, T32678.1, AW399587.1, AW398501.1, AA955194.1, C77542.1, AL161639.4, AL160008.1, AL139416.1, AC021689.2, AL138786.3, AL355818.2, AC021626.3, AC010872.4, AC024551.3, AC060776.2, AC063963.3, AC021399.3, AC025482.2, AC022015.2, AC007147.7, AC011210.3, AC016474.2, AC010118.5, AC020189.1, AC017393.1, U82205.1, AL356126.1, AC026877.4, AC064824.2, AC053519.2, AC027322.2, AC008494.7, AC016942.4, AC010289.3, AC019282.2, AC027620.3, AC023888.6, AC037442.1, AC026047.2, AC013693.3, AC021769.3, AC020577.1, AC019338.4, AC013718.3, AC015469.2, AC023823.2, AC013415.3, AC020230.1, AC021758.1, AC016495.1, AC013276.2, AC013485.1, AC012667.1, AC007515.1, AL355532.4, AL356008.1, AL354918.3, AL079302.3, AP002010.1, AP001807.1, AP001642.1, AP001638.1, AP001461.2, AP001324.1, AP001104.1,

SEQ ID NO. 117

NGO-Br-40

MK121/T7 3'

45 NM_004120.2, M55543.1, AK001823.1, NM_002053.1, M55542.1, NM_010259.1, M63961.1, M55544.1, M80367.1, NM_010260.1, AF109168.1, AF077007.1, AJ007970.1, AC022522.2, AC006487.7, AC005028.1, AL163226.2, AL121963.10, AP001681.1, AL035640.2, Y10720.1, AP001137.1, AC007236.4, AC018769.2, NM_007199.1, AF178650.1, AF113136.1, AC006241.1, U78259.1, AL163235.2, AL135749.2, AL109984.14, AP001690.1, AP000476.2, AB005234.1, AW614912.1, AI830004.1, AW001215.1, AA876142.1, AW058212.1, AI760378.1, AI439472.1, AW078537.1, AI983562.1, AA075477.1, AI870195.1, AA622193.1, AW341927.1, W37755.1, W37973.1, AA642656.1, AI492530.1, AI500507.1, AA837842.1, AI865686.1, AA587444.1, AA635989.1, AI285460.1, AI862178.1, AA937007.1, AA903286.1, AI289455.1, AA533156.1, AI084027.1, AA627607.1, AW373870.1, AA075671.1, AA532369.1, AA579973.1, AA917383.1, AW026936.1, AW793466.1, AI138455.1, T29528.1, AW577433.1, AI073859.1, AI371522.1, AI702366.1, AW609821.1, W01896.1, AI500511.1, AW468007.1, AI969542.1, AI859339.1, AI922648.1, AA586545.1, AA487528.1, AA315174.1, AI081732.1, AI075062.1, AA937600.1, AW449506.1, AA827350.1, AA131800.1, AA810201.1, AA650178.1, AI280597.1, AA424529.1, AW799191.1, AI910674.1, AA486850.1, AA837672.1, AA834863.1, AI905784.1, AI905719.1, AI861968.1, AI251115.1, AW817431.1, AW304126.1, AA564905.1, AA056488.1, AW363341.1, AW805514.1, AW796865.1, AW804484.1, AA424397.1, AI372935.1, AA587703.1, H05300.1, AI246407.1, AW820994.1, AW799183.1, W37972.1, AW821048.1, AW470713.1, AW363352.1, AW797212.1, AI760921.1, AI007134.1, AA175795.1, AA139382.1, AI386222.1, AI036133.1, AA153027.1, AA153021.1, AL161639.4, AL139416.1, AL160008.1, AC060233.1, AC026091.3, AC013475.4, AC025799.2, AC012246.3, AC016190.3, AC027133.1, AC022895.2, AL121573.10, AL355373.1, AC012264.8, AC022330.9, AC018461.18, AC026777.2, AC026737.3, AC026704.3, AC022418.3, AC010230.3, AC009051.5, AC009050.4, AC025073.2, AC027110.2, AC027630.4, AC027453.2, AC010159.7, AC027168.2, AC026590.2, AC015972.3, AC021149.4, AC025790.2, AC021688.2,

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SEQ ID NO. 118

5 NGO-Br-40

MK221/T3 5'

NM_004120.2, M55543.1, NM_002053.1, M55542.1, M80367.1, NM_010259.1, M63961.1, M55544.1, AK001823.1, NM_010260.1, AF109168.1, AF077007.1, AJ007970.1, U44731.1, NM_008620.1, M81128.1, X77129.1, Z95388.1, AC004930.1, NC_001143.1, AF085699.1, AC007980.1, AC005669.1, AL109935.39, AB038490.1, Z28127.1, X72016.1, 10 AB015429.1, AB020867.1, NM_001567.2, AC005917.2, AE003603.1, NM_013134.1, NM_006460.1, AC006312.8, AC004798.1, AC003111.1, AL161516.2, AL133304.2, AL049487.1, L36818.1, Y14385.1, AB021179.1, M29249.1, X93922.1, AI906045.1, AA131850.1, AW368079.1, AW362711.1, AW815880.1, W72748.1, AW297239.1, AW820994.1, AI902944.1, AW578905.1, AW861558.1, AA044192.1, H05350.1, AA486849.1, F06345.1, AW804456.1, W77927.1, AW821048.1, AW804484.1, AI969542.1, AI962517.1, AI683358.1, AA911189.1, AA164464.1, AW468007.1, 15 AI989871.1, AI528561.1, AW474440.1, AI683206.1, AA878690.1, AA487367.1, F07031.1, AW804431.1, AA487747.1, AI905784.1, AI905719.1, AA873192.1, AI922648.1, AW320458.1, AW211765.1, AA122936.1, AW820809.1, AW106727.1, AA174655.1, T83604.1, T75545.1, AW817439.1, AW609764.1, AI811907.1, AW817360.1, AA610352.1, F05698.1, AI859339.1, AW797814.1, AA471169.1, AA880099.1, AW577433.1, AI500511.1, AA044017.1, T87056.1, AI922921.1, AA848004.1, AA506001.1, AV362793.1, AA582749.1, W13273.1, AI651570.1, AI075062.1, AA690573.1, 20 AA665504.1, AA057242.1, AW665096.1, AW454822.1, AL135036.1, AW166154.1, AI811680.1, AI796944.1, AV046437.2, AA955194.1, AI383864.1, AI216433.1, AA928789.1, AA927260.1, AA909971.1, AA890309.1, T43327.1, AA719024.1, C77542.1, AA099506.1, N33318.1, N21081.1, R65420.1, H36685.1, H16325.1, T41892.1, Z44502.1, AL161639.4, AL160008.1, AL139416.1, AL138786.3, AL355818.2, AC021689.2, AL137851.3, AP000831.1, AC024150.5, AC034166.2, AC024303.2, AC016696.4, AC011860.3, AL158849.7, AL158070.2, AC036129.2, AC021630.4, 25 AC018354.6, AC012053.2, AC025975.2, AC027743.1, AC024047.2, AC026047.2, AC025865.2, AC013612.3, AC022854.3, AC022679.3, AC020753.2, AC018814.3, AC018497.4, AC023201.2, AC006295.8, AC013759.2, AC017228.1, AF166490.1, AL354770.2, AL356008.1, AL355990.1, AL161658.3, AL160006.2, AP001385.1, AP001157.1, AP000812.1, AP000593.1, AP000485.2,

30 SEQ ID NO.119

NGO-Br-40

MK221/T7 3'

NM_004120.2, M55543.1, AK001823.1, NM_002053.1, M55542.1, NM_010259.1, M63961.1, M55544.1, M80367.1, AC022522.2, NM_010260.1, AF109168.1, AF077007.1, AJ007970.1, AC006642.1, U28927.1, AL163226.2, AL049555.6, 35 AP001681.1, U40937.1, AP001137.1, AE002269.1, AC006241.1, AC004558.1, AF052729.1, AL163235.2, AP001690.1, Y10720.1, AP000476.2, AB005234.1, AB026654.1, M97632.1, AA876142.1, AW001215.1, AI830004.1, AW614912.1, AW058212.1, AI760378.1, AI439472.1, AW078537.1, AI983562.1, AA075477.1, AI870195.1, AW341927.1, AI492530.1, W37755.1, AA622193.1, W37973.1, AA642656.1, AI500507.1, AA837842.1, AI865686.1, AA635989.1, AI862178.1, AA587444.1, AI285460.1, AA937007.1, AA903286.1, AI289455.1, AA533156.1, AA627607.1, AI084027.1, AA532369.1, 40 AA579973.1, AW373870.1, AA917383.1, AA075671.1, AW026936.1, AI138455.1, AI073859.1, AW793466.1, T29528.1, AI702366.1, AW577433.1, AI371522.1, W01896.1, AW609821.1, AI500511.1, AW468007.1, AI969542.1, AI859339.1, AI922648.1, AA586545.1, AI280597.1, AA131800.1, AA487528.1, AA315174.1, AW796865.1, AI081732.1, AI075062.1, AW449506.1, AA937600.1, AI905784.1, AI905719.1, AI251115.1, AA827350.1, AW817431.1, AW799191.1, AI910674.1, AA810201.1, AA650178.1, AA486850.1, AW804484.1, AA424529.1, AA837672.1, AA834863.1, 45 AI861968.1, AW304126.1, AA564905.1, AA056488.1, AW805514.1, AW363341.1, AA424397.1, AW820994.1, AI372935.1, AI246407.1, AI400402.1, AA587703.1, AW799183.1, AW804508.1, W37972.1, AW821048.1, AW799555.1, AW797212.1, AI760921.1, AA947554.1, H05300.1, AI007134.1, AA175795.1, AA139382.1, AL161639.4, AL139416.1, AL160008.1, AC026091.3, AC013475.4, AC027453.2, AC016190.3, AC021149.4, AC027133.1, AC021688.2, AC016774.2, AC006883.2, AC022330.9, AC018461.18, AC022418.3, AC010230.3, AC009051.5, AC009050.4, 50 AC011784.3, AC027168.2, AC009625.3, AC026590.2, AC015972.3, AC016686.4, AC024403.2, AC013404.1, AC012545.1, AL139275.6, AL139274.6, AL354758.3, AL157714.3, AL160058.3, AL157818.2, AL158072.2,

SEQ ID NO.120

NGO-Br-40

55 MK241/T3 5'

NM_004120.2, M55543.1, NM_002053.1, M55542.1, AK001823.1, NM_010259.1, M63961.1, M55544.1, M80367.1, NM_010260.1, AF109168.1, AF077007.1, AJ007970.1, U44731.1, NM_008620.1, M81128.1, AC006112.2, X77129.1, Z95388.1, Z78546.1, AE003472.1, AC004969.1, AC005053.1, AC005061.2, AF085699.1, AC007980.1, AC005557.1, AL109935.39, AL133283.9, AL008639.15, X92112.1, AL117265.1, AB015429.1, AB020867.1, AF257304.1, AF257303.1, 60 AE003459.1, NM_013134.1, AC007177.1, AC004798.1, AC003111.1, AF003626.1, U69633.1, AL117319.1, AL034426.4, AL031587.3, U29614.1, M29249.1, AW297239.1, AW368079.1, AI962517.1, AW362711.1, AW815880.1, AI795779.1, AI528561.1, AW320458.1, AA122936.1, AA880099.1, AA424070.1, AW211765.1, AA100063.1, AA305909.1, AA354725.1, AI906045.1, AW629741.1, AA131850.1, AA347633.1, AW239153.1, AA709608.1, AA296543.1, W77927.1, AA911189.1, AA878690.1, AA873192.1, AA337079.1, F14838.1, AW106727.1, AA576498.1, W72748.1, AW428394.1,

- AI905784.1, AI905719.1, AW820809.1, AA487747.1, T83604.1, T75545.1, AW817439.1, AW609764.1, AA296485.1, AW817360.1, F14828.1, AW578905.1, AW861558.1, AW669464.1, AA158924.1, AU076892.1, AI626652.1, AI979397.1, AI922921.1, AI980812.1, AA848004.1, AA506001.1, AA582749.1, W13273.1, AI651570.1, AI529783.1, AI194988.1, AA889865.1, C05965.1, R54285.1, R54280.1, F06574.1, T34309.1, T32678.1, AW399587.1, AW398501.1, AW256377.1, AV046437.2, AA955194.1, C90826.1, C77542.1, AL161639.4, AL160008.1, AL139416.1, AC021689.2, AL138786.3, AL355818.2, AC021626.3, AC007223.1, AC010872.4, AC024551.3, AC060776.2, AC063963.3, AC034166.2, AC021399.3, AC025482.2, AC022015.2, AC024303.2, AC016696.4, AC011210.3, AC016474.2, AC010118.5, AC020825.2, AC019249.3, AC017393.1, U82205.1, AL356126.1,
- 10 SEQ ID NO.121
NGO-Br-40
MK241/T7 3'
NM_004120.2, M55543.1, AK001823.1, NM_002053.1, M55542.1, NM_010259.1, M63961.1, M55544.1, M80367.1, NM_010260.1, AF109168.1, AF077007.1, AJ007970.1, AC006487.7, AC005028.1, AF235093.1, AC022522.2, U97404.1,
- 15 AL163226.2, AL163210.2, AP001681.1, AJ010598.1, AL035640.2, AP001137.1, AE002269.1, NM_007199.1, AF113136.1, AC006241.1, U41556.1, AL163235.2, AL109984.14, Z82288.2, Z81102.1, Z70285.1, AP001690.1, U37429.1, Y10720.1, Z73419.1, AP000476.2, AB005234.1, AW614912.1, AI830004.1, AW001215.1, AA876142.1, AW058212.1, AW078537.1, AI760378.1, AI439472.1, AA075477.1, AI870195.1, AI983562.1, AI492530.1, AW341927.1, AA622193.1, W37755.1, AI500507.1, AA642656.1, AA837842.1, AI865686.1, W37973.1, AA635989.1, AI862178.1,
- 20 AA587444.1, AI285460.1, AA903286.1, AA937007.1, AI289455.1, AA533156.1, AI084027.1, AA532369.1, AA627607.1, AA579973.1, AA917383.1, AW026936.1, AI138455.1, AW373870.1, AI073859.1, AA075671.1, AI371522.1, AI702366.1, W01896.1, AW793466.1, T29528.1, AW577433.1, AW609821.1, AI922648.1, AA131800.1, AI280597.1, AI500511.1, AA487528.1, AA315174.1, AW468007.1, AI969542.1, AI859339.1, AW449506.1, AI081732.1, AI075062.1, AA937600.1, AA486850.1, AW799191.1, AI910674.1, AA837672.1, AA834863.1, AA827350.1, AA810201.1, AA650178.1,
- 25 AA424529.1, AW796865.1, AW304126.1, AI861968.1, AA564905.1, AA056488.1, AA586545.1, AW363341.1, AI246407.1, AA587703.1, AI372935.1, AW805514.1, H05300.1, AA424397.1, AW799183.1, AW470713.1, AI905784.1, AI905719.1, AW817431.1, AW797212.1, AI251115.1, AI400402.1, AI760921.1, AW804484.1, AW820994.1, AA947554.1, AI007134.1, AA175795.1, AA139382.1, AW821048.1, AA153021.1, AI386222.1, AA153027.1, W37972.1, AL161639.4, AL139416.1, AL160008.1, AC060233.1, AC026091.3, AC013475.4, AC025799.2, AC016190.3,
- 30 AC063948.3, AC012264.8, AC024102.5, AC018461.18, AC026737.3, AC026704.3, AC022418.3, AC027630.4, AC027168.2, AC026590.2, AC026549.2, AF235106.1, AC015972.3, AC034223.1, AC012148.2, AC025790.2, AC008248.2, AC009256.7, AC024403.2, AC020798.2, AC022290.2, AC013404.1, AC008031.3, AC012545.1, AL139275.6, AL139274.6, AL136380.2, AL355820.2, AL162421.1,
- 35 SEQ ID NO. 122
NGO-Br-40
MK255/T7 3'
NM_004120.2, M55543.1, AK001823.1, NM_002053.1, M55542.1, NM_010259.1, M63961.1, M55544.1, M80367.1, NM_010260.1, AF109168.1, AF077007.1, AJ007970.1, AC022522.2, AC006487.7, AL135749.2, AC005028.1,
- 40 AL162873.1, AE003782.1, AL163226.2, AP001681.1, AL035640.2, AP001137.1, AB011093.1, AF227618.1, AE002269.1, AC007347.3, NM_007199.1, AF113136.1, AC006241.1, AL163235.2, AC002094.1, AL133246.2, AL109984.14, Z49910.1, AP001690.1, X56844.1, Y10720.1, AP000476.2, AB005234.1, AI830004.1, AW001215.1, AA876142.1, AW058212.1, AI760378.1, AW614912.1, AI983562.1, AI439472.1, AW078537.1, AA075477.1, AI870195.1, W37973.1, AA622193.1, AI492530.1, AW341927.1, W37755.1, AA642656.1, AI500507.1, AA837842.1, AI865686.1, AA635989.1,
- 45 AA587444.1, AI862178.1, AI285460.1, AA903286.1, AA937007.1, AI289455.1, AA533156.1, AW373870.1, AI084027.1, AA075671.1, AA532369.1, AA627607.1, AA579973.1, AA917383.1, AW026936.1, AW793466.1, AI138455.1, AW577433.1, AI073859.1, T29528.1, AI371522.1, AI702366.1, AW609821.1, AI500511.1, AW468007.1, AI969542.1, AI859339.1, W01896.1, AA586545.1, AI922648.1, AI905784.1, AI905719.1, AI251115.1, AW817431.1, AA131800.1, AA487528.1, AA315174.1, AI280597.1, AI081732.1, AI075062.1, AW804484.1, AW449506.1, AA937600.1,
- 50 AA827350.1, AW799191.1, AI910674.1, AA810201.1, AA650178.1, AA486850.1, AA837672.1, AA834863.1, AA424529.1, AW304126.1, AI861968.1, AA564905.1, AA056488.1, AW820994.1, AW796865.1, AW804456.1, AW797814.1, AI902944.1, AW797815.1, AW797793.1, AW363341.1, AI372935.1, AA587703.1, AW805514.1, AI246407.1, AW821048.1, AA424397.1, H05300.1, AW799183.1, W37972.1, AW470713.1, AA175795.1, AA139382.1, AA153021.1, AI386222.1, AA153027.1, AL161639.4, AL139416.1, AL160008.1, AC060233.1, AC026091.3,
- 55 AC013475.4, AC008878.6, AC008373.6, AC010630.3, AC025799.2, AC016190.3, AC027133.1, AC011764.5, AC014685.1,
- SEQ ID NO.123
NGO-Br-40
MK303/T3 5'
NM_004120.2, M55543.1, NM_002053.1, M55542.1, AK001823.1, NM_010259.1, M63961.1, M55544.1, NM_010260.1, AF109168.1, AF077007.1, AJ007970.1, M80367.1, AC004930.1, AL135749.2, AP000350.1, NC_001143.1, NM_000379.1, AC002288.1, AC005669.1, AF077537.1, AL121654.1, U39487.1, U39646.1, Z28127.1, X72016.1, U06117.1, D10044.1, D11456.1, NM_001567.2, AC009890.12, AC010489.4, AC007048.4, AC005917.2, AC006832.2,

- AE003603.1, AE003479.1, AC005781.1, AC002526.1, NM_006460.1, AF202730.1, AC003661.1, AC008125.9, U40939.1, AC007504.3, AC007785.1, L21934.2, AC004596.1, AC000028.1, AC005837.1, U81031.1, AC005215.1, AC003047.1, AC002094.1, AL161516.2, Z81088.1, AL049487.1, L36818.1, X15209.1, X15750.1, Y14385.1, AB021179.1, AW820994.1, AW804484.1, AW468007.1, AI969542.1, AI902944.1, AW804456.1, AI922648.1, AW821048.1, AI859339.1, AI500511.1, AW577433.1, AI251115.1, AW797814.1, AW797815.1, AA471169.1, AA044192.1, AI683358.1, AW861558.1, AW578905.1, AA586545.1, AW001215.1, AW793466.1, AI989871.1, AI683206.1, AW474440.1, AI906045.1, AA164464.1, AA075671.1, AI830004.1, AI811907.1, AW797793.1, AW058212.1, AI983562.1, AA876142.1, H05350.1, AA131850.1, W72748.1, AI439472.1, AA486849.1, F06345.1, AW804431.1, AW373870.1, AA174655.1, AW817431.1, AI905784.1, AI905719.1, F23076.1, AA044017.1, AA610352.1, AA487747.1, AW609821.1, AI760378.1, AW078537.1, AA487367.1, AW614912.1, T87056.1, T29528.1, W37973.1, F07031.1, W37972.1, AA263171.1, AI492530.1, AA424397.1, AI865686.1, AA487528.1, AA294979.1, AW138402.1, AI386222.1, AI180927.1, AI036133.1, AA184762.1, AA153027.1, AA153021.1, AV362793.1, AA315174.1, F05698.1, AW815880.1, AW363341.1, AW362711.1, AA622193.1, AA057242.1, AI796944.1, T41892.1, AL161639.4, AL160008.1, AL139416.1, AL138786.3, AL355818.2, AC009158.3, AC024026.2, AL138782.5, AL138934.2, AL138889.2, AC024150.5, AC008373.6, AC010630.3, AC021689.2, AC048369.1, AC015803.3, AC019071.2, AC010743.4, AP001809.1,

SEQ ID NO. 124

NGO-Br-40

MK303/T7 3'

- NM_004120.2, M55543.1, AK001823.1, NM_002053.1, M55542.1, NM_010259.1, M63961.1, M55544.1, M80367.1, NM_010260.1, AF109168.1, AF077007.1, AJ007970.1, AC022522.2, AC006487.7, AL135749.2, AC005028.1, AF178650.1, AL163226.2, AP001681.1, AL035640.2, Y10720.1, AP001137.1, AC011282.3, AE002269.1, AC006142.1, NM_011369.1, NM_007199.1, AF113136.1, AF017152.1, AC006241.1, AF064699.1, AF069670.1, AF069669.1, AF057284.1, AL163235.2, AC002094.1, AL109984.14, AL139296.2, AL121871.8, AL161581.2, AL136132.15, U86532.1, AP001690.1, AL034567.1, X56844.1, AP000476.2, AB005234.1, L11794.1, L11777.1, X99948.1, AW001215.1, AW058212.1, AI830004.1, AA876142.1, AI760378.1, AW614912.1, AI983562.1, AI439472.1, AW078537.1, AA075477.1, AI870195.1, AA622193.1, W37973.1, AW341927.1, W37755.1, AA642656.1, AI492530.1, AI500507.1, AA837842.1, AI865686.1, AA635989.1, AA587444.1, AI285460.1, AI862178.1, AA937007.1, AA903286.1, AI289455.1, AA075671.1, AW373870.1, AA533156.1, AI084027.1, AA627607.1, AA532369.1, AA579973.1, AW793466.1, AW577433.1, AA917383.1, AW026936.1, AI138455.1, T29528.1, AI500511.1, AI859339.1, AI073859.1, AI969542.1, AW468007.1, AI371522.1, AI702366.1, AW609821.1, W01896.1, AA586545.1, AI251115.1, AI922648.1, AW804484.1, AW820994.1, AI905784.1, AI905719.1, AW817431.1, AA131800.1, AA487528.1, AA315174.1, AI280597.1, AI081732.1, AI075062.1, AW449506.1, AA937600.1, AA827350.1, AW799191.1, AI910674.1, AA810201.1, AA650178.1, AA486850.1, AA424529.1, AA837672.1, AA834863.1, AI861968.1, AW796865.1, AW304126.1, AA564905.1, AA056488.1, AW804456.1, AI902944.1, AW363341.1, AW805514.1, AW821048.1, AI372935.1, AI246407.1, AA587703.1, AW797815.1, AW797814.1, AA424397.1, W37972.1, AW799183.1, H05300.1, AW470713.1, AI007134.1, AA175795.1, AA139382.1, AA153021.1, AI386222.1, AA153027.1, AL161639.4, AL139416.1, AL160008.1, AC060233.1, AC026091.3, AC013475.4, AC068832.1, AC008373.6, AC010630.3, AC025799.2, AC016190.3, AC027133.1, AC018807.4, AC016720.4, AC012444.3, AC036136.2, AC023395.2, AC012264.8, AC022330.9, AC053477.2, AC023347.3, AC018461.18, AC027820.2, AC032036.2, AC026737.3, AC026704.3, AC022418.3, AC010369.5, AC010230.3, AC010396.3, AC008780.4, AC009051.5, AC009050.4, AC027780.2, AC027630.4, AC060807.1, AC027168.2, AC009614.4, AC017106.3, AC026590.2, AC027646.3, AC040964.1, AC015972.3, AC025790.2, AC011080.2, AC022247.2, AC024026.2, AC016686.4, AC024403.2, AC018408.1, AC013404.1, AC010874.2, AC012545.1, AL157771.3, AL139815.3, AL139275.6, AL139274.6, AL136380.2, AL355820.2, AL355886.1, AL354929.1, AL162453.4, AL096870.1, AL157818.2, AP002001.1, AP001985.1, AP001388.1, AP001241.1, AP001230.1,

SEQ ID NO. 125

NGO-Br-40

MK353/T3 5'

- NM_004120.2, M55543.1, NM_002053.1, M55542.1, AK001823.1, NM_010259.1, M63961.1, M55544.1, NM_010260.1, AF109168.1, AF077007.1, AJ007970.1, M80367.1, AC004930.1, NC_001143.1, NM_000379.1, AC005669.1, AL121654.1, U39487.1, Z28127.1, X72016.1, U06117.1, D10044.1, D11456.1, NM_001567.2, AC007048.4, AC005917.2, AC024882.1, AE003603.1, AE003479.1, NM_006460.1, AF202730.1, AC002565.1, AC008125.9, AC007785.1, AF125463.1, AL163210.2, AL135749.2, AL132880.2, AL161581.2, AL161516.2, AL117204.1, Z81088.1, AL078588.9, AL117193.1, AL034449.1, AL049487.1, AL034567.1, L36818.1, X15209.1, X15750.1, Y14385.1, AB021179.1, AW820994.1, AW804484.1, AI902944.1, AW468007.1, AI969542.1, AW804456.1, AW821048.1, AI922648.1, AI859339.1, AI500511.1, AW577433.1, AI906045.1, AI251115.1, AA131850.1, AW578905.1, AA044192.1, AW861558.1, AW797814.1, AW797815.1, AA471169.1, AI683358.1, AA586545.1, AW001215.1, AW793466.1, AA164464.1, AI989871.1, AW474440.1, AI683206.1, AA075671.1, AI830004.1, AI811907.1, W72748.1, AW797793.1, H05350.1, AW058212.1, AI983562.1, AA876142.1, AA486849.1, F06345.1, AI439472.1, AA174655.1, AW373870.1, AW804431.1, AW817431.1, AA487747.1, F23076.1, AI905784.1, AI905719.1, AA610352.1, AW609821.1, AA044017.1, AI760378.1, AA487367.1, AW078537.1, W37973.1, F07031.1, AW614912.1, T29528.1, T87056.1, W37972.1, AI492530.1, AA263171.1, F05698.1, AI865686.1, AI386222.1, AI180927.1, AI036133.1, AA184762.1, AA153027.1,

- AA153021.1, AW815880.1, AW362711.1, AW400386.1, AV362793.1, AW363341.1, AI075062.1, AA487528.1, AA424397.1, AA315174.1, AA294979.1, AA057242.1, T41892.1, AL161639.4, AL160008.1, AL139416.1, AL138786.3, AL355818.2, AC021689.2, AL138889.2, AL136985.1, AC024150.5, AC024038.5, AC019071.2, AC010743.4, AP001809.1, AC009770.4, AC023395.2, AC036129.2, AC027820.2, AC035140.2, AC008373.6, AC010630.3, 5 AC008731.4, AC063979.1, AC017106.3, AC040911.1, AC024047.2, AC027362.1, AC012241.4, AC015975.3, AC006295.8, AC013759.2, AC017228.1, AC015394.1, AF166490.1, AC006916.1, AC006719.1, AL121796.4, AL353796.2, AL022594.18, AL035066.20, Z98858.1, Z98855.1, AL021573.1, AP001385.1, AP001157.1, AP000812.1, AP000593.1, AP000485.2,
- 10 SEQ ID NO.126
NGO-Br-40
MK451/T3 5'
NM_004120.2, M55543.1, M80367.1, NM_010259.1, M63961.1, M55544.1, NM_010260.1, AF109168.1, AF077007.1, AJ007970.1, NM_002053.1, M55542.1, AK001823.1, AC004930.1, AF085699.1, AC007980.1, AL109935.39, X77129.1, 15 Z95388.1, AB015429.1, AB020867.1, AC005103.3, NM_013134.1, NM_006460.1, U44731.1, AF047825.1, AC004798.1, AC003111.1, AB021179.1, M29249.1, AI906045.1, AA131850.1, AW368079.1, AW362711.1, AW815880.1, W72748.1, AW297239.1, AW820994.1, W77927.1, AI902944.1, AW861558.1, AW578905.1, AA878690.1, H05350.1, AA044192.1, AA486849.1, F06345.1, AI905784.1, AI905719.1, AI528561.1, AA911189.1, F07031.1, AI962517.1, AA873192.1, AW474440.1, AW820809.1, AA487747.1, AI989871.1, AA487367.1, AA164464.1, AI683358.1, AI683206.1, 20 AW320458.1, T83604.1, T75545.1, AW817439.1, AW609764.1, AW211765.1, AW817360.1, AA122936.1, AW821048.1, AW804484.1, AW804456.1, AW106727.1, AW804431.1, AI811907.1, AI922921.1, AA174655.1, AA848004.1, AA506001.1, AW468007.1, AV362793.1, AA582749.1, W13273.1, AI651570.1, AA880099.1, AW665096.1, AW454822.1, AW166154.1, AI811680.1, AI796944.1, AV046437.2, AA955194.1, AI383864.1, AI216433.1, AA928789.1, AA927260.1, AA909971.1, AA890309.1, AA719024.1, C77542.1, AA514692.1, AA099506.1, N33318.1, N21081.1, 25 HI6325.1, Z44502.1, AL161639.4, AL160008.1, AL139416.1, AL138786.3, AC034166.2, AC016696.4, AL158849.7, AC036129.2, AC018354.6, AC012053.2, AC021689.2, AC024047.2, AC026047.2, AC024303.2, AC020883.2, AC006295.8, AF166490.1, AL356008.1, AL161658.3,
- 30 SEQ ID NO.127
NGO-Br-41
MK264/T3 5'
NM_004602.1, AF061941.1, AF061940.1, AF061939.1, AF061938.1, AJ132258.1, NM_011490.1, AF061942.1, NM_007344.1, X83973.1, AC004585.1, NM_014865.1, NM_014393.1, AC004002.1, AC007542.2, AF038608.1, AC006064.9, U32712.1, AL121877.13, Y19062.1, AK002152.1, AK001576.1, X67320.1, AB015752.1, M31229.1, 35 L04287.1, L03711.1, X68492.1, D63880.1, AC006142.1, AC010186.6, AC008078.11, AC004131.1, U46596.1, AL121775.2, AL096802.11, AL034345.3, X89870.1, AP000497.1, AW351909.1, AW403841.1, AW836710.1, AW320695.1, AA240112.1, AA218774.1, AA270608.1, AW351905.1, AW141293.1, AA135261.1, U69197.1, H17179.1, T31173.1, T31172.1, AW581619.1, AA153656.1, T74327.1, W28253.1, AL045575.1, AA191685.1, R95466.1, AA209495.1, T06248.1, AA025528.1, AA285302.1, AW366804.1, AW153775.1, AI958903.1, AJ244015.1, AI386266.1, 40 AI326431.1, AA562089.1, AA104976.1, W82776.1, AI353217.1, AA813637.1, AA700898.1, AV182864.1, AA918411.1, AA890493.1, U25927.1, AV398409.1, AV344143.1, AW123407.1, AA388686.1, AA156216.1, AL133174.11, AC063967.1, AC055879.1, AC011492.5, AC051627.3, AC068845.1, AC016960.6, AC015624.2, AC069023.1, AC027538.2, AC025512.2, AC022909.4, AC015944.3, AC009842.7, AC015989.3, AC015809.2, AC022403.3, AC023263.2, AC012595.3, AC012161.7, AC006739.1, AL355854.1, AL160399.2, AL157885.2, AP001397.1,
- 45 SEQ ID NO.128
NGO-Br-41
MK264/T7 3'
AJ132258.1, NM_004602.1, AF061941.1, AF061940.1, AF061939.1, AF061938.1, AL109755.14, NM_011490.1, AF061942.1, AL163222.2, AP001677.1, AP000946.3, AC006717.1, AF196972.1, AE001740.1, AC005318.1, Z81142.1, 50 AL031007.1, X06997.1, AC024077.2, AC007559.3, AC004988.2, AF134199.1, AC005520.2, AC006518.17, AF063866.1, AE001142.1, AC005544.1, U47023.1, AF076274.1, AC004051.1, AC005337.1, AC004100.1, AL161946.1, AL161499.2, AL050326.3, AL022722.1, AB019438.1, L00608.1, L00607.1, L06312.1, L06135.1, X57002.1, X60725.1, X57001.1, X69496.1, D37813.1, AB009052.1, Y10614.1, AI983007.1, AI802592.1, AI190464.1, U69197.1, AA889669.1, 55 AA157806.1, AI925182.1, AA846829.1, AA191622.1, AA609322.1, AA910279.1, AI333376.1, H16250.1, AA034036.1, AI557117.1, H11397.1, N45294.1, AW169049.1, AA907298.1, AI819766.1, N71642.1, AW263961.1, T15527.1, AI362641.1, AI472734.1, T89105.1, AI433939.1, AW183696.1, AA931425.1, AA594141.1, AA847184.1, AW105669.1, AA658226.1, AI419995.1, AW194431.1, AI340359.1, AA160287.1, N22707.1, AW576192.1, AI740524.1, AI017580.1, AL044093.1, AA858303.1, AA610333.1, AL044094.1, AI803720.1, AW166420.1, AW069464.1, AA903241.1, 60 AI864144.1, AI216722.1, AI921819.1, AI190687.1, AA074277.1, N51259.1, F10050.1, AA427905.1, AI814813.1, AA541311.1, H96787.1, AA904093.1, AA669068.1, AA206434.1, AI268881.1, AI150891.1, AI061243.1, AA747271.1, AA135198.1, AA593048.1, AA135111.1, AA207148.1, Z41528.1, AA135106.1, AW272442.1, AI963361.1, AW090441.1, AI262450.1, AA043331.1, T10553.1, T11277.1, AI138341.1, N66837.1, AI383429.1, N67513.1, N31181.1, D20243.1, AI868926.1, AA886271.1, AA578579.1, AW384062.1, AI160470.1, AA043332.1, AI687569.1, AI970644.1, T94064.1,

AI799396.1, AA620459.1, AA741223.1, AA090084.1, AW464265.1, AL133174.1, AC011492.5, AL158850.2, AC063967.1, AC068736.1, AC009429.3, AC067887.2, AC024935.8, AC026678.4, AC021057.3, AC021056.3, AC025928.2, AC015929.4, AC013364.7, AC025738.1, AC022049.3, AC017061.3, AC021682.1, AL158840.4, AL133284.12, AC026333.2, AC013625.3, AC009047.4, AC012215.3, AC027402.2, AC007383.3, AC055805.1, 5 AC019088.3, AC026588.2, AC015825.4, AC021186.2, AC022903.3, AC024732.2, AC015834.3, AC021011.2, AC022820.2, AC016930.5, AC010974.4, AC021980.1, AC009642.2, AC005282.1, AL139084.4, AL353709.1, AL354723.1, AP001394.1,

SEQ ID NO. 129

10 NGO-Br-42 combined

AC005069.2, AB011102.1, L23077.1, NM_013889.1, AF017806.1, AP001253.1, AE001788.1, AL133417.10, AF262044.1, AC008051.3, AF237670.1, AC021043.4, AF022974.1, L14730.1, AL031056.1, Z83313.1, AP001426.1, X01441.1, AB017192.1, AP000606.1, AB025611.1, AB018115.1, AL134426.1, AA972711.1, AW157207.1, AW770787.1, AW468156.1, AW473852.1, AI266259.1, AA599244.1, AI817665.1, AA837101.1, AI377803.1, AW163183.1, 15 AA527031.1, AA721095.1, N33849.1, AA167375.1, AI572106.1, AI251893.1, AI241041.1, H84943.1, AA279430.1, AW609920.1, AA764886.1, AI699744.1, AA725331.1, AI302964.1, AI567039.1, AW379942.1, AI593485.1, D52427.1, D55742.1, AI956843.1, AA210577.1, T10410.1, C01624.1, AA165991.1, AA825378.1, AI642382.1, AA611337.1, AW214633.1, AI551647.1, AW489266.1, AI467091.1, N85349.1, AA473146.1, AA167374.1, D55908.1, AA471246.1, AI956621.1, AI606224.1, AA726787.1, R98544.1, AA292113.1, AA279626.1, AW385669.1, W45824.1, AI810043.1, 20 H33984.1, R21996.1, AW416485.1, AV403226.1, AW260960.1, AW222072.1, AV227797.1, AW077780.1, AI820616.1, AV061748.1, AV042292.2, AI632719.1, AI423781.1, AI395491.1, AI014647.1, AA918760.1, AA829983.1, AA395972.1, AA363407.1, AA274077.1, AL139274.6, AL160258.3, AL137180.3, AL138875.3, AL137000.3, AC025451.3, AC023608.1, AC023276.3, AC068334.1, AC027596.2, AC008276.2, AC006451.2, AC019240.4, AC005308.6, AC010109.4, AC014418.1, AL138727.2,

25

SEQ ID NO. 130

NGO-Br-42

MK182/T3 5'

AC005069.2, AB011102.1, L23077.1, NM_013889.1, AF017806.1, AL133417.10, AC004485.1, AC008082.12, 30 AF022974.1, AE003628.1, AE003579.1, AE003420.1, AC012654.2, AC000096.13, AC005137.1, AC003063.7, AC016163.4, AC006317.3, AC004973.1, AC007649.12, AC005454.1, AL132976.2, AL122126.2, AC000392.1, AL121806.2, Z69838.1, AL022722.1, AL049571.1, U64875.1, AJ000521.1, D89336.1, AW163183.1, N33849.1, H84943.1, AA721095.1, AL134426.1, AI642382.1, AA611337.1, AA972711.1, AW609920.1, AW157207.1, AW770787.1, AA726787.1, AI266259.1, AI817665.1, AA837101.1, AA167375.1, N85349.1, AW473852.1, AI699744.1, AI251893.1, 35 AW468156.1, AI572106.1, AA825378.1, AA764886.1, AA599244.1, AA165991.1, AA279626.1, AI956843.1, AI593485.1, AI942680.1, AV403226.1, AW334920.1, AW214633.1, AV227797.1, AW077780.1, AI820616.1, AI014647.1, AL139274.6, AL137180.3, AL160258.3, AC067751.1, AC026297.2, AC022907.3, AC016212.3, AC023608.1, AC069075.1, AC068778.3, AC044835.2, AC023276.3, AC069019.1, AC021870.6, AC068334.1, AC008276.2, AC053489.1, AC021598.4, AC024718.3, AC019240.4, AC024646.2, AC005308.6, AC018580.4, AC024632.1, 40 AC018519.3, AL158166.6, AL158158.4, AL157393.1,

SEQ ID NO. 131

NGO-Br-42

MK182/T7 3'

45 AC005069.2, AB011102.1, L23077.1, NM_013889.1, AF017806.1, AL163231.2, AP001686.1, AP001253.1, AE001788.1, AF262044.1, AF237670.1, AC021043.4, AE003478.1, AF229187.1, AC004658.1, AL163276.2, AL118512.8, L14730.1, Z83313.1, AP001731.1, AP001426.1, X01441.1, AB017192.1, AP000163.1, AB025611.1, AP000021.2, NC_001136.2, AC009415.2, AE003824.1, AC004460.1, NM_011261.1, AC008072.3, AC005046.3, AF115517.1, AC005467.1, U24703.1, AE000943.1, AL049834.3, AL049546.3, Z93374.1, AL021939.1, Z74123.1, X51895.1, Z78583.1, D63520.1, 50 AW157207.1, AA972711.1, AW770787.1, AW468156.1, AI266259.1, AA599244.1, AI377803.1, AA527031.1, AI572106.1, AA279430.1, AA725331.1, AI302964.1, AI567039.1, AW379942.1, D52427.1, D55742.1, AI593485.1, AI956843.1, T10410.1, AA210577.1, C01624.1, AA165991.1, AW214633.1, AI551647.1, AW489266.1, AI467091.1, AA473146.1, D55908.1, AI606224.1, AW163183.1, R98544.1, AA292113.1, AW385669.1, W45824.1, AI810043.1, H33984.1, R21996.1, AW222072.1, AI632719.1, AI423781.1, AA829983.1, AA395972.1, AA274077.1, AA030373.1, W20048.1, AL139274.6, AL137180.3, AL160258.3, AL138875.3, AL137000.3, AC027490.3, AC025451.3, AC010432.4, 55 AL137249.6, AC069145.1, AC069071.1, AC018473.9, AC006451.2, AC027189.2, AC023844.2, AC021677.3, AC010109.4, AL135932.4, AL137013.3, AC041025.2, AC012211.3, AC027600.1, AC024254.2, AC024026.2, AC023153.2, AC012369.2, AC018873.1, AF188032.1, AL139418.1, AP001813.1,

60 SEQ ID NO. 132

NGO-Br-42

MK203/T3 5'

AC005069.2, AB011102.1, L23077.1, NM_013889.1, AF017806.1, AC016678.4, AE003694.1, AE003528.1, AF063866.1, AP000606.1, AB018115.1, AC016749.4, AC019209.3, AE003706.1, AE003579.1, AE003462.1, AF240628.1,

AC011284.3, AF224669.1, AC006317.3, AC005534.2, AC003037.1, U70823.1, AC004642.1, AL163224.2, AL049588.11, AL161516.2, AL161514.2, AL117386.1, AL078599.19, AL035693.19, Z81089.1, Z69838.1, Z95329.1, AL022722.1, AL035090.10, AP001679.1, AL049571.1, U64875.1, AJ000521.1, AL049482.1, L33820.1, L33819.1, AP001251.1, M76616.1, X61589.1, D89336.1, AP000001.1, AL134426.1, AW473852.1, AA837101.1, AI817665.1, AA721095.1, 5 AA167375.1, AI251893.1, AW609920.1, AI241041.1, AA764886.1, N33849.1, AI699744.1, H84943.1, AW163183.1, AA825378.1, N85349.1, AI642382.1, AA611337.1, AA279626.1, AV424771.1, AW416485.1, AW260960.1, AV061748.1, AV042292.2, AL139274.6, AL160258.3, AL137180.3, AC026297.2, AC025494.2, AL109926.2, AC027596.2, AC020987.4, AC023957.3, AC016187.4, AC062033.1, AC025104.2, AC025526.2, AC022744.2, AC024632.1, AC022691.1, AC009818.4, AC010204.8, AC008250.15, AC020418.1, AC009588.4, AC012259.2, AC014418.1, 10 AC007692.3,

SEQ ID NO. 133

NGO-Br-42

MK2410/T3 5'

15 AC005069.2, AB011102.1, L23077.1, NM_013889.1, AF017806.1, AC016678.4, AE003694.1, AF063866.1, AL049874.3, AP000606.1, AB018115.1, NC_001134.1, AC016749.4, AE003831.1, AE003528.1, AC011284.3, AF224669.1, U91318.1, AC006317.3, AC006004.1, AC005534.2, AC006221.1, U17503.1, U70823.1, AL049588.11, AL133512.10, Z69838.1, Z95329.1, AL035090.10, L33820.1, L33819.1, Z36160.1, X76053.1, AB020865.1, M76616.1, X61589.1, AP000001.1, AL134426.1, AW473852.1, AA837101.1, AI817665.1, AA167375.1, AI241041.1, AI251893.1, AA721095.1, 20 AW609920.1, AA764886.1, AI699744.1, AA825378.1, N85349.1, N33849.1, AA167374.1, AA471246.1, H84943.1, AI956621.1, AW163183.1, AI642382.1, AA611337.1, AV042292.2, AW646457.1, AW642567.1, AW416485.1, AW260960.1, AV061748.1, AI395491.1, AL139274.6, AL160258.3, AL137180.3, AL139223.2, AC016904.2, AC026297.2, AC025494.2, AC016469.4, AC012219.3, AC020987.4, AC023957.3, AC016187.4, AC025104.2, AC009818.4, AC010204.8, AC008250.15, AC020418.1, AC012259.2, AC007692.3, AL157389.3, AC037489.2, 25 AC015846.3, AC037434.2, AF267167.1, AC023156.3, AC010543.4, AC009128.5, AC007716.2, AC009547.3, AC010902.3, AC019171.3, AC008271.3, AC018797.3, AC062007.1, AC026829.2, AC025656.2, AF235099.1, AC026225.2, AC025660.2, AC009562.5, AC021619.3, AC016667.2, AC007413.4, AC007330.5, AC012182.3, AC025348.1, AC010894.3, AC011564.3, AC014418.1, AC013270.2, AC014124.1, AC010826.2, AC007414.4, AL162579.4, AL161647.5, AL157779.4, AL136311.3, AL355312.3, AL354893.3, AL136319.7, AL354711.1, AL157836.3, 30 AL122125.1, AP001448.1, AP001023.1, AP000813.1, AP000675.1, AP000624.1,

SEQ ID NO. 134

NGO-Br-42

MK2410/T7 3'

35 AC005069.2, AB011102.1, L23077.1, NM_013889.1, AF017806.1, AL163231.2, AP001686.1, AP001253.1, AF262044.1, AF237670.1, AC021043.4, AE003478.1, AF229187.1, AC008072.3, AC004658.1, AL163276.2, AL118512.8, L14730.1, Z83313.1, AP001731.1, AP001426.1, X01441.1, AB017192.1, AP000163.1, AB025611.1, AP000021.2, NC_001136.2, AC009415.2, AC004460.1, AC005046.3, AF115517.1, AL049834.3, AL049546.3, Z93374.1, AL021939.1, Z74123.1, D00702.1, X51895.1, Z78583.1, AW157207.1, AA972711.1, AW468156.1, AW770787.1, AI266259.1, AA599244.1, 40 AI377803.1, AA527031.1, AI572106.1, AA279430.1, AA725331.1, AI302964.1, AI567039.1, AW379942.1, D55742.1, T10410.1, D52427.1, AI593485.1, AI956843.1, C01624.1, AA210577.1, AA165991.1, AW214633.1, AI551647.1, AW489266.1, AI467091.1, AA473146.1, D55908.1, AW163183.1, AI606224.1, R98544.1, AA292113.1, AW385669.1, AW061815.1, H33984.1, R21996.1, AW728990.1, AW222072.1, AI810043.1, AI632719.1, AI423781.1, AA829983.1, AA030373.1, AL139274.6, AL137180.3, AL160258.3, AL138875.3, AL137000.3, AC027490.3, AC025451.3, 45 AC010432.4, AL137249.6, AC069145.1, AC019230.3, AC034127.2, AC024687.3, AC006451.2, AC027189.2, AC020695.3, AC009407.3, AC021677.3, AC023095.2, AC010109.4, AC019599.1, AL135932.4, AL137013.3, AC069071.1, AC024223.7, AC018473.9, AC012323.4, AC024272.2, AC044797.2, AC027215.2, AC034298.1, AC016350.3, AC016031.2, AC027600.1, AC024254.2, AC024026.2, AC011272.3, AC023153.2, AC013409.3, AC012369.2, AC011231.3, AC011619.2, AC016407.1, AF188032.1, AL121943.13, AL353786.2, AL161417.5, 50 AL139418.1, AP001813.1,

SEQ ID NO. 135

NGO-Br-42

MK245/T7 3'

55 AC005069.2, AB011102.1, L23077.1, NM_013889.1, AF017806.1, AL163231.2, AP001686.1, AP001253.1, AF262044.1, AF237670.1, AC021043.4, AE003478.1, AF229187.1, NM_011692.1, AC004901.1, U96760.1, AC004658.1, AL163276.2, AL118512.8, L14730.1, Z83313.1, X01441.1, AP001731.1, AP001426.1, AB017192.1, AP000163.1, AB025611.1, AP000021.2, AC005046.3, AC007887.8, AL032637.1, Z78016.1, AL031825.1, AL049546.3, AL031644.1, Z93374.1, AL021939.1, Z74123.1, Z68252.1, X51895.1, Z78583.1, AA972711.1, AW157207.1, AW468156.1, AW770787.1, 60 AI266259.1, AA599244.1, AI377803.1, AA527031.1, AI572106.1, AA279430.1, AA725331.1, AI302964.1, AW379942.1, AI567039.1, AI593485.1, D52427.1, D55742.1, AI956843.1, T10410.1, AA210577.1, C01624.1, AA165991.1, AW214633.1, AI551647.1, AW489266.1, AI467091.1, AA473146.1, D55908.1, AW163183.1, AI606224.1, R98544.1, AA726787.1, W45824.1, AI942680.1, H33984.1, R21996.1, AI632719.1, AI423781.1, AA829983.1, AA030373.1, AL139274.6, AL137180.3, AL160258.3, AL138875.3, AL137000.3, AC027490.3, AL137249.7, AC069145.1,

AC018473.10, AC069071.2, AC025451.3, AC010432.4, AC006451.2, AC020695.3, AC021677.3, AC010109.4, AC019599.1, AL135932.4, AL137013.3, AL138725.4, AC012014.5, AC012323.4, AC024272.2, AC044797.2, AC027215.2, AC016350.3, AC027600.1, AC024254.2, AC024026.2, AC016878.3, AC011272.3, AC012369.2, AF188032.1, AL157936.3, AL139418.1, AP001813.1, AP001198.1,

5

SEQ ID NO. 136

NGO-Br-43

AB023420.1, L12723.1, X67643.1, AF077354.1, NM_008300.1, D85904.1, X67641.1, X67642.1, X67640.1, AC011013.17, U23921.1, NM_014278.1, AB023421.1, NM_011020.1, D49482.1, AB001926.1, NM_006644.1, AF039695.1, AB003334.1, AB003333.1, D86956.1, Z47807.1, NM_013559.1, L40406.1, D67017.1, D67016.1, AB005279.1, AE003433.1, AC010072.5, AC004674.1, AL078621.19, AL096821.2, Z71263.1, Y13478.1, AC008545.3, AC011751.2, AC009489.3, AE003820.1, AE003518.1, M96150.1, AC007453.1, AC006409.2, AC006502.2, AC002350.1, AC003006.1, AL132793.24, AL121904.13, AL135879.1, AL132994.2, AL121790.2, AL133033.1, AJ251914.1, Z73907.1, AL008713.1, AL034348.5, AL034551.14, AL033522.1, AL008628.1, AP000555.1, AB028948.1, AL135032.1, AW609809.1, AW391888.1, AW609816.1, AW817219.1, AI567970.1, AW578992.1, AI925201.1, AW363570.1, AW085727.1, AI188118.1, AI560115.1, AI754819.1, AI956648.1, AA493400.1, AW754210.1, AA191559.1, AA173193.1, AW367717.1, AW583074.1, AI907727.1, AI627184.1, AW513086.1, AI952125.1, AW609784.1, AW192860.1, AW489091.1, AW578990.1, AA205597.1, AI274739.1, AI014766.1, AA913650.1, AW363562.1, AI230094.1, AI140781.1, AI375447.1, AI983708.1, W74245.1, AW613658.1, AA913187.1, AA633656.1, AA162193.1, AI678576.1, AW817504.1, AA518224.1, AA210820.1, AW819755.1, AA216635.1, AI866008.1, AA354293.1, AA874242.1, AA761335.1, AA103602.1, AW545353.1, AA227204.1, AW545094.1, AW537735.1, AA991908.1, AW819997.1, AW578928.1, AW262251.1, AI408846.1, AW542227.1, AA125191.1, AA437859.1, AA821679.1, AW754207.1, AA542289.1, AA121736.1, AA591244.1, AW861588.1, AI909282.1, N50726.1, AW582514.1, AI956869.1, AW196018.1, AW609842.1, AW372094.1, AI799801.1, AW817153.1, AW609769.1, AW582510.1, AW817315.1, AW371571.1, AW817164.1, AW817496.1, AW817372.1, AW582499.1, AW391901.1, AW381775.1, AA870633.1, AA498893.1, AA687763.1, AW817440.1, AW371552.1, AW371548.1, RI1513.1, AW817445.1, AI314009.1, AI760838.1, AC020834.2, AC015501.3, AC021286.3, AC022550.1, AL137142.8, AC048384.2, AC065723.1, AC063302.1, AC039237.1, AC034727.1, AC034094.1, AC025168.3, AC013883.1, AL135795.3, AL160402.2, AL121814.1, AC034304.2, AC021076.3, AC036128.2, AC068226.1, AC025689.3, AC067810.1, AC027184.2, AC017102.5, AC023692.2, AC018288.1, AL121956.4, AL138965.3,

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SEQ ID NO. 137

NGO-Br-43

MK132/T3 5'

AB023420.1, L12723.1, X67643.1, AF077354.1, NM_008300.1, D85904.1, NM_006644.1, AF039695.1, AB003334.1, AB003333.1, D86956.1, NM_014278.1, NM_011020.1, U23921.1, AB023421.1, D49482.1, AB001926.1, U81260.1, AI132792.1, NM_013559.1, AE003820.1, AE003518.1, AC007453.1, AC006409.2, U76309.1, AL121775.2, AL133033.1, AL034348.5, AL034551.14, AL008628.1, L40406.1, AP000555.1, AB028948.1, D67017.1, D67016.1, AF245116.1, AC008865.3, AC007171.4, AC006200.2, AC006624.1, NM_013513.1, AE003750.1, AE003571.1, AC011809.2, AC012380.1, AC011198.2, U78296.2, AF106589.1, Y14213.1, AL078594.36, Z70757.1, Z77657.1, AL049861.18, AL115647.1, AL113847.1, AL111874.1, U04056.1, U04055.1, U03487.1, AB005279.1, AB005275.1, U00035.1, M57719.1, L35933.1, X56682.1, M59962.1, AW578992.1, AW363570.1, AW609809.1, AW391888.1, AW609816.1, AW817219.1, AW367717.1, AW578990.1, AA191559.1, AW363562.1, AW583074.1, AL135032.1, AW609784.1, AI909282.1, AI907727.1, AW754210.1, AW817504.1, AA626524.1, T29047.1, AA370218.1, W26511.1, AA755774.1, AW817215.1, AA125191.1, AW609842.1, AW817153.1, AW609769.1, AW582510.1, AW582514.1, AW817164.1, AW817496.1, AW817440.1, AW817372.1, AW817318.1, AW817315.1, AW817234.1, AW582499.1, AW391901.1, AW381775.1, AW372094.1, AW371556.1, AW371553.1, AW371550.1, AW817445.1, AW817442.1, AW601252.1, AW582504.1, AW371571.1, AW371552.1, AW371548.1, AW817364.1, AW817319.1, AA543642.1, AA437859.1, AW371570.1, AW817432.1, AW372116.1, AW819755.1, AW371546.1, AW609859.1, AW609807.1, AW371549.1, AW609846.1, AW578928.1, AW609867.1, AW609856.1, AA518224.1, AW609844.1, AW384296.1, AI760838.1, AA870633.1, AA117945.1, AI956648.1, AW748834.1, AI827505.1, D29434.1, AA615363.1, AA445826.1, AJ396671.1, AW819997.1, W22433.1, AW839103.1, AA874242.1, AW754207.1, AA103602.1, AW125594.1, AA919208.1, AW366794.1, AW371561.1, AI314009.1, R54223.1, AW371568.1, AI567970.1, AW861588.1, AW229772.1, AA645750.1, AA212025.1, AA821679.1, AV312929.1, AW391883.1, AC020834.2, AL137142.8, AC027421.2, AC025860.2, AC055864.2, AC065723.1, AC063302.1, AC039237.1, AC034727.1, AC034094.1, AC022301.6, AC068812.8, AC012157.9, AC034304.2, AC009781.5, AC009321.5, AC023056.7, AC027672.3, AC025689.3, AC027184.2, AC016065.4, AC009899.5, AC010563.3, AC013243.4, AC018288.1, AC015160.1, AC005450.4, AL356425.1, AL356303.2, AL121589.12, AC002417.1, AL139108.2, AP001180.1,

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SEQ ID NO. 138

NGO-Br-43

MK132/T7 3'

AB023420.1, NM_008300.1, D85904.1, AF077354.1, X67643.1, L12723.1, NM_011020.1, U23921.1, D49482.1, AB001926.1, AC010072.5, Z71263.1, AC009489.3, AC024817.1, AE003641.1, AE003408.1, AC012039.10, AC004614.1,

- AF164299.1, NM_008229.1, AC006355.3, AF071221.1, AC007172.6, AC005856.1, AC005495.1, AC004671.1, U31758.1, AE001016.1, AL031853.1, AL023804.1, X59603.1, L39125.1, D01021.1, A1567970.1, A1925201.1, AW085727.1, A1188118.1, A1560115.1, A1754819.1, AA493400.1, AA173193.1, A1627184.1, AW513086.1, A1952125.1, AW192860.1, AA205597.1, A1274739.1, A1014766.1, AA913650.1, A1140781.1, A1375447.1, A1983708.1, AW613658.1, AA913187.1, AA633656.1, A1678576.1, AA210820.1, AA216635.1, A1866008.1, AA761335.1, AW545353.1, AA227204.1, AW754210.1, AW545094.1, AW537735.1, AA991908.1, AW262251.1, A1408846.1, AW542227.1, AW819755.1, AW819997.1, AW861588.1, N50726.1, A1956869.1, AW196018.1, A1799801.1, AW578928.1, AA687763.1, C76500.1, AW529607.1, R11513.1, AW754207.1, R54223.1, AA061925.1, C81619.1, AW604699.1, A1347806.1, AA558925.1, A1593463.1, AA179753.1, AA542420.1, AW682076.1, AU020108.1, W27793.1, C81004.1, AA180330.1, AA121181.1, Z18817.1, AA823019.1, A1911599.1, AW060626.1, R60452.1, AW583074.1, A1197516.1, AA935133.1, AU015665.1, AA671121.1, AW604696.1, AW366794.1, A1760838.1, N74649.1, AW071627.1, AA408319.1, AA407913.1, A1501198.1, AA799083.1, AA543635.1, AW213908.1, A1576267.1, AV165705.1, AA434598.1, AA703912.1, AW071628.1, AV294079.1, AW754208.1, N79564.1, AW371893.1, AA655993.1, R56469.1, A1569348.1, AA948300.1, A1655547.1, AV301839.1, AC048384.2, AC002518.1, AL160402.2, AC068975.1, AC026382.3, AC020551.2, AC021393.2, AV301839.1, AC048384.2, AC002518.1, AL160402.2, AC068975.1, AC026382.3, AC020551.2, AC021393.2, AC036128.2, AC021573.4, AC068383.1, AC066588.1, AC027012.2, AC018990.4, AC026061.2, AC021717.3, AC024037.2, AC015653.3, AC019002.3, AC022038.2, AC017901.1, AC006911.1, AL121834.8, AL160290.3, AL157819.2,
- 20 SEQ ID NO.139
NGO-Br-43
MK261/T3 5'
AB023420.1, X67643.1, L12723.1, NM_008300.1, AF077354.1, D85904.1, X67641.1, X67642.1, AC011013.17, U23921.1, NM_014278.1, AB023421.1, NM_011020.1, D49482.1, AB001926.1, AL132776.11, AL078621.19, Y13478.1, AC011751.2, AC009489.3, AC006502.2, AC002350.1, AC003006.1, AL135879.1, AL121790.2, AC007244.2, AC019183.3, AC010361.3, AC011292.2, AF248484.1, NM_013559.1, AC004459.1, AC003984.1, AC002460.1, AC004612.1, AC004822.1, AC006322.2, AC004988.2, AC005050.2, AC008173.2, AC004772.1, AC005406.2, AC006559.6, AC009248.6, AC008071.2, AC007794.1, AF101874.2, AF064254.1, AC003689.1, AC003678.1, AF068862.1, AC004075.1, AC004043.1, U01882.1, AL163207.2, Z72001.1, AL160192.2, AL049555.6, AL078595.12, U50871.1, AL035661.16, AL080316.8, AL050334.12, AL109854.10, AL096802.11, Z68873.1, AL031000.1, AL023806.1, Z97987.1, Z98748.1, Z84477.1, AL021307.1, L40406.1, AP001065.1, D67017.1, D67016.1, W74245.1, AA121736.1, AA542289.1, AA591244.1, AA498893.1, AA354293.1, AA162193.1, A1314009.1, AW489091.1, N85657.1, A1956648.1, A1230094.1, R56974.1, AW861596.1, AV226442.1, AV226379.1, AA063966.1, AA821679.1, AA896038.1, AL135032.1, AA874242.1, AW578931.1, AW578926.1, AA103602.1, AA518224.1, AA499765.1, AA385978.1, AV320109.1, AA121221.1, AV226463.1, H93522.1, AA247166.1, W20649.1, A1956324.1, AW385268.1, AW385266.1, A1396671.1, AW502280.1, AW501910.1, AW501774.1, AW274501.1, AU037061.1, A1085867.1, AA747312.1, AA102000.1, H23069.1, H10565.1, AC020834.2, AC015501.3, AC021286.3, AL355143.4, AC025168.3, AC016767.3, AL353608.2, AL135795.3, AC036128.2, AC010814.5, AC017022.3, AC022968.2, AC022760.2, AC009875.2, AL353625.2, AL121956.4, AP001587.1, AC021053.7, AC018474.9, AC034305.2, AC068992.3, AC040969.2, AC040965.2, AC040960.2, AC023410.3, AC023538.2, AC026698.3, AC025182.2, AC024569.2, AC022433.3, AC022430.3, AC022135.3, AC008773.6, AC008968.4, AC010234.3, AC011346.3, AC008673.6, AC021595.3, AC062017.2, AC023116.4, AC010133.2, AC058804.1, AC018978.5, AC040961.1, AC026493.3, AC021464.2, AC023858.2, AC021948.3, AC018443.5, AC016763.5, AC021208.3, AC015823.3, AC022039.2, AC023560.2, AC009666.4, AC024010.2, AC010895.3, AC012669.2, AC021319.1, AC012502.2, AC013259.1, AL139375.7, AL355345.2, AL139803.7, AL136087.6, AL158147.4, AL354875.3, AL138702.5, AL353151.2, AL162492.3, AL034378.2, AP001986.1, AP001828.1,
- 50 SEQ ID NO.140
NGO-Br-43
MK2912/T3 5'
AB023420.1, X67643.1, L12723.1, AF077354.1, NM_008300.1, D85904.1, X67641.1, X67640.1, AC011013.17, X67642.1, U23921.1, NM_014278.1, AB023421.1, NM_011020.1, D49482.1, AB001926.1, AL078621.19, AL096821.2, Y13478.1, NM_006644.1, AC004003.1, AF039695.1, AF117829.1, AF069291.1, AC002350.1, AB003334.1, AB003333.1, D86956.1, L43098.1, L43082.1, AC010352.4, AC007730.2, AC007662.2, AF240629.1, AF123535.1, AC002124.1, AF130247.2, AC005228.1, AC009248.6, AF081491.1, AF081490.1, AF081489.1, AF081488.1, AF081487.1, AF165138.1, AF064254.1, AF112117.1, U96409.1, AC005900.1, AC004636.1, AC004472.1, U69258.1, AL163224.2, AL163206.2, AL161537.2, X15901.1, Y08502.1, Z68873.1, AL022727.1, AL022097.1, AL031073.1, AL035528.2, AP001679.1, AP000957.2, AW489091.1, A1230094.1, A1956324.1, A1956249.1, AA591244.1, A1316935.1, AW069322.1, AA498893.1, AW318627.1, A1506418.1, AA542289.1, AA840049.1, AA205624.1, A1314009.1, AA499765.1, AV320109.1, W74245.1, AA726333.1, AA408320.1, AA247166.1, AW755799.1, AW755396.1, AW568012.1, AW567990.1, AW397511.1, AW234798.1, AA162193.1, AW681906.1, AL045611.2, A1851924.1, AL044212.1, AL043449.1, AA793473.1, AA690112.1, AA675583.1, AA360776.1, AA183406.1, AA120371.1, AV131040.1, AV047607.2, AV047086.2, A1046570.1, AA499782.1, AA498000.1, AA144603.1, AA139245.1, AA138950.1, AA110497.1, AA062258.1, AA060083.1, H23069.1, H10565.1, R59827.1, R28864.1, AC020834.2, AC015501.3, AC021286.3, AC022550.1,

AC022089.4, AC010428.4, AC011403.2, AC025168.3, AC021755.4, AC016767.3, AL163541.6, AL353608.2, AL135795.3, AL163545.4, AL160031.4, AC026084.2, AC026562.3, AC051613.3, AC008483.4, AC046137.3, AC068226.1, AC016002.5, AC031979.1, AC015578.4, AC019235.2, AC019228.4, AC017102.5, AC008519.2, AC016281.2, AC135627.2, AL139823.2, AL137142.8, AL353625.2, AL121956.4, AL138965.3, AL136456.3,

SEQ ID NO. 141

NGO-Br-43

MK466/T3 5'

AB023420.1, X67643.1, L12723.1, AF077354.1, NM_008300.1, D85904.1, X67641.1, X67642.1, X67640.1, AC011013.17, U23921.1, NM_014278.1, AB023421.1, NM_011020.1, D49482.1, AB001926.1, AL078621.19, AL096821.2, Y13478.1, AL121904.13, AJ251914.1, AC010352.4, AC007662.2, NM_013559.1, AE003537.1, AC004492.1, AC009248.6, AC007388.3, AF064254.1, U96409.1, AC004636.1, AL121821.5, AL161537.2, Z48006.1, Z68873.1, AL022097.1, AL035528.2, L40406.1, M26221.1, D67017.1, D67016.1, AW489091.1, AL230094.1, AA591244.1, AA498893.1, W74245.1, AA542289.1, AI314009.1, AI956324.1, AA121736.1, AI956249.1, AI316935.1, AA162193.1, N85657.1, AW069322.1, AI506418.1, AV226442.1, AI956648.1, AA499765.1, AA354293.1, AV320109.1, AW318627.1, AA205624.1, AA063966.1, R56974.1, AV226379.1, AA247166.1, AA840049.1, AW385268.1, AW385266.1, AA726333.1, AV340213.1, AI870749.1, AV047607.2, AV047086.2, AI046570.1, AA747312.1, C39670.1, AA499782.1, AA498000.1, AA144603.1, AA139245.1, AA138950.1, AA110497.1, AA062258.1, AA060083.1, H23069.1, H10565.1, R59827.1, AC020834.2, AC015501.3, AC021286.3, AC025168.3, AC021755.4, AC016767.3, AL163541.6, AL353608.2, AL135795.3, AL163545.4, AL160031.4, AC026084.2, AC026562.3, AC064862.2, AC016002.5, AC019235.2, AC017102.5, AL353625.2, AL121956.4,

SEQ ID NO. 142

NGO-Br-43

MK691/T3 5'

AB023420.1, X67643.1, L12723.1, NM_008300.1, D85904.1, AF077354.1, X67642.1, NM_014278.1, AB023421.1, NM_011020.1, U23921.1, D49482.1, AB001926.1, NM_006644.1, AF039695.1, AB003334.1, AB003333.1, D86956.1, AE003433.1, AC004674.1, AC008545.3, AC011751.2, AC009489.3, NM_013559.1, AC006502.2, AC003006.1, AL132793.24, AL135879.1, AL121790.2, AL008713.1, L40406.1, Z47807.1, M38250.1, D67017.1, D67016.1, AC010879.2, AC012082.6, AC020943.5, AC006200.2, AF248484.1, AC009311.2, AC004459.1, AC004745.1, AC003984.1, AC002452.1, AC002461.1, AC004612.1, AC004741.1, AC004930.1, AC002519.1, AC008173.2, AC005406.2, AC006559.6, AC003666.1, AF101874.2, AC003689.1, AC003678.1, AC005393.1, AC004075.1, AC004043.1, U01882.1, U80460.1, AL160192.2, AL049555.6, AL035665.29, AL078595.12, U50871.1, AL050334.12, AL096802.11, Z97987.1, Z92844.1, Z98748.1, Z84475.1, AL009176.1, U41995.1, AB005275.1, Y15994.1, AB016880.1, AB020870.1, AI956648.1, AA354293.1, AL135032.1, AA162193.1, W74245.1, AA821679.1, AA121736.1, AA103602.1, AA874242.1, AA518224.1, AI907727.1, AA121221.1, AW861596.1, N85657.1, AA542289.1, AW582514.1, AW372094.1, AW817315.1, AW371571.1, R56974.1, AW817219.1, AW817496.1, AW817372.1, AW817364.1, AW817164.1, AW817153.1, AW609859.1, AW609846.1, AW609816.1, AW609809.1, AW609769.1, AW582510.1, AW582499.1, AW391901.1, AW381775.1, AW371552.1, AW371546.1, AA437859.1, AW609842.1, AW371550.1, AW817440.1, AW817432.1, AW817319.1, AW609867.1, AW609856.1, AW391888.1, AW384296.1, AW371549.1, AW371548.1, AW817445.1, AW817442.1, AW609844.1, AW371570.1, AW817504.1, AW371556.1, AW817234.1, AW371553.1, AW817318.1, AA870633.1, AA125191.1, AW609784.1, AW582504.1, AW372095.1, AA191559.1, W20649.1, AW601252.1, AA896038.1, AI314009.1, AA543642.1, AW372116.1, AA498893.1, AV226442.1, AW578931.1, AV226379.1, AW578926.1, AA063966.1, AA385978.1, AJ396671.1, AW371561.1, AI827505.1, D29434.1, AW748834.1, AA591244.1, AW371568.1, W26511.1, AW229772.1, H93522.1, AV226463.1, AA549649.1, AW577563.1, AL042714.2, AI656127.1, AI633338.1, AI267631.1, AI203278.1, AA714219.1, AA580845.1, AA311379.1, AW210124.1, X85639.1, AC020834.2, AC021286.3, AL137142.8, AC013883.1, AL133489.1, AL121814.1, AC069108.1, AC068732.1, AC021076.3, AC067810.1, AC010814.5, AC023692.2, AC009875.2, AP001587.1, AP001180.1, AC034305.2, AC068992.3, AC040960.2, AC026998.2, AC044809.2, AC023410.3, AC025752.4, AC022433.3, AC022430.3, AC022135.3, AC008961.4, AC008968.4, AC011346.3, AC008561.3, AC008539.3, AC021595.3, AC017100.3, AC010133.2, AC010810.3, AC009657.3, AC026824.2, AC027281.2, AC021548.3, AC011954.5, AC023858.2, AC015681.4, AC025411.2, AC021948.3, AC013321.4, AC025218.2, AC013368.4, AC011055.6, AC017082.3, AC015943.3, AC021208.3, AC015823.3, AC016421.4, AC013297.4, AC022039.2, AC023560.2, AC023034.2, AC025599.1, AC012451.3, AC021350.2, AC021319.1, AC007799.4, AC013759.2, AC011107.2, AC007914.1, AL355345.2, AL160407.4, AL157785.2, AL139344.4, AL355599.2, AL355332.1, AL353143.2, AL161913.2, AL353624.1, AL158819.2, AL133255.9, AL157759.2, AL158140.2, AL034378.2, AP001488.1, AP001336.1,

SEQ ID NO. 143

NGO-Br-44

MK062/T3 5'

AF210818.1, AF134894.1, AB014540.1, NM_009302.1, AF053974.1, AE003678.1, AE003692.1, AC004260.1, AC005244.1, AL162633.2, AL138996.2, AL049522.1, AL035603.11, AE003589.1, AE002906.1, AC006926.1, AC002080.1, U91322.1, AC006043.1, AC005082.2, AF128252.1, AF128251.1, AF128249.1, AF128247.1, AC005548.1, AC005269.1, U32723.1, AL022598.2, AL133391.5, AL121656.2, Z35601.1, AL034561.4, AL033530.1, U35657.1,

- K01711.1, AB027827.1, AB027454.1, M20865.1, J04355.1, Z66517.1, A1181303.1, AW824953.1, AW123265.1, AW504308.1, AW824368.1, AW425515.1, AJ392422.1, AW202793.1, AW029904.1, AW487421.1, AV070180.1, AU013359.1, AC025788.2, AC026250.3, AC011979.3, AC026628.2, AC009800.6, AC023126.2, AC014216.1, AC009539.5, AL160255.5, AL138790.2, AC055752.5, AC055875.2, AC053484.3, AC021515.3, AC024494.1, AC021857.2, AC010097.4, AC016475.1, AC012199.4, AC013013.1, AL031726.16, AL133259.23, AL355073.1, AL353152.2, AL137183.1, AP001852.1, AC024905.7, AC024890.7, AC008713.5, AC011376.2, AC008856.4, AC026958.2, AC024595.2, AC026259.3, AC025966.2, AC025818.2, AC022735.3, AC024387.2, AC022040.2, AC023375.2, AC017402.1, AC009610.1, AL356358.1, AL355293.2, AL008872.1,
- 10 SEQ ID NO.144
NGO-Br-44
MK062/T7 3'
AB014540.1, AF134894.1, AC004834.2, AC006538.1, Z97054.1, AF111168.2, AL109914.16, AL121586.28, AC002094.1, AC006457.3, AL031985.10, AC002400.1, U80017.1, AF030453.1, AL031846.2, Z95152.1, AC005031.1, AL049874.3, Z72006.1, AC007386.3, AC000353.27, AC005207.1, AC003002.1, AL160191.2, AL034429.1, AC004552.1, AC004195.1, AL078639.5, AF168787.1, AC002477.1, AC005796.1, AC005500.2, AP000689.1, AC005081.2, AC002492.1, AC004815.2, AC005049.2, AC006064.9, AC005839.1, AC002350.1, AL163292.2, AP001747.1, AC005412.5, AC003104.1, AL049569.13, AP000505.1, AP000045.1, AC011890.4, AC007225.2, AC005102.1, AL136295.2, Z85994.1, AL050321.8, AC005227.2, AC003663.1, AC008115.3, AC011311.11, AC005793.1, AL024507.7, AL096800.20, AL049795.20, AW467233.1, AA186857.1, AW572140.1, AW473996.1, AW327624.1, AI889579.1, AI049630.1, H68343.1, AW850230.1, AI733856.1, AA135761.1, AA583386.1, AW873261.1, AW833047.1, AI754421.1, AA838091.1, AA468923.1, AA176605.1, AW157005.1, AI452836.1, AI090377.1, AA152253.1, AI474127.1, AI192465.1, AI064786.1, AA721645.1, AI799569.1, AI283938.1, H47736.1, AW798093.1, AI340151.1, AA992126.1, AI762528.1, AI309943.1, AW769687.1, AW089625.1, AW008184.1, AA857812.1, AW167202.1, AA630854.1, AA298365.1, AI310343.1, AW589345.1, AI859906.1, AI249365.1, AA302978.1, AW674631.1, AW516080.1, AW243808.1, AW069227.1, AI634187.1, AI457313.1, AI431513.1, AW242031.1, AW328331.1, AL038936.1, AI446336.1, AA827383.1, AA502991.1, AA487569.1, AA130647.1, AW574899.1, AI815210.1, AI696878.1, AA642809.1, AA176257.1, AI336771.1, AI285493.1, AI797998.1, AI653515.1, AA612727.1, AA218631.1, AI791659.1, AI278972.1, H57439.1, AI065038.1, N38991.1, AA601218.1, AI362442.1, AI066711.1, AA832175.1, AI653776.1, AA604149.1, AI446623.1, AA877992.1, AW082104.1, AI962030.1, F29968.1, AI049845.1, AA287570.1, AA284247.1, AW852684.1, AA633981.1, AA443390.1, AI633294.1, AA594220.1, AA429197.1, AA429020.1, AA290878.1, AA569648.1, AC026250.3, AL356218.1, AC018751.22, AL159970.7, AC027272.2, AC008630.3, AL136222.3, AC008616.3, AC019157.4, AL161671.5, AC012306.3, AC023232.3, AC015795.3, AL135839.3, AC019268.3, AL355001.3, AC011771.3, AC013355.3, AC012652.3, AL158828.4, AC044797.2, AL158039.2, AF235092.1, AC024561.3, AC008379.5, AC009149.4, AL354720.3, AC027472.2, AL137849.2, AC009041.5, AC011423.1, AL355076.1, AC020922.5, AC011895.3, AC026051.3, AL161911.3, AC021016.3, AC025395.2, AC008026.2, AC008745.4, AC015920.4, AL138762.5, AP001462.1, AC011488.5, AC018557.4,
- 40 SEQ ID NO.145
NGO-Br-45
MK506/T3 5'
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- 60 SEQ ID NO.146
NGO-Br-46
MK283/T3 5'
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- AL121985.13, AB026643.1, J03902.1, AC007188.6, AC002461.1, AP000457.3, AB005240.1, AA485189.1, R20183.1, AW431383.1, F06553.1, AW431576.1, AI153796.1, AV249408.1, AL079586.1, AV295325.1, AV296868.1, AV304343.1, AV335031.1, AV251198.1, AA713956.1, AV323916.1, AV351047.1, R14337.1, AW242991.1, AA296993.1, AV318231.1, AV298138.1, AW820697.1, AV407971.1, AV407307.1, AW611599.1, AW571035.1, AW570959.1, AW570812.1, AW163609.1, AW162962.1, AI506067.1, T86264.1, AW775546.1, AV439780.1, AW696915.1, AW693997.1, AW690655.1, AW589802.1, AW470688.1, AW255547.1, AW243044.1, AW195535.1, AW135177.1, AI912938.1, AI823378.1, AI816820.1, AI809563.1, AI803416.1, AV146241.1, AI770033.1, AI766212.1, AI766190.1, AI632787.1, AI478418.1, AI280988.1, AI246187.1, AI242863.1, AI160538.1, AI143611.1, AI091619.1, AI055903.1, AI034050.1, AI032880.1, AI015057.1, AA988532.1, AA922855.1, AA863243.1, AA811866.1, AA731602.1, AA524142.1, AA375259.1, AA001674.1, W80645.1, W56179.1, W39715.1, W32984.1, W31210.1, R40471.1, AA524073.1, AL353899.3, AL133418.3, AL161423.4, AC010092.3, AL136366.4, AL049185.4, AC021804.3, AC005140.6, AC004153.5, AC022648.1, AC017725.1, AF181450.1, AC006858.1, AL157786.2, AC064811.2, AC027723.2, AF254982.1, AC025820.3, AC027691.1, AC018982.1, AL354653.2, AL049180.3,
- 15 SEQ ID NO. 147
NGO-Br-46
MK283/T7 3'
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- 20 SEQ ID NO. 148
NGO-Br-46
MK482/T3 5'
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- 30 SEQ ID NO. 149
NGO-Br-46
MK482/T7 3'
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- 35 116374.1, AB030181.1, AF227899.1, AF208045.1, AF214114.1, AF245512.1, AF083249.1, AC027657.1, S57162.1, S57160.1, S57153.1, AC006420.3, U23522.2, NM_002892.1, AC007032.2, AC004440.1, S66427.1, Z48784.1, AC002461.1, AC005207.1, AC004048.1, AL031595.4, AP001819.1, AA485189.1, R20183.1, AL079586.1, AW431383.1, F06553.1, AW431576.1, AW242991.1, AA296993.1, AI153796.1, AV249408.1, AV295325.1, AV296868.1, AV304343.1, AV335031.1, AV251198.1, AV323916.1, AA713956.1, AV351047.1, AV318231.1, AA743290.1, AW496257.1, AV298138.1, AW820697.1, AW611599.1, AW571035.1, AW570959.1, AW570812.1, AW162962.1, H34667.1, T86264.1, AW754057.1, AV439780.1, AW696915.1, AW693997.1, AW690655.1, AW341096.1, AW270194.1, AW207299.1, AV318321.1, AW057255.1, AW043594.1, AV146241.1, AI698675.1, AI698047.1, AI570113.1, AI506941.1, AI393132.1, AI361113.1, AI246187.1, AI222232.1, AA962426.1, AA926638.1, AA837710.1, AA829497.1, C68432.1, C57364.1, AA370189.1, C10349.1, W88641.1, N73528.1, H69420.1, H50563.1, H24328.1, H24314.1, H23256.1, F02811.1, C11969.1, AL133418.3, AL353899.3, AC011267.2, AL136366.4, AC020604.4, AC068607.1, AC008570.3, AC021804.3, AC022944.2, AC022648.1, AC017725.1, AL121987.2, AC064811.2, AC021183.2, AC027723.2, AC026384.2, AF254982.1, AC027412.2, AC009881.3, AC013653.2, AC018982.1, AL034557.7, AL049180.3,
- 40 116374.1, AB030181.1, AF227899.1, AF208045.1, AF214114.1, AF083249.1, AF245512.1, NC_001137.2, U18916.2, AC007032.2, L77119.1, AC005687.1, AP001073.1, AP000969.1, AC002038.1, AC007882.3, AC007188.6, AC009230.3, AC007379.2, AE003827.1, AE003758.1, AE003644.1, AE003410.1, AC002041.1, AC004161.1, AC018359.6, AC004827.1, AC004890.2, AC004896.1, AC009322.1, AC006352.3, AC006359.3, AC004671.1, U40947.1, AC005207.1, U00176.1, U67526.1, AL355921.1, AF004387.1, AL080287.1, AL050333.18, AL117353.6, AL034563.1, AL132769.1, U66528.1, Y00354.1, U33010.1, U33008.1, M18061.1, AP000391.1, AP000543.1, J05080.1, AL079586.1, AW242991.1, AA296993.1, AA743290.1, AA485189.1, AW496257.1, R20183.1, AI153796.1, AV318231.1, T61718.1, F06553.1, AV295325.1, AV249408.1, AV304343.1, AV296868.1, AV251198.1, AV335031.1, AV323916.1, AW431383.1, AW875017.1, AW875016.1, AW571035.1, AW570959.1, AW570812.1, T86264.1, AW696915.1, AW693997.1, AW690655.1, AW773470.1, AV439780.1, AW472410.1, AV351047.1, AW056097.1, AW021051.1, AI963428.1, AI741526.1, C93293.1, AA668233.1, C23844.1, W36281.1, T14884.1, AL133418.3, AC010092.3, AC019046.3, AC007990.2, AC023145.4, AC016789.4, AC011267.2, AL136366.4, AC017057.5, AC068607.1, AC008570.3, AC068444.1, AC068256.1, AC067904.1, AC021804.3, AC023200.2, AC016697.2, AP000742.1, AC019071.3, AC064811.2, AC068761.2, AC026273.5, AC021183.2, AC068541.2, AC026740.3, AC008480.3, AC027723.2, AF254982.1, AC010791.2, AC026897.2, AC016108.3, AC025610.2, AC024972.2, AC019110.3, AC024025.3, AC024315.2, AC007908.2, AC023202.2, AC023576.1, AC009209.5, AC010683.3, AC011231.3, AC009981.5, AC021671.1, AC009982.6, AC017924.1, AC014837.1, AL356288.1, AL034557.7, AP001017.2, AP001007.1, AP001109.1,
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SEQ ID NO.150

NGO-Br-46

MK712/T3 5'

- 5 NM_016374.1, AB030181.1, AF245512.1, AF178849.1, Y17968.1, AC004537.1, AL118523.15, AK000096.1, AL021396.5, AL118494.1, S51239.1, AB032988.1, NM_008671.1, NM_008665.1, NM_001978.1, AF004294.1, U28389.1, U28734.1, X92352.1, L19713.1, AC002039.1, AF222800.1, S79939.1, D86076.1, Z46939.1, D83650.1, D31729.1, NM_008253.1, NM_003449.1, AC004186.1, U59897.1, AF022465.1, U09825.1, U17837.1, AC007844.32, NM_005381.1, AF132047.1, AC006289.1, AE001393.1, AC004659.1, AF030001.1, AL035527.1, X86100.1, U15800.1, AB010266.1, 10 L04162.1, AK001314.1, AK000250.1, AK000221.1, AB015639.1, AB020693.1, AP000344.1, L08135.1, L22219.1, NM_003204.1, AC007870.3, D37887.1, X84060.1, L14750.1, L24123.1, X77366.1, U08853.1, NM_010238.1, AF069772.1, AC006925.6, AF045462.1, AF017349.1, AL121754.18, AL132977.1, AL009226.1, U14731.1, D89801.1, AB011480.1, D84418.1, NM_015866.1, NM_014977.1, NM_012749.1, AF124726.1, AF133520.1, AF019611.1, U17838.1, AL163217.2, U89340.1, U19361.1, AP001672.1, U12825.1, D45132.1, AB014570.1, AC018721.1, 15 NM_008252.1, AC002302.1, AF085279.1, AC006070.1, U46900.1, Z83117.1, Z46757.1, M15825.1, AW431576.1, AA485189.1, AW431383.1, W84569.1, W67770.1, AA262427.1, R20183.1, AW369401.1, F06553.1, AI036486.1, AV340693.1, AV249408.1, AV295325.1, AI153796.1, AV296868.1, AV304343.1, AV335031.1, AA713956.1, AV251198.1, R14337.1, AV323916.1, AV351047.1, AI102488.1, AJ397247.1, AW158536.1, AA960471.1, AL079721.1, AU060883.1, F08518.1, M79841.1, AW281090.1, AI573315.1, AV407435.1, AW561908.1, AW099610.1, AI931397.1, 20 AI505223.1, AI159593.1, AA939911.1, AA838901.1, AA413260.1, D22328.1, AI044390.1, AW366844.1, AI908284.1, H33616.1, R54825.1, AW531362.1, AW162962.1, AI746770.1, AI579779.1, AI579345.1, AI575698.1, AI558058.1, AI408526.1, AI408307.1, AW681502.1, AW398648.1, AU061751.1, AU060420.1, AU053145.1, AU053100.1, AA685125.1, AW682367.1, AW681399.1, AW681336.1, AW619893.1, AW553956.1, AW553928.1, AW550476.1, AW549664.1, AW548257.1, AW547813.1, AW546306.1, AW545571.1, AW545015.1, AW543191.1, AW542602.1, 25 AW541865.1, AW536650.1, AW536323.1, AW320463.1, AW320328.1, AV111141.1, AV071436.1, AI376890.1, AI183692.1, AI182809.1, AU015986.1, C85885.1, C85603.1, AA795177.1, AA636994.1, C80539.1, AA607084.1, AA606813.1, AA590440.1, AA420329.1, T52646.1, AL353899.3, AC040981.1, AC012588.5, AC023288.6, AC018745.2, AC068493.3, AC053536.2, AC025669.2, AC026017.2, AC026462.1, AC006279.6, AC007340.3, AC024173.1, AC020757.2, AC016876.1, AC005136.1, AL163051.1, AC026581.1, AC024111.6, AC002317.1, AL136382.3, 30 AL136998.12, AL355576.1, AL355366.1, AL158172.1, AC026532.2, AC034245.2, AC016569.3, AC068147.1, AC027275.1, AC021768.3, AC016171.4, AL121953.13, AL049796.27, AL133375.3, AP000448.1, AC068909.3, AC012055.6, AC034126.2, AC044806.1, AC019128.3, AC020879.2, AC017104.3, AC021627.2, AC020632.4, AC041041.2, AC021142.4, AC026163.2, AC015535.4, AC016989.4, AC020988.3, AC024625.1, AC015901.3, AL356459.1, AL157895.1, AP001488.1, AP001024.1, AC016142.6, AC020940.4, AC019028.3, AC009717.4, 35 AC023364.3, AC013334.6, AC022565.3, AC020509.1, AC017725.1, AC004123.1, AC005861.2, AL354874.1, AL034557.7, AC009361.17, AC015891.10, AC063968.1, AC027650.2, AC025364.2, AC012296.3, AC022310.2, AC023571.2, AC023284.1, AC009962.3, AC021444.1, AL035477.5,

SEQ ID NO.151

40 NGO-Br-47

MK265/T3 5'

- NM_004987.1, U09284.1, AK000906.1, AE003678.1, AF078907.1, AF035583.1, U41021.1, AE003528.1, NM_000888.1, AL137129.2, AL050403.13, Z69648.1, M35198.1, AC007380.3, AE003454.1, NM_008407.1, AC004300.1, AE000795.1, Z71186.1, X70393.1, Z99123.1, Z80360.1, X95584.1, AW504514.1, AI327306.1, AA299595.1, AA289280.1, AI862555.1, 45 AI609736.1, AA968535.1, AI608376.1, AA037783.1, AI948956.1, AI956192.1, AA201027.1, AI152133.1, AI195455.1, AI089674.1, AA198689.1, AA732465.1, AA766629.1, AA989985.1, H58225.1, AA970328.1, AW787078.1, AW787072.1, AI450546.1, AA799637.1, AW742584.1, AA510363.1, AA450826.1, AA504265.1, AA110054.1, AI854549.1, AI195654.1, AI986356.1, AI943339.1, AW142146.1, AA102210.1, AI593658.1, Z42656.1, AI722835.1, AI353353.1, H58562.1, AW493431.1, AI237400.1, AA848258.1, AA636357.1, AA220130.1, AW347458.1, AI464258.1, AI408319.1, 50 AW481822.1, AW417049.1, AW312785.1, AW140389.1, AA119018.1, R58438.1, AJ398975.1, AW017114.1, AI386040.1, AA066359.1, AI981121.1, AI262403.1, AA646588.1, AA358612.1, AJ392355.1, AA064613.1, AI986343.1, AA511616.1, AW140647.1, AI929976.1, AV203690.1, AV198544.1, AV194653.1, AV194457.1, AV187669.1, C48705.1, C48492.1, C48145.1, C45906.1, C41445.1, AA471768.1, D76144.1, AW216171.1, AA269965.1, AA069994.1, AA016593.1, T73549.1, AC010095.3, AC011919.3, AC013271.1, AC011922.2, AC010976.4, AC027815.1, AC012487.3, 55 AC014215.1, AC016057.3, AC016797.3, AC022102.3, AC016575.6, AC021017.3, AC020993.3, AC013658.3, AC024522.1, AC010066.5, AC014423.1, AL136985.1, AC026261.3, AC027627.3, AC008864.4, AC008740.3, AC037456.4, AC025781.5, AC025706.3, AC024453.2, AC018914.3, AC021788.2, AC023463.2, AC019902.1, AL022281.20, Z98874.1,

60 SEQ ID NO.152

NGO-Br-48

MK124/T3 5'

AJ251245.1, AC004890.2, NM_009477.1, D44464.1, AC007371.16, AL034423.18, AL096761.1, AE003806.1, AF022713.2, AF133262.1, AF133263.1, U69607.1, AC004287.1, U65480.1, AF007190.1, AL035420.15, AW630547.1,

- AI769091.1, T58810.1, AA403044.1, AW436458.1, AI713670.1, AI712879.1, AI060054.1, AI412971.1, AJ010977.1, AW318411.1, AW012719.1, AA817712.1, AA943539.1, AA404342.1, AW121356.1, AI837465.1, AI823387.1, AI877170.1, AL118479.1, AI325217.1, AA023318.1, AA020155.1, W34889.1, AI099015.1, W08125.1, R51103.1, AW820705.1, AA475225.1, AA411125.1, AA171085.1, AL160054.4, AC021561.3, AP001490.1, AC027461.1, AC027462.2, AC023571.2, AL355353.3, AC018714.3, AC016883.3, AC022244.2, AC027559.1, AC018671.5, AC016402.1, AL353782.3, AL161937.5, AL022335.6, AP001000.1, AC021874.12, AC021023.4, AC018352.8, AC018656.5, AC012674.7, AC022504.9, AC055882.3, AC018752.3, AC010396.3, AC008596.3, AC013747.5, AC068557.1, AC034137.2, AC024948.2, AC007944.2, AC022830.2, AC024504.2, AC011635.3, AC012378.5, AC021874.11, AC016346.2, AC021250.2, AC018352.7, AC020957.1, AC017056.3, AC020077.1, AC016510.1, AC012123.1, AL356217.2, AL122125.1, AL031301.1, AP001888.1, AP001123.1, AP000850.1,
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- SEQ ID NO.153
NGO-Br-48
MK124/T7 3'
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- AI251245.1, NM_006703.1, AF062530.1, AF062529.1, AL117352.12, AJ249395.1, Z98036.1, AC010305.3, AC006474.3, AC002098.1, AC000396.1, AL078603.4, Z66560.2, M20162.1, AE003687.1, AE003539.1, AE003452.1, AC005005.1, AC004466.1, AC005268.1, AF015725.1, AL163300.2, AL163268.2, Z73972.1, Z99714.2, Z83001.1, Z97200.1, AJ011930.1, AP001068.1, AB012242.1, AB008267.1, AJ229042.1, Z48305.1, X14710.1, AI270576.1, AA349855.1, H60027.1, AA639612.1, R25924.1, AW392280.1, AW450452.1, AI014725.1, AA092495.1, W58640.1, AW022648.1, AI179962.1, AW431718.1, N55875.1, AI178673.1, AW427283.1, R14767.1, AI179961.1, AW868962.1, D21042.1, AW062717.1, AW062693.1, AI654799.1, AI652271.1, AI493530.1, AI435022.1, AI289025.1, AI126256.1, AI086076.1, AI032793.1, AA838460.1, AA781029.1, AA643067.1, AA629918.1, AA594551.1, AA573873.1, AA505932.1, AA479474.1, AA447455.1, AA446652.1, AA256802.1, AA150300.1, AA148791.1, AA086458.1, AA030012.1, W05069.1, N51389.1, R34884.1, AI158210.1, AW785190.1, AV305650.1, AU080152.1, AI987624.1, AI810108.1, AI764741.1, AI607860.1, AI546326.1, AI388669.1, AU033961.1, AI144326.1, AI113962.1, AI020516.1, AA951467.1, AA736165.1, AA701889.1, AA700625.1, AA504833.1, AA404221.1, AA404687.1, AA159318.1, H84256.1, H34335.1, H05385.1, AC021561.3, AP001490.1, AC025405.2, AC011945.3, AL354740.4, AL137801.1, AC068548.2, AC027395.2, AC018358.6, AC068739.2, AC026022.2, AC021088.2, AC068386.1, AC020552.3, AC018966.3, AC007721.15, AC016427.3, AC015622.3, AC009703.2, AC005910.4, AC002320.1, AL161452.3, AP001257.1, AL022276.1, AC009522.3, AC063940.4, AC025005.2, AC016572.4, AC008513.6, AC027074.2, AC012184.3, AC016883.3, AC011794.4, AC009871.5, AC010966.2, AC015676.3, AC024237.3, AC018232.1, AC018272.1, AF165146.1, AC006171.1, AC004847.1, AL356461.1, AL159154.3, AL162399.3, AL133410.10, AL162589.1, AL136001.1, AP001078.1, AP000899.2, AP001029.2, AP001113.1, AL008875.1,
- SEQ ID NO.154
NGO-Br-49
MK4111/T3 5'
- NM_004349.1, S78158.1, D14821.1, D43638.1, D14289.1, D13979.1, X79990.1, NM_009822.1, X79989.1, D32007.1, S78159.1, D14823.1, AF018276.1, AF018275.1, AF018283.1, D14822.1, AF018274.1, NM_009824.1, AF038029.1, AB010420.1, AB010419.1, AF018277.1, AB013280.1, AF052215.1, S74096.1, NM_005187.2, AF069747.1, NM_005093.1, AF068266.1, AF052210.1, AF013970.1, AF039200.1, AF212198.1, AF076455.1, AL034421.4, AC007842.1, AF022978.1, AB037757.1, AC023838.1, AC004011.1, AC006208.3, AE001039.1, AC002297.1, AC001229.1, AL133445.2, AL049766.14, AL096843.11, AL008634.1, Z84466.1, AL022721.1, AJ005682.1, U01337.1, AJ005077.1, L24038.1, AP000385.1, X77694.1, H18342.1, AW659083.1, AL134801.1, H18378.1, R91340.1, AW409814.1, AA597034.1, AW411004.1, AI880924.1, AW047315.1, AW526016.1, AW319793.1, AW319604.1, AW125686.1, AW060692.1, AV127503.1, AI606504.1, AA996736.1, AI407074.1, AI176767.1, AI171652.1, AI152215.1, AI046358.1, AA914494.1, AA822901.1, AA674424.1, AA529559.1, AA261311.1, AA222118.1, AA222011.1, AA963424.1, W39519.1, N75171.1, R70443.1, AV170567.1, AA924939.1, AI169429.1, W89980.1, AA015563.1, AC015952.3, AC013551.1, AF181450.1, AC068674.1, AC011671.3, AC009149.4, AC021125.2, AL121906.12, AC031998.2, AC013552.4, AL158160.1, AC012485.4, AC009989.6, AC006431.8, AC021193.3, AC022029.3, AC009438.2, AC027023.2, AC019055.3, AC007779.2, AC015667.3, AC027146.1, AC021291.3, AC023300.3, AC023545.2, AC015598.3, AC023438.2, AC020713.2, AC016279.2, AC007936.1, AL109823.21, AL160211.1, AL135961.1, AP001892.1, AP001637.1, AP000798.1, AP000662.1,
- SEQ ID NO.155
NGO-Br-49
MK4111/T7 3'
- NM_004349.1, D14821.1, D43638.1, D14289.1, D13979.1, X79990.1, S78158.1, NM_009822.1, D32007.1, X79989.1, AF018282.1, AC007161.1, AC003006.1, AE000663.1, AC011494.2, AC012147.7, AC004846.2, AC005058.1, AC007630.3, AF109907.1, M13209.1, AL034365.1, Z70782.1, AL031176.7, S55844.1, X67119.1, X16144.1, X01978.1, K03329.1, J02070.1, K01729.1, M17293.1, AJ224792.1, AJ224790.1, D49508.1, AI420591.1, AI033811.1, H94855.1, AW411005.1, AI167424.1, AW409570.1, AI264845.1, AA904353.1, F02579.1, N75054.1, AU041415.1, AW192965.1, AA992855.1, R38996.1, AV162276.1, N86959.1, AA247686.1, AV240937.1, AJ078840.1, AV245662.1, F01701.1, AI080687.1, AV347330.1, N88058.1, AA463390.1, AA095305.1, AI825475.1, H46432.1, AW450741.1, AW063104.1,

AI723657.1, AI604144.1, AI574526.1, AA257797.1, AW859690.1, AW177930.1, AW849569.1, AW849241.1, AW575067.1, AW257554.1, AV332137.1, AV153186.1, AI476165.1, AI445297.1, AI445224.1, AI181996.1, AI116642.1, AA469797.1, AA469776.1, AA194741.1, AA125063.1, AC015952.3, AF181450.1, AC068674.1, AC010295.4, AC017222.1, AC008197.2, AL136968.4, AL096708.33,

5

SEQ ID NO.156

NGO-Br-49

MK571/T3 5'

10 NM_004349.1, S78158.1, D14821.1, D43638.1, D14289.1, D13979.1, X79990.1, NM_009822.1, X79989.1, D32007.1, S78159.1, D14823.1, AF018276.1, AF018283.1, AF018275.1, S74096.1, D14822.1, AF018274.1, NM_009824.1, AF038029.1, AF018277.1, AB010420.1, AB010419.1, AB013280.1, AF052215.1, NM_005187.2, AF018278.1, AF069747.1, NM_005093.1, AF068266.1, AF052210.1, AF013970.1, AF039200.1, AF212198.1, AF076455.1, AL034421.4, AC010285.4, AC007842.1, AF022978.1, AB037757.1, AC023838.1, AC004011.1, U91322.1, AC006208.3, AE001039.1, AC001229.1, AL133445.2, AL049766.14, AL096843.11, AL031682.1, AL008634.1, Z84466.1, AL022721.1, 15 AJ005682.1, U01337.1, AJ005077.1, L24038.1, AP000385.1, X77694.1, H18342.1, AW659083.1, AL134801.1, H18378.1, R91340.1, AW409814.1, AA597034.1, AW411004.1, AI880924.1, AW047315.1, AW526016.1, AW319793.1, AW319604.1, AW125686.1, AW060692.1, AV127503.1, AI606504.1, AA996736.1, AI407074.1, AI176767.1, AI171652.1, AI152215.1, AI046358.1, AA914494.1, AA822901.1, AA674424.1, AA529559.1, AA261311.1, AA222118.1, AA222011.1, AA963424.1, W39519.1, N75171.1, R70443.1, AW433933.1, AV170567.1, AI555661.1, AA924939.1, 20 AI169429.1, AA196015.1, AA120052.1, W89980.1, AA015563.1, AC015952.3, AC013551.1, AF181450.1, AC068674.1, AC011671.3, AC009149.4, AC021125.2, AL121906.12, AC031998.2, AC013552.4, AL158160.1, AC025418.5, AC010313.4, AC016533.5, AC023924.2, AC011094.2, AC027737.2, AC050049.1, AC038905.1, AC013648.3, AC012485.4, AC009989.6, AC012154.9, AC006431.8, AC021193.3, AC012626.4, AC009078.4, AC022029.3, AC009438.2, AC027023.2, AC019055.3, AC007779.2, AC026911.2, AC026958.2, AC015667.3, AC027146.1, 25 AC021291.3, AC023300.3, AC023545.2, AC015598.3, AC006404.20, AC023438.2, AC020713.2, AC016279.2, AC009878.3, AC007936.1, AL160211.1, AL135961.1, AP001892.1, AP000798.1, AP000662.1,

SEQ ID NO. 157

NGO-Br-49

30 MK571/T7 3'

NM_004349.1, D14821.1, D43638.1, D14289.1, D13979.1, X79990.1, S78158.1, NM_009822.1, D32007.1, X79989.1, AF018282.1, AE003739.1, AC007161.1, AC003006.1, AE000663.1, AC012147.7, AC004846.2, AC005058.1, AC007630.3, AL031176.7, S55844.1, X67119.1, X01978.1, AI420591.1, AI033811.1, H94855.1, AW411005.1, AI167424.1, AW409570.1, AI264845.1, AA904353.1, F02579.1, N75054.1, AU041415.1, AW192965.1, AA992855.1, 35 R38996.1, AV162276.1, N86959.1, AA247686.1, AV240937.1, AI078840.1, AV245662.1, F01701.1, AI080687.1, AV347330.1, AA463390.1, N88058.1, AI825475.1, AA095305.1, H46432.1, AW450741.1, AW063104.1, AI885714.1, AI723657.1, AI604144.1, AI574526.1, AA257797.1, AW859690.1, AW575067.1, AW257554.1, AV332137.1, AV153186.1, AI476165.1, AI445297.1, AI445224.1, AI181996.1, AI116642.1, AA469797.1, AA469776.1, AA194741.1, AA125063.1, AC015952.3, AF181450.1, AC068674.1, AC017222.1, AC008197.2, AL096708.33, AC011005.4, 40 AC024483.2, AC012431.5,

SEQ ID NO.158

NGO-Br-50

MK253/T3 5'

45 NM_013235.1, AF116910.1, AK001121.1, AE003484.1, AL135784.4, L33180.1, L22858.1, Z83744.1, L35905.1, X71415.1, AF178030.1, Z95126.1, Z98266.1, AB025632.1, X78287.1, AC008969.5, AC027659.1, AC024799.1, AC013453.1, AC007038.3, AC007591.2, AC005284.1, Y14344.1, AA543176.1, AW237908.1, AA153374.1, AA144562.1, AA114761.1, AA460045.1, AW834734.1, H34369.1, AA549506.1, AA623764.1, AA797275.1, AW246359.1, AW702080.1, AA083888.1, AA199399.1, AA461807.1, AW860954.1, AI681138.1, C72137.1, AW836479.1, 50 AW416148.1, AV141668.1, AI678836.1, AI035692.1, C84814.1, AA768917.1, AA722287.1, R66162.1, R59232.1, AC008768.4, AC008159.1, AC026712.3, AC008419.4, AC010348.3, AC008550.3, AC018857.3, AC013905.1, AC008035.8, AC046148.2, AC010243.3, AC016555.4, AC026300.2, AC012586.6, AC015725.3, AC009591.3, AC010897.3, AC016998.1, AC012338.2, AL136987.2, AC021874.12, AC021023.4, AC018916.6, AC012041.8, AC011312.5, AC055789.2, AC067752.2, AC026780.2, AC010457.5, AF260012.1, AC026167.2, AC011050.4, 55 AC011148.4, AC016099.3, AC026205.3, AC023780.2, AC023571.2, AC024598.2, AC020755.2, AC021874.11, AC020856.1, AC024159.1, AC006595.1, AC006788.1, AL355353.3, AL139143.4, AL138885.4, AL355482.1, AL354864.1, AL161639.4, AL160008.1, AP001280.1, AP001085.2, AP000577.1,

SEQ ID NO.159

60 NGO-Br-50

MK253/T7 3'

NM_013235.1, AF116910.1, AK001121.1, AC006349.3, AL023807.6, AC008082.12, AC008160.11, AF060568.1, AF016679.1, U51999.1, X52871.1, M15387.1, AE003826.1, AC007056.4, AF088189.1, AC006216.1, AF099810.1, AC002397.1, AE000092.1, AL163221.2, U96131.1, AL117672.3, AL049758.11, AL035427.17, AL022578.1, AP001676.1,

- D87952.1, AP000403.1, AW246572.1, AA827562.1, AA514488.1, AI190270.1, AL135673.1, AI539185.1, AA778031.1, AA083889.1, AW874309.1, AA255533.1, AW662264.1, AI539830.1, AA532881.1, FI9104.2, AA459956.1, AW701839.1, AA749416.1, AI972095.1, AI874853.1, AW656237.1, AW793352.1, AW793354.1, AA247961.1, AW246359.1, AW793373.1, AU042596.1, N66268.1, AA271691.1, AI630888.1, AW522844.1, AA255505.1, AI502808.1, AA384265.1, 5 AW438881.1, AA729375.1, AA364111.1, AW363733.1, AW638275.1, AA538198.1, AV084911.1, AA702934.1, AI940043.1, AW428205.1, AV008608.1, AW702080.1, AL134250.1, AI159057.1, AA711797.1, AA120508.1, T06791.1, AV319126.1, AA739069.1, AV319605.1, AV038838.1, U94841.1, AA461807.1, AW803473.1, AI937621.1, AI673094.1, AI105163.1, AA638281.1, AA559086.1, AA473595.1, AA331632.1, H87048.1, AC026712.3, AC008768.4, AC008159.1, AC068577.1, AC020880.2, AC021229.2, AC012557.7, AC021482.4, AC022782.2, AC024656.2, AC020742.2, 10 AC019262.3, AL354712.2, AL354656.1, AP000908.1, AC024898.7, AC009716.3, AC068132.2, AC020930.4, AC010393.4, AC010266.7, AC010500.4, AC034195.2, AC023478.2, AC024928.4, AC049149.1, AC021380.3, AC023761.2, AC016498.4, AC026219.1, AC026198.1, AC026188.1, AC025978.1, AC005653.8, AC017064.4, AC011981.3, AC022668.3, AC022335.6, AC022002.2, AC022989.2, AC021141.2, AC016397.4, AC009673.2, AC013573.2, AC017933.1, AC008031.3, AC010167.1, AF165425.1, AC007715.1, AL096868.7, AL353585.3, 15 AL160403.3, AL160281.3, Z82199.1, AL132638.1, AP001445.1, AP001194.1, AP001130.1,

SEQ ID NO.160

NGO-Br-50

MK496/T3 5'

- 20 NM_013235.1, AF116910.1, AK001121.1, AE003484.1, L33180.1, L22858.1, Z83744.1, L35905.1, X71415.1, Z98266.1, AC008969.5, AE003629.1, AC000370.1, AC013453.1, AC007591.2, AE001718.1, AC004673.1, AC005751.1, AC002995.1, AL031670.6, Z81133.1, AL035467.23, AA460045.1, AA153374.1, AA144562.1, AW246359.1, AA549506.1, AW834734.1, AA623764.1, AA083888.1, AA114761.1, AL134250.1, AA543176.1, AW702080.1, AA797275.1, AA199399.1, AW428205.1, AA461807.1, AA711797.1, AW237908.1, AA538198.1, AA120508.1, 25 AI987530.1, AI681138.1, C72137.1, AW836479.1, AW559878.1, AW416148.1, AU039592.1, R66162.1, R59232.1, AC026712.3, AC008768.4, AC008159.1, AC046148.2, AC013905.1, AC010190.7, AC063946.3, AC025265.5, AC010243.3, AC016555.4, AC026300.2, AC015725.3, AC010897.3, AL136987.2, AC021874.12, AC021023.4, AC011312.5, AC012114.2, AC067752.2, AC010457.5, AC010381.4, AC025546.3, AC009135.6, AC068121.1, AC067828.1, AC025700.3, AC018508.4, AC025039.3, AC022526.4, AC016099.3, AC021736.3, AC010785.3, 30 AC021242.3, AC023860.2, AC024598.2, AC021874.11, AC020856.1, AF230637.1, AC016906.3, AC015747.1, AC020115.1, AC007300.5, AC004387.1, AL353194.6, AL138885.4, AL355482.1, AL354933.1, AP001869.1,

SEQ ID NO.161

NGO-Br-51

MK071/T3 5'

- 35 NM_003137.1, U09564.1, NM_016795.1, AB012290.1, AJ224115.1, Z99128.1, NM_009274.1, U92456.1, AB006036.1, NM_003138.1, U88666.1, AF043288.1, AC005070.1, AE003811.1, AF133093.1, AF043289.1, AB017067.1, AC023279.2, AC005220.1, AL160231.2, AL023634.1, AB023037.1, D13447.1, AE003484.1, AF002725.1, AE000541.1, AE001458.1, AF052290.1, AL021127.2, AL021180.1, AL022311.5, AB035133.1, AB006605.1, AW611721.1, AA060080.1, 40 AA492926.1, AL048784.3, AW006865.1, AU051027.1, AL046120.2, AA382461.1, AW500688.1, AW637436.1, AW701629.1, AJ396085.1, AA864027.1, AA211241.1, AI605657.1, AW635365.1, AW422773.1, AW421817.1, AW128008.1, AI722256.1, AW629710.1, AW381192.1, AW153931.1, AI626169.1, N28924.1, AI595541.1, AI038250.1, AI854277.1, AI787785.1, AI599584.1, W92175.1, AA428487.1, N23469.1, AW701402.1, AW462697.1, AI848239.1, AI414590.1, AI184192.1, AA553654.1, AW149364.1, AW016345.1, AI869878.1, AI830963.1, AI808855.1, AI808450.1, 45 AI555245.1, AI248681.1, AI247996.1, AI200995.1, AI199780.1, AI127471.1, AI075315.1, AI032748.1, AI018413.1, AI018139.1, AI000892.1, AA573426.1, AA479899.1, W92176.1, N35218.1, H98745.1, AA537749.1, AI296396.1, W12836.1, AW668908.1, AW392218.1, AI810017.1, AA968079.1, AA062255.1, AW736509.1, AW705048.1, AW704786.1, AW277878.1, AW277356.1, AW277342.1, AV375020.1, AV293419.1, AV287373.1, AV284759.1, AV234361.1, AW099987.1, AW036092.1, AI960739.1, AV174923.1, AI794688.1, AV118805.1, AI703778.1, AI507200.1, 50 AA972378.1, AA891069.1, AA863700.1, AA086829.1, AL133507.3, AC022452.2, AC017471.1, AC022525.3, AC023305.2, AC022106.2, AC011540.2, AC010787.3, AC021963.3, AC023913.4, AC016956.6, AC060815.2, AC068798.4, AC024102.5, AC023158.4, AC020570.3, AC023052.13, AC025765.3, AC025178.3, AC022444.3, AC022423.3, AC008411.3, AC008803.3, AC023779.2, AC024479.3, AC037484.1, AC016985.4, AC019298.3, AC027165.1, AC009072.2, AC016956.5, AC013441.2, AC013907.1, AC008108.1, AL160162.4, AL133356.3, 55 AL157696.2, AL009027.1,

SEQ ID NO.162

NGO-Br-51

MK071/T3 5'

- 60 Z99128.1, NM_003137.1, U09564.1, NM_016795.1, AB012290.1, AJ224115.1, AJ005937.1, AE003588.1, AC004116.1, AL031534.1, AL137450.1, AL023534.1, AW594310.1, AW082913.1, AI672149.1, AI126291.1, AW338805.1, AA490202.1, AA629288.1, AW848261.1, AA921804.1, R78142.1, AI076709.1, AW510886.1, AW275479.1, AW376532.1, T77446.1, AA284106.1, R29335.1, AA323127.1, R78141.1, W25929.1, AW123035.1, AI648020.1, AA899108.1, AU024203.1, AU020306.1, N76402.1, N77083.1, AA383402.1, AW674276.1, AW275654.1, AW103361.1,

AW091907.1, AW039956.1, AW008221.1, AI799557.1, AI598063.1, AI458262.1, AA915976.1, AA373583.1, AA059466.1, W73010.1, N36259.1, N24536.1, H26379.1, AW727130.1, AW702067.1, AW489711.1, AW421443.1, AW144384.1, AV167622.1, AV060461.1, AI697622.1, AI630968.1, AI325483.1, AI235699.1, AI210173.1, AI152339.1, AI034064.1, AI006140.1, AA798365.1, AA764641.1, AA450512.1, AA408261.1, AA122933.1, AA097370.1, AA024303.1, W36820.1, W11581.1, W08677.1, D19317.1, D24037.1, AL157823.3, AP001449.1, AL139347.2, AC026566.1, AC018197.1, AC024107.9, AC021650.9, AC008810.4, AC026466.3, AC026959.2, AC023271.3, AC024193.2, AC009792.4, AC020730.2, AC021155.2, AF178220.1, AP000794.1,

SEQ ID NO.163

10 NGO-Br-52

MK111/T3 5'

NM_003373.2, NM_014000.1, M33308.1, NM_009502.1, L18880.1, J04126.1, Y00312.1, L13300.1, S52276.1, S52271.1, AF067624.1, AL163852.1, AL138646.2, AC007138.1, AF047564.1, U82828.1, AL161552.2, AL161493.2, AL161492.2, U55724.1, Z98946.15, AL080253.2, X52256.1, AC007347.3, AC002485.1, AF107675.1, AC005026.1, AC008170.2, AC007560.3, AF147259.1, AC004063.1, AL163290.2, AL132793.24, AL161506.2, AL049871.3, AP001745.1, AP001619.1, AP001800.1, X91233.1, AB033053.1, AL048129.1, AA853564.1, AA375439.1, AV441119.1, AA585825.1, AW202184.1, AW577790.1, AW498327.1, AV404553.1, AV402299.1, AU004063.1, AU004045.1, AU003308.1, AI042965.1, AJ003662.1, AC025425.4, AC021191.3, AC006874.1, AC025212.2, AC011797.4, AC025104.2, AC015687.3, AL354652.3, AP001925.1, AP001808.1, AP000838.1, AC024933.7, AC023598.10, AC022072.8, AC051642.2, AC015891.10, AC068973.1, AC055869.2, AC068886.1, AC025477.3, AC018753.3, AC008859.4, AC026557.2, AC068246.1, AC022993.3, AC012211.3, AC046149.2, AC012068.3, AC026824.2, AC026087.3, AC034111.1, AC025061.2, AC020672.3, AC012252.4, AC026566.1, AC018911.4, AC015938.3, AC018973.3, AC022041.2, AC023916.2, AC011298.2, AC021950.1, AF216674.1, AC013695.1, AF191252.1, AL118506.16, AL161442.7, AL139157.4, AL138744.7, AL136980.3, AL354744.1, AL354696.1, AL137022.7, AP001954.1,

SEQ ID NO.164

NGO-Br-52

MK111/T7 3'

NM_003373.2, NM_014000.1, M33308.1, AL121751.12, AC007237.3, AC005405.1, Z50070.2, AC006332.3, NM_005509.1, AE003635.1, AC006979.2, AF204929.1, AF185647.1, U80443.2, AC000104.1, AL138478.2, AL078605.30, AJ005821.1, D90900.1, AB017062.1, AL043388.1, AL048130.1, AW613219.1, AL042874.1, AL047646.1, AI564569.1, AW338462.1, AI871828.1, AW341948.1, AI744828.1, AI754173.1, AI889651.1, C06476.1, AI564600.1, AW189900.1, AI583605.1, AW316646.1, AA776250.1, AW268882.1, AW268623.1, AI833189.1, AA564112.1, AA486728.1, AA458903.1, AW067932.1, AW026609.1, AA284505.1, AI808349.1, AI041865.1, AA744683.1, AA744677.1, N35013.1, AI367320.1, AW070464.1, AA723251.1, AA478033.1, AI161355.1, AA521095.1, AI956152.1, AI753120.1, AA653613.1, AI890467.1, AA173528.1, AA160880.1, AA653144.1, W72421.1, AA031689.1, AI095313.1, AI243169.1, AA744691.1, N27658.1, AA909152.1, AI381956.1, AA548423.1, AI240491.1, AA705238.1, AA150688.1, W76280.1, H24935.1, AI290052.1, AI953995.1, AA099284.1, AI003089.1, AI041158.1, AA299485.1, H47593.1, R87481.1, H06272.1, AA670014.1, AI750559.1, AW081510.1, H62215.1, T92938.1, F32136.1, W15223.1, H28559.1, AA045285.1, H57205.1, AW438657.1, AA490932.1, R78919.1, AA165451.1, AI206471.1, AA370855.1, AI952389.1, AA853565.1, AW118302.1, AW193451.1, T92716.1, H51597.1, AA831147.1, H38452.1, AA776247.1, T23463.1, T93331.1, AI694888.1, H97605.1, T92712.1, AA904909.1, R62767.1, AC025425.4, AL110115.28, AL138753.3, AL139114.3, AC015970.4, AC010278.5, AC008883.3, AC008446.3, AC012583.3, AC021516.4, AC011944.3, AC024317.2, AL139042.3, AL162411.1, AL023673.1, Z81488.1, AC041006.2, AC036146.2, AC068429.1, AC068020.1, AC026458.3, AC024492.2, AC015873.2, AC022770.4, AC010579.8, AC025134.1, AC023828.1, AC011066.4, AC011750.3, AC019782.1, AC013663.1, AC010213.2, AC009339.1, AL096888.26, AL161671.5, AL161653.7, AL160172.4, AL109824.23, AL135901.4, AL162759.1, AL136301.4, AL136985.1, AL137785.2, AP000863.1, AP000784.1,

50 SEQ ID NO.165

NGO-Br-53

MK282/T3 5'

X98494.1, AL133363.1, AE002611.1, Z83848.1, AF036707.1, AF118145.1, AC002060.3, AF022981.2, AF125969.1, D87023.1, AC008757.5, AE003498.1, U76408.1, AC009303.2, AF197947.1, AF242181.1, AE003844.1, AE003477.1, NM_011241.1, AF098623.1, AF098622.1, AF098621.1, AF098620.1, AF098619.1, AF098618.1, AF098617.1, U48809.1, AF046092.1, AF046084.1, U53154.1, AF057293.1, AE000661.1, U20857.1, Y14591.1, AJ242625.1, Y18000.1, Y14592.1, D87010.1, AC010252.3, AC008174.2, AF216973.1, AF220200.1, AF030052.1, Z73905.1, U10577.1, U67889.1, AL031652.1, AK001686.1, AP000501.1, AB011164.1, AA848124.1, AW365568.1, T24602.1, AW365559.1, AA603307.1, AI844833.1, W33952.1, W75630.1, W64795.1, AV113531.1, AV113797.1, AV114982.1, AI709759.1, AW365540.1, AI137651.1, AI070777.1, AW376006.1, AI546038.1, C94041.1, AV294399.1, AI959638.1, AI793667.1, AI406906.1, L37652.1, AV427570.1, AV409781.1, AW638224.1, AW560695.1, AW517166.1, AJ398790.1, AW345759.1, AW187449.2, AV314465.1, AV312363.1, AW128487.1, AI994267.1, AV024242.1, AV020965.1, AI641607.1, AA388279.1, R90246.1, T75711.1, AV420624.1, AW703701.1, AW604496.1, AW579832.1, AW443988.1, AW373650.1, AW361293.1, AW361221.1, AL038706.1, C99888.1, AI384793.1, AA147878.1, W26394.1, T92366.1, T90227.1,

5 AC007881.3, AC007345.2, AC007342.2, AC009673.2, AC016033.2, AC025138.2, AC018348.1, AC023310.1, AC027794.1, AC026150.1, AC036148.2, AC022113.4, AC020980.3, AC016621.4, AC027472.2, AC018409.3, AC018491.7, AC014030.1, AC011402.5, AC026275.3, AC009792.4, AF178220.1, AC006844.1, AC027245.1, AC013451.7, AC012931.1, AC009682.3, AC023659.2, AC025303.1, AL355178.2, AC034214.3, AC027621.3, AC064793.1, AC025856.2, AC015454.3, AC022783.2, AC018510.3, AC015672.3, AC014497.1, AL353612.5, AL163151.1,

SEQ ID NO.166

NGO-Br-53

10 MK282/T7 3'

X98494.1, AF135002.1, AI760199.1, AI742680.1, AW384883.1, AI284853.1, AI222419.1, AA992199.1, AW044708.1, AI862023.1, AI681988.1, AI867639.1, AI955575.1, AA992130.1, AI087795.1, AI263606.1, AA025657.1, AA083314.1, AI094541.1, AA847842.1, AA731098.1, AA047545.1, AI420376.1, W80758.1, AA770202.1, AI357730.1, AW592097.1, AA909134.1, AW369791.1, AI271912.1, AA810790.1, N68965.1, AI806559.1, T97061.1, AI056034.1, AW591044.1, 15 AA668325.1, AA504113.1, AA347116.1, AW606827.1, AW608731.1, AI244315.1, AA837327.1, Z25156.1, AI809694.1, AA888598.1, H88801.1, F00393.1, AW130117.1, AI884600.1, AI679865.1, AI679289.1, AI386428.1, AI000365.1, AA162148.1, AW556570.1, AA213194.1, H89025.1, AI177638.1, T96950.1, AA881872.1, AV146345.1, AA916136.1, AW539498.1, AV077858.1, AI647220.1, AI326008.1, AA590060.1, C02251.1, AI406906.1, AW632369.1, AW532104.1, AA817668.1, AV218492.1, AA619205.1, AC007881.3, AC021225.3, AC027794.1,

20

SEQ ID NO.167

NGO-Br-54

MK123/T3 5'

25 AK001917.1, AF035606.1, NM_013232.1, U58773.1, NM_011051.1, U49112.1, AC008925.3, AC007790.1, AC004485.1, AC004025.1, AC004923.2, AC008078.1, AC002288.1, AE001146.1, AC000385.1, U73627.1, AC000389.1, AL078590.27, AL049839.3, Z73424.1, Z95397.2, U40412.1, X14938.1, U03396.1, AB020682.1, AB020863.1, D89223.1, AC010083.5, AF203377.1, AE003750.1, AE003637.1, AE003550.1, AC007514.5, AC010198.8, AC012039.10, AC004893.1, AC004128.1, AF090189.1, AC006207.5, AC005007.1, AC005891.1, AC002366.1, AL031664.1, AL161587.2, AL161577.2, AL133453.2, U22376.1, Z46267.1, Z97055.1, AL049649.4, AL049713.19, AL035246.13, 30 AL031177.1, AL023805.1, AL021879.3, AL031599.1, AL022198.1, AL109787.1, AL022604.1, U49956.1, AB012766.1, AB022220.1, L20858.1, AW439592.1, AW058001.1, AI982775.1, AI912340.1, AA825538.1, AW513884.1, AW074361.1, AI872206.1, AI798286.1, AI522238.1, AI758821.1, AW474823.1, AI572080.1, AA831357.1, AW337178.1, AI690445.1, AI360561.1, AA775261.1, AI140796.1, AA835492.1, AI361820.1, AW004890.1, AA100279.1, AI277190.1, AW517943.1, AI917776.1, AI469550.1, AI015234.1, AA581345.1, AI689240.1, AI744762.1, AW769512.1, D20022.1, AA122332.1, 35 AI811224.1, AI355770.1, AW265061.1, AA485257.1, AA092467.1, AI471817.1, AI702026.1, T34498.1, AI597962.1, AW545016.1, AW544484.1, AI852320.1, AI839826.1, AV173766.1, AI646046.1, AI415428.1, AA959713.1, AA855573.1, AA116476.1, C85464.1, AW545749.1, AV269112.1, AV262681.1, AI884872.1, AV169832.1, AV064737.1, AV012020.1, AU019447.1, AV299656.1, AV154525.1, AV335637.1, AV301925.1, AI835781.1, AV160371.1, AV139152.1, AV138338.1, AV065117.1, AV051902.1, AV245530.1, AV338545.1, AV273829.1, AV214086.1, AV251164.1, 40 AV249977.1, AV234666.1, AV163377.1, AV167956.1, AV136391.1, AV064067.1, AV062993.1, AV061701.1, AV057279.1, AV028650.1, AV232758.1, AV064377.1, AV063220.1, AV062771.1, AV059304.1, AV244517.1, AV215643.1, AV301794.1, AI706252.1, AW254397.1, AA956495.1, AI180308.1, AW465410.1, AC061974.2, AC060789.2, AC019267.3, AC026124.3, AC021067.5, AC025543.2, AC018428.3, AC024418.2, AC021067.4, AL163533.5, AL355887.1, AC068587.1, AC032016.2, AC009664.4, AC027523.2, AC026135.2, AC025830.2, 45 AC013389.3, AC015474.3, AC023518.3, AC011774.4, AC012552.2, AF231129.1, AC016460.1, AC013750.4, AC015980.1, AL161658.3, AL050340.7, AL136373.2, AP001848.1, Z99293.1,

SEQ ID NO.168

NGO-Br-54

50 MK123/T7 3'

AK001917.1, AF035606.1, NM_013232.1, U58773.1, NM_011051.1, U49112.1, AC008925.3, AC007790.1, AC004485.1, AC004923.2, AC008078.1, AE001146.1, AC000385.1, U73627.1, AC000389.1, AL049839.3, Z95397.2, U03396.1, D89223.1, AW439592.1, AW058001.1, AI982775.1, AI912340.1, AA825538.1, AW513884.1, AW074361.1, AI872206.1, AI798286.1, AI522238.1, AI758821.1, AW474823.1, AW337178.1, AI690445.1, AI572080.1, AA831357.1, AI360561.1, 55 AA775261.1, AI140796.1, AW517943.1, AW004890.1, AI361820.1, AA835492.1, AI917776.1, AA100279.1, AI277190.1, AI469550.1, AI015234.1, AI689240.1, AW769512.1, AA581345.1, AI744762.1, D20022.1, AA122332.1, AI811224.1, AI355770.1, AI471817.1, AI702026.1, AW265061.1, AA485257.1, AI597962.1, AA092467.1, T34498.1, AI624976.1, AI811439.1, AV262681.1, AV249977.1, AW545749.1, AV269112.1, AW545016.1, AW544484.1, AV335637.1, AV303323.1, AV299656.1, AV324700.1, AV273829.1, AV269112.1, AV251768.1, AV235453.1, AV232758.1, AV214086.1, 60 AI852320.1, AI839826.1, AI835781.1, AV173766.1, AV138338.1, AV070618.1, AV065117.1, AV064737.1, AV063220.1, AV062993.1, AV062771.1, AV061701.1, AV057279.1, AV051902.1, AV028650.1, AV012020.1, AI646046.1, AA959713.1, C85464.1, AA116476.1, AV303717.1, AV338545.1, AV301925.1, AV296289.1, AV259612.1, AV245530.1, AV244517.1, AV234666.1, AV215643.1, AV210921.1, AV167956.1, AV154525.1, AV153177.1, AV152413.1, AV136391.1, AV132769.1, AV064791.1, AV064377.1, AV064067.1, AV059304.1, AC061974.2, AC060789.2,

AC019267.3, AC027145.1, AL163533.5, AC011699.5, AC025164.7, AC026102.5, AC055810.2, AC068587.1, AC034259.2, AC032016.2, AC025615.2, AC027523.2, AC026135.2, AC025965.2, AC025543.2, AC013389.3, AC023518.3, AC018428.3, AC011774.4, AC011699.4, AF231129.1, AF228730.1, AC013750.4, AC007310.1, AL096888.26, AL353663.2, AL050340.7, AP001848.1,

5

SEQ ID NO. 169

NGO-Br-56

MK271/T3 5'

U13369.1, X03205.1, M10098.1, K03432.1, X00686.1, X82564.1, M11188.1, X01117.1, V01270.1, X06778.1, K01593.1, X00640.1, AF173638.1, AF173637.1, AF173636.1, AF173635.1, AF173634.1, AF173633.1, AF173632.1, AF173631.1, AF173629.1, AF173628.1, AF173627.1, AF173625.1, AF173624.1, AF173623.1, AF173622.1, AF173621.1, AF173620.1, AF173619.1, AF173618.1, AF173617.1, AF173616.1, AF173615.1, D84514.1, AF173630.1, AF173626.1, AF173613.1, X04025.1, X59734.1, AF173612.1, AF173610.1, AF173609.1, AF173608.1, AF173607.1, AF173606.1, M97576.1, X59733.1, M91180.1, AF173611.1, AF115860.1, X02995.1, J00999.1, K01373.1, AF173614.1, AF173605.1, AF169014.1, X98843.1, M91182.1, M91179.1, M91183.1, M91181.1, X98841.1, X98846.1, L11288.1, X98844.1, AF102857.1, AJ270031.1, AJ279506.1, U87963.1, X98840.1, X98837.1, NM_007841.1, D50494.1, X98842.1, X98838.1, X98836.1, AJ277531.1, X98839.1, X98845.1, AF030250.1, M33066.1, AJ270032.1, L24123.1, M59402.1, M97575.1, M59384.1, M97573.1, AF157625.1, M59401.1, M59393.1, M59392.1, AF021880.1, M59386.1, M59385.1, AF236803.1, AF236802.1, AJ007613.1, M59396.1, M59390.1, AW794857.1, AW579814.1, AW580540.1, AW601150.1, AW601147.1, AW601146.1, AW803842.1, AW773277.1, AW773263.1, AW579819.1, AW864483.1, AW801020.1, AW579820.1, AW802332.1, AW795520.1, AA409121.1, AW869663.1, AW820465.1, AW860385.1, AW601994.1, AJ241168.1, AU080818.1, AW866280.1, AW841972.1, AW802330.1, AW601111.1, AW866367.1, AW866279.1, AW804859.1, AW604972.1, AW602533.1, AW866444.1, AW803373.1, AW206333.1, AA900286.1, AW866441.1, AW804923.1, AW801069.1, AW607233.1, AW804888.1, AJ058227.1, AW793732.1, AW750335.1, AW867019.1, AW868469.1, AW864482.1, AW866513.1, AW803865.1, AW784679.1, AW803389.1, AW841701.1, AW580567.1, AW806873.1, AU023662.1, AW802360.1, AW868472.1, AW841735.1, AW579825.1, AW862813.1, AW802322.1, AW581425.1, AW803866.1, AW802405.1, AW864515.1, AW804909.1, AW802410.1, AW797997.1, AW601124.1, AW864460.1, AW577599.1, AW804949.1, AW869661.1, AW363080.1, AW841738.1, AW804307.1, AW864524.1, AW804302.1, AW601130.1, AW601094.1, AW868926.1, AW602408.1, AW868199.1, AW773266.1, AW773181.1, AW773102.1, AW868212.1, AW804283.1, AW868207.1, AW864334.1, AW804702.1, AW581420.1, AW803872.1, AW527555.1, AW864530.1, AW864525.1, AW804289.1, AW773310.1, AW864624.1, AW864534.1, AW868455.1, AL353644.2, AL158197.6, AC011630.2, AC023572.3, AC027604.2, AC068192.1, AC026915.1, AC064866.2, AL355134.1, AC069087.1, AC025654.2, AC064825.3, AC025630.1, AC010970.2, AC010554.1, AC018688.4, AC025968.1, AC064844.1, AC027174.1, AC068900.1, AC016828.4, AC006763.1, AL049183.5, AC019020.4, AC025330.2, AP000639.1, AC012647.15, AC008031.3, AC005806.2, AC012386.9, AC060712.1, AC064263.1, AC067527.1, AC067410.1, AC065739.1, AC065644.1, AC065474.1, AC064126.1, AC064016.1, AC063445.1, AC062950.1, AC062797.1, AC062782.1, AC060627.1, AC060379.1, AC060840.1, AC059708.1, AC059318.1, AC059021.1, AC058845.1, AC058431.1, AC057969.1, AC057826.1, AC056563.1, AC057287.1, AC057204.1, AC057180.1, AC056774.1, AC051336.1, AC051335.1, AC050735.1, AC050283.1, AC050278.1, AC050261.1, AC048611.1, AC048549.1, AC043304.1, AC043037.1, AC045314.1, AC044975.1, AC042630.1, AC042522.1, AC041360.1, AC041109.1, AC039370.1, AC039308.1, AC039109.1, AC038920.1, AC038318.1, AC037587.1, AC036362.1, AC036088.1, AC035291.1, AC034717.1, AC034385.1, AC034335.1, AC030306.1, AC030238.1, AC029865.1, AC029864.1, AC029705.1, AC035311.1, AC034638.1, AC033832.1, AC029523.1, AC027847.1, AC056957.1, AL157407.2, AC025184.3, AC011135.2,

45

SEQ ID NO.170

NGO-Br-57

MK3710/T3 5'

AF025438.1, AL050353.1, AE003680.1, AC005539.1, AL024458.1, AC004680.2, AC004455.1, AC005966.1, U63928.1, Y18930.1, Z48544.1, X79080.1, AW161135.1, W58718.1, N32746.1, AA313566.1, AA024784.1, AA236836.1, AA007319.1, R72404.1, AA236656.1, AJ090162.1, AJ630438.1, AA701988.1, AA852227.1, AA137279.1, AA541923.1, AA000683.1, AI337332.1, AW161742.1, AW427494.1, AJ828070.1, AI935340.1, AI760923.1, AI765742.1, W10638.1, AI630424.1, H30501.1, R17187.1, AI964006.1, AI304319.1, W43974.1, AI765022.1, AA236789.1, AW051324.1, H25699.1, AW592648.1, N56244.1, AW485468.1, AA865602.1, AI631687.1, AA000401.1, AI765999.1, N66532.1, AI888263.1, AW557853.1, H35482.1, AA003291.1, AJ076924.1, AI461713.1, AW466965.1, AA637410.1, AW805299.1, AI808237.1, AW536613.1, AA687041.1, AA452088.1, AA916723.1, AI585560.1, AA024685.1, AW152251.1, AI430072.1, AA007455.1, AA759800.1, AA546383.1, AW614505.1, AW772254.1, AA916358.1, AW272790.1, AI336121.1, AA607321.1, AI599140.1, AA521369.1, AI167263.1, AI283104.1, AI140745.1, AA345744.1, AW645427.1, AA995467.1, AA451907.1, N23163.1, AI753758.1, AI841918.1, R77800.1, AA505618.1, AA110039.1, AI685071.1, AU024430.1, AA959647.1, AA913049.1, AW636012.1, AI538205.1, AA385531.1, AI073755.1, AW823008.1, AU024429.1, AI352390.1, R72405.1, R41738.1, AU022981.1, AL119291.1, AI171338.1, AL136131.7, AL355349.1, AL138706.1, AC032027.2, AP000831.1, AP000713.1, AC013237.1, AL160276.2, AC069160.1, AC011168.4, AC046152.2, AC017106.3, AC023448.2, AC012335.2, AC006279.6, AC013779.3, AC007345.2, AC007342.2, AC015860.2, AC012273.1, AL353640.6, AL354937.2, AL159996.4, AL138815.4, AL157366.3, AL161780.3,

60

AL163973.1, AL136298.1,

SEQ ID NO. 171

NGO-Br-57

5 MK3710/T7 3'

AL050353.1, AF025438.1, AL121924.12, U42838.1, AL031055.1, AL121931.10, AL139076.2, AL024458.1, AC004680.2, AC010889.2, NM_007050.2, AF043644.4, AE003844.1, AE003787.1, AE003676.1, AE003533.1, AE003519.1, AE003480.1, AF003422.1, AE003217.1, AE002799.1, AC004455.1, AC009320.7, AC007478.1, AC007123.1, AC005548.1, AL163232.2, AC000389.1, AL035633.18, AL032654.1, Z68335.1, AL024473.1, Z92844.1, AL110503.1, 10 AP001687.1, AP001297.1, AP000459.3, AB005234.1, D17799.1, D17798.1, D17797.1, AB009052.1, AB006621.1, AI964006.1, AI337332.1, AI765742.1, AA236789.1, AI304319.1, AA701988.1, AW592648.1, AI765022.1, AA865602.1, AI828070.1, AI765999.1, AI760923.1, N66532.1, AI631687.1, AI935340.1, AA916723.1, AW161742.1, AA024685.1, AW152251.1, AW772254.1, AA916358.1, AI336121.1, AW614505.1, AW051324.1, AI888263.1, N23163.1, AA007455.1, AW272790.1, AI167263.1, AI283104.1, AA451907.1, AA995467.1, AI753758.1, AA505618.1, AI073755.1, AA913049.1, 15 AI538205.1, AA670386.1, AI352390.1, AA680352.1, AW151295.1, AA720562.1, AA723980.1, AI808237.1, AW466965.1, AI081040.1, AA992256.1, AI267913.1, AA532854.1, R41738.1, AA928158.1, AW117185.1, AA016221.1, AA345744.1, R72405.1, AI140745.1, AI084344.1, AI079153.1, AA852226.1, H89982.1, AI539552.1, AA385531.1, AA236836.1, N50079.1, AI090162.1, AW557853.1, AA858049.1, AW536613.1, AI461713.1, AI599140.1, AI678339.1, AW172462.1, AA637410.1, AI678340.1, R77800.1, AI198148.1, AA546383.1, AW433804.1, AI841918.1, AI585560.1, 20 AW823008.1, AA541923.1, AU024430.1, AA959647.1, AA924460.1, AU022981.1, H30501.1, AA024784.1, T26930.1, AI630424.1, AA137279.1, AI630438.1, AW161135.1, W58718.1, AA607321.1, AU024429.1, AA963706.1, AA765777.1, AI505865.1, AI963259.1, AL136131.7, AL355349.1, AL138706.1, AL050335.24, AC016073.2, AC023651.2, AL354992.1, AC026285.4, AC055116.2, AC012133.3, AC006756.1, AC012031.7, AC007953.7, AC027502.3, AC008926.5, AC009679.3, AP000841.1, AP000783.1, AC012151.5, AC022226.7, AC018728.2, AC068509.1, AC026961.2, 25 AC011036.3, AL136231.5, AL157824.2,

SEQ ID NO.172

NGO-Br-58

MK436/T3 5'

30 AF118652.1, NM_006541.1, AJ010841.1, AF118649.1, AF118650.1, AF118651.1, AC021044.4, W73086.1, AA307154.1, W58564.1, AA363862.1, AW327841.1, AI902183.1, T06444.1, AW014738.1, AI822071.1, AI813451.1, AA452335.1, W15560.1, H78479.1, H59799.1, F11379.1, R63123.1, T83390.1, N24488.1, T83556.1, F07471.1, N76641.1, T36308.1, H17884.1, AW743314.1, AL024195.1, AI892878.1, AI541284.1, AI121283.1, AA423088.1, AA124189.1, AA119742.1, AA086801.1, W14808.1, AA222785.1, AA293188.1, AA985756.1, AA711181.1, AA218282.1, W33933.1, AI685717.1, 35 TI0785.1, AA815685.1, AA273544.1, AA238334.1, AA157103.1, AI595622.1, AI316625.1, AI119458.1, AA879644.1, AA879757.1, AA390040.1, AA220693.1, AA217769.1, AA106608.1, W90901.1, W85535.1, AA050409.1, AA000754.1, W57189.1, W36243.1, AA120515.1, AI929984.1, AA623076.1, AA939357.1, AA914937.1, AA674174.1, W16243.1, AA009010.1, AA536703.1, W01696.1, AL117714.1, AW652677.1, AA929573.1, AA667299.1, AA561056.1, AA177257.1, AA172553.1, AA117786.1, AA066010.1, W16154.1, AA048263.1, W76881.1, C83514.1, C82658.1, R84921.1, 40 AA198255.1, H96310.1, W23637.1, AA833367.1, AA822615.1, AA140412.1, AI561434.1, AA545088.1, AA049167.1, AW672942.1, AA222090.1, AA212687.1, AA866363.1, AA867450.1, AL161648.5, AL139123.2, AL138831.2, AC050138.1, AL158828.4, AL353613.2,

SEQ ID NO.173

45 NGO-Br-58

MK436/T7 3'

NM_006541.1, AJ010841.1, AC020610.6, AC005666.1, AC004381.1, AC005972.1, AC004099.1, AC005519.2, AC005899.1, AL034343.17, AL008582.11, AC005516.1, AC004601.1, AL110120.11, AC018511.4, AC005726.1, AL035420.15, Z99128.1, AL022159.1, U91323.1, AC005520.2, AJ011930.1, AC002036.1, AC007676.19, AF205588.1, 50 AC004525.1, AC004961.2, AL117337.25, U07000.1, AL034427.1, AL020997.1, AC009946.2, AC004584.1, AC003043.1, AC002070.1, AC004552.1, AC005232.1, AC002425.1, AC006312.8, AC004968.1, AC005480.3, AC004821.2, U72787.1, AL355916.1, AL117375.12, Z83840.7, Z94801.1, AL008718.23, AC007240.2, AC004463.2, AC004771.1, AL160231.2, AL121825.19, AL022322.1, AL022238.1, AL021391.2, AL031296.1, AL031681.13, AC005015.2, AC007435.12, AL163262.2, AL121658.2, AL121655.1, Z84486.1, AP001717.1, AC010285.4, AC000003.1, AC004883.2, AC005288.1, 55 AL163265.2, AL133396.1, Z83819.1, AP001720.1, AC009516.19, Z82243.1, AC009145.4, AC002544.1, AC005562.1, U52111.1, AC011449.6, AC022149.3, AC005907.1, AL133243.1, AL035699.4, AC006509.15, AC007055.3, AL049779.4, AL035658.7, Z82245.1, AP000557.2, AL049759.10, AC006581.16, AL049712.12, AC005778.1, AC002558.1, Z85996.1, AL024474.1, AL008716.1, AC005755.1, AC003002.1, AI074462.1, H99205.1, AI038375.1, AL119361.1, AA299728.1, AA732982.1, AA602488.1, AI963281.1, AI345497.1, AI371278.1, AA570441.1, AA487512.1, AW149972.1, AI829381.1, 60 AL079763.1, AA614595.1, AA491864.1, AW768439.1, AL135639.1, AI963725.1, AI858632.1, F25696.1, AI610602.1, AI370302.1, AI285709.1, AA618392.1, AA618346.1, AA602468.1, AA306530.1, H70245.1, H66503.1, AA708669.1, AA620386.1, AA362670.1, M77904.1, AW877774.1, AW467676.1, AI469586.1, AI375374.1, AI052628.1, AA700279.1, AA613177.1, AA528405.1, AA515254.1, AA504694.1, AA382130.1, AA347199.1, AA338281.1, AA174071.1, AA167567.1, R86266.1, AL134669.1, AI745457.1, AI734060.1, AI734052.1, AI732085.1, AI370199.1, AI288162.1,

- AA876148.1, AA846808.1, AA678733.1, AA631915.1, AA489797.1, AA226144.1, AA226095.1, AA225949.1, AW500075.1, AW177901.1, AW177895.1, AW177822.1, AW177816.1, H41308.1, AI073735.1, AA601218.1, AA482054.1, AI174701.1, AW074405.1, N38996.1, AI500315.1, H62161.1, AW847624.1, AI597931.1, AW084237.1, AI791265.1, AI468269.1, AI382183.1, AA194502.1, C05882.1, AA001398.1, AA828783.1, AA688148.1, AA455088.1, AA194944.1, AA487225.1, AI005219.1, H73907.1, AA280681.1, N55212.1, AI082472.1, AA578774.1, AI161648.5, AI139123.2, AI109615.18, AC020603.3, AC068727.1, AC011355.3, AI109843.17, AP001885.1, AC068847.1, AC068583.1, AC021991.3, AC011022.4, AC010481.4, AC009038.5, AL050329.11, AC046162.2, AI136458.2, AI162733.2, AC008474.6, AI139815.3, AC005047.2, AC026495.1, AL353596.2, AP001809.1, AI135787.8, AI157789.1, AC024096.7, AC026603.2, AC007217.2, AI109823.21, AL355837.1, AL353641.1, AP001447.1, AC036206.2, AC008403.5, AC004873.1, AP001787.1, AC063950.3, AC018462.3, AI139384.3, AI139327.12, AC068785.4, AC063962.3, AP000717.1, AC010277.3, AC008484.3, AC064860.2, AC025692.3, AC020781.4, AC023183.2, Z93015.7, AL355392.2, AL354932.4, AI139324.5, AC025265.5, AC026115.10, AC008622.4, AC025778.2, AC025277.2, AC011486.5, AC022307.7, AC012659.3, AC010260.3, AC008671.3, AC025142.2, AI133458.12, AI161789.3, AC009027.4, AC023089.2, AL356009.2, AP001855.1, AC068077.1, AC022795.3, AC020754.2, AL353794.1, AP001279.1, AC008121.13, AC023831.3, AC019255.2, AP000846.1, AL353691.2, AI158153.2, AC022156.4, AC016701.2, AC016525.3, AI161756.1, AI139396.1, AC008158.3, AC068786.4, AC009021.3, AC010503.5, AC008614.4, AC009120.5, AC027394.2, AL353622.3, AC064835.3, AC011445.4, AP001187.1, AL354760.1, AC012635.1,
- 20 SEQ ID NO. 174
NGO-Br-59
MK337/T3 5'
- X56687.1, M61725.1, NM_014233.1, X53461.1, X53390.1, L42571.1, M61726.1, NM_011551.1, X60831.1, L42570.1, M61724.1, AC004596.1, U65487.1, AF241726.1, X59863.1, X57201.1, X57561.1, X65698.1, X65697.1, AF164119.1, AF102773.1, AL078477.5, AC010083.5, AC018765.4, AF157625.1, AC006254.10, U78553.1, AC002986.1, AE000747.1, AE000803.1, AL353815.2, AL163290.2, U49246.1, AL049659.2, AL163812.1, AI117200.2, Z83125.1, Y09788.2, L20418.1, U41548.1, AP001745.1, AP001618.1, X73942.1, AB014538.1, AA683270.1, AI990923.1, AI652105.1, W56216.1, AI424653.1, AI361257.1, AW373605.1, AI263742.1, W28568.1, AA134165.1, AW867502.1, AI407688.1, AV098625.1, AW607456.1, AI121071.1, AA322474.1, AA494480.1, AA254648.1, AW362484.1, AA306865.1, AI947817.1, AV207877.1, AV140171.1, AV122483.1, AI594085.1, AI551499.1, AI463712.1, C85526.1, AA606502.1, AV083972.1, AI267702.1, AV392783.1, AV392203.1, AV392190.1, AV392165.1, AV387615.1, FI5738.2, AI047080.1, C65313.1, AA437706.1, AC011606.6, AC060757.2, AC021999.2, AC020754.2, AC011606.5, AC024234.4, AC024899.4, AI158052.2, AC068918.2, AC026801.2, AC008795.5, AC008855.4, AC011145.3, AC023857.2, AC007555.1, AI137780.2, AI138811.1, AC016955.9, AC012522.7, AC011318.8, AC024891.8, AC061979.2, AC025638.3, AC037426.2, AC034103.4, AC062039.1, AC009237.2, AC021015.3, AC023582.2, AC040893.1, AC019008.4, AC019250.3, AC015801.3, AC013713.4, AC024253.2, AC022302.3, AC025598.1, AC022609.2, AC019251.2, AC024119.1, AC016490.2, AC012499.3, AC018665.2, AC012340.2, AC009408.2, AL049715.21, AI157875.4, AL355535.1, AL355506.1, AI162582.2, AI162372.3, AI161615.2, AI136447.4, AP001769.1, AP000941.2, AP000869.1, AP000846.1, AP000827.1,
- 40 SEQ ID NO.175
NGO-Br-59
MK337/T7 3'
- NM_014233.1, X53461.1, X53390.1, X56687.1, NM_011551.1, X60831.1, AC004596.1, U65487.1, L42571.1, L42570.1, M61725.1, M61726.1, X56688.1, AF241726.1, AF170811.1, AC007372.4, AC004912.1, AC007011.1, AC005295.1, AI132896.1, AL049837.4, AJ009934.1, AC004983.2, NM_014771.1, AC005782.1, AI121934.15, AB040880.1, AK000425.1, AK000265.1, AP000696.1, AB014561.1, AW373933.1, AW373896.1, AA626575.1, AA374794.1, AI915777.1, AI798277.1, AI521078.1, AI087037.1, AW249403.1, W31280.1, AA651656.1, R36455.1, AA919770.1, AA664208.1, AA329246.1, R36454.1, AA134166.1, AA961221.1, AA914265.1, AA911482.1, D56068.1, D56028.1, AI907998.1, AA623692.1, AA413864.1, AA308880.1, AI740529.1, AA637361.1, AW793731.1, AA889124.1, AA377594.1, AI907995.1, AA377898.1, AA438075.1, AA211953.1, W83843.1, AI762169.1, AA611296.1, AW519549.1, AW390831.1, AI893975.1, AA500491.1, AA492907.1, W80099.1, W77364.1, W33457.1, AI105117.1, AA518740.1, AW814069.1, AW814073.1, AI154308.1, AW438655.1, AW298403.1, AW243881.1, AW166393.1, AW001988.1, AI989406.1, AI971828.1, AI831668.1, AI208785.1, AI077671.1, AI027548.1, AA890545.1, AA768775.1, AA577311.1, AA056073.1, AA022622.1, AA021002.1, AA020748.1, AA019643.1, AA013126.1, H84980.1, H85537.1, AW819846.1, AW556048.1, AW433907.1, AI968114.1, AI678953.1, AI651215.1, AI202697.1, AA220802.1, AW196586.1, AW175973.1, AI513981.1, AI348282.1, AI297541.1, AI257079.1, AI187754.1, AA973975.1, AA942224.1, AA816918.1, AA478079.1, AA127812.1, H39217.1, AA183999.1, W79356.1, AC011606.6, AC060757.2, AC021999.2, AC020754.2, AC011606.5, AC009237.2, AC017099.3, AP001769.1, AP000827.1, AI162372.3, AC024234.4, AC021987.2, AP000668.1, AC026803.2, AC008749.4, AC026930.2, AC026285.4, AC018761.4, AC023154.4, AC012482.3, AC011200.2, AL353609.2, AI139423.4, AI161662.1, AC010189.4, AC007834.20, AC053546.3, AC007339.3, AC022197.3, AC015867.2, AC022783.2, AC000005.1, AC020968.1, AL355293.2,
- 60

SEQ ID NO.176

NGO-Br-62

MK804/T3 5'

- 5 NM_005134.1, AF111106.1, AC007736.3, AC008168.3, NM_013658.1, AC005324.1, X85991.1, AC004539.1, NM_009134.1, AC006287.1, AF075627.1, AL122020.3, U58743.1, Y09108.1, AC009486.3, AE003769.1, AC004888.1, AC005013.1, AC007463.3, AC008067.3, AF189157.1, AE001980.1, AC009888.1, AC005549.1, AL008733.10, Z68760.2, L46672.1, X94768.1, AP001278.1, AP000816.1, M24411.1, Z99105.1, AB006424.1, AW673704.1, AW371829.1, AW382321.1, AW371827.1, AJ081867.1, AW382320.1, AW371825.1, AJ687366.1, AL120881.1, N41948.1, AW239384.1, AI286014.1, N40656.1, AW382480.1, AA161066.1, AW367894.1, AA332078.1, AW382482.1, AW659290.1, AW500241.1, AA611470.1, AW392387.1, AA906014.1, AW535590.1, AW534364.1, AW533907.1, AW534600.1, 10 AW535963.1, AI552086.1, AW535977.1, AW535929.1, AW535612.1, AW535599.1, AW535574.1, AW535542.1, AW535538.1, AW535507.1, AW535217.1, AW534451.1, AW534434.1, AW534374.1, AW534356.1, AW534229.1, AW534224.1, AW534199.1, AW534112.1, AW534076.1, AW534005.1, AW533992.1, AW533915.1, AW532274.1, AW532226.1, AW532183.1, AW532169.1, AW531827.1, AW531069.1, AW530797.1, AW530120.1, AW530107.1, AW529979.1, AW529973.1, AW254242.1, AW254201.1, AW251947.1, AW251307.1, AW251102.1, AI709485.1, 15 AI578408.1, AI555305.1, AI549564.1, AI549513.1, AI549263.1, AI549090.1, AI548886.1, AI548373.1, AI548339.1, AI547780.1, AI547618.1, AI547615.1, AI535377.1, AI535100.1, AI535055.1, AI535053.1, AI511474.1, AI501242.1, AA900666.1, AI137299.1, AI072600.1, AI072263.1, AI072230.1, AI071899.1, AI071691.1, AI071396.1, AI071193.1, AI071165.1, AI070019.1, AI058437.1, AI045860.1, AI045612.1, AI044996.1, AC021927.3, AP001381.1, AC015956.3, AC007140.1, AC026964.2, AC018989.3, AC024046.2, AC012596.3, AC009574.3, AC021114.3, AC018940.4, 20 AC022971.2, AC011172.4, AC016068.2,

SEQ ID NO.177

NGO-Br-62

MK804/T7 3'

- 25 AF100744.1, U79267.1, NM_005134.1, AF111106.1, AE003449.1, AL163301.2, NM_000236.1, AC016041.5, M29193.1, AL035653.12, AL023807.6, Z84475.1, J03895.1, M35432.1, J03540.1, X07228.1, D83548.1, AC010102.3, AC006283.5, AE003514.1, AE003440.1, AC005690.8, AC006465.2, AC008075.2, AF101438.1, AL163302.2, AL163254.2, AL163233.2, AL136018.2, AL133097.1, AL109627.18, Z76735.1, AP001709.1, AP001688.1, U23442.1, AP000950.2, AP000204.1, AP000244.1, AP000126.1, AI076775.1, AI215696.1, AI601253.1, AA581865.1, AI371049.1, H97837.1, 30 AI131196.1, AI184641.1, AI754673.1, AI139064.1, AI142447.1, AI374783.1, AI204302.1, AA772102.1, AA435767.1, AI659941.1, AA860292.1, AI569647.1, AA706309.1, AA732402.1, AA706694.1, AA192742.1, N56938.1, AA766582.1, AA171536.1, N59159.1, AI336886.1, N49858.1, AA994358.1, AI191899.1, N47550.1, AA074753.1, N30433.1, AA536150.1, AI348314.1, AI342660.1, N29328.1, AA401497.1, AA854769.1, AI220586.1, AI025515.1, AA936114.1, AA825278.1, AA492553.1, N77882.1, AA804953.1, AW068965.1, AA860331.1, N89882.1, AA769019.1, N47895.1, 35 N63879.1, Z39560.1, AA805421.1, W73239.1, N66463.1, T62952.1, AI093651.1, AW839754.1, R68907.1, W57588.1, AI970730.1, W92205.1, AA602432.1, F10765.1, AA074836.1, R22227.1, AA255616.1, AA987948.1, F03184.1, AA852934.1, H04250.1, R42968.1, AW503224.1, R67269.1, AI621152.1, AI536774.1, AW503670.1, H83900.1, AI743459.1, AW439253.1, AI571914.1, T92192.1, AW264100.1, AW172934.1, F04772.1, AI588862.1, H56904.1, R40975.1, AI915335.1, AW467646.1, AI678364.1, R43639.1, AI625453.1, AA643894.1, AI560721.1, R00485.1, 40 W73294.1, AW270022.1, AA397947.1, AC015956.3, AC021927.3, AP001381.1, AL121900.7, AL121780.3, AC026570.2, AL354706.2, AC046148.2, AC027566.1, AC008658.2, AC015405.1, AL133499.1, AC016956.6, AC024153.10, AC008019.37, AC027489.2, AC016994.3, AC025130.2, AC016956.5, AL356377.1, AL121759.19, AL162381.3, AL139094.5, AC068908.2, AC069028.4, AC023057.6, AC012117.3, AC046161.2, AC010631.4, AC009118.6, AC021471.2, AC009639.3, AC026967.2, AC027067.2, AC027059.2, AC026505.3, AC022050.2, AC019334.3, 45 AC016910.2, AC012585.4, AC009384.5, AC012071.3, AC017069.3, AC012855.1, AC015230.1, AL356140.3, AL353578.2, AL158146.2, AL160057.4, AL162759.1, AL136975.1, AP001392.1,

SEQ ID NO.178

NGO-Br-63

MK467/T3 5'

- 50 NM_014731.1, AB011124.1, AF123659.1, AF123658.1, AF123657.1, AF123656.1, AF123655.1, AF123653.1, AL133215.16, AE003506.1, NM_003980.1, AJ242502.1, AJ242501.1, AL023284.1, X73882.1, AF130782.1, AF190465.1, AC006544.19, AC005033.1, AC003065.1, AC006985.2, U84269.1, U84268.1, AC003047.1, AL031295.1, AE001862.1, U51197.1, AC004231.1, AP000279.1, AB004043.1, AB004042.1, AB002339.1, AW416906.1, D56085.1, AW263065.1, 55 AJ281091.1, AI911142.1, AI501468.1, W45377.1, AW530214.1, AW140903.1, AA819761.1, AI293560.1, AI230840.1, AA799815.1, C25135.1, AA086491.1, AW727488.1, AW657062.1, AW648093.1, AW581571.1, AW576745.1, AV306266.1, AW138828.1, AW045957.1, AI892415.1, AV014939.1, AI325725.1, AI069094.1, AA727234.1, AA400580.1, AL121891.18, AC025853.2, AC012162.9, AC012693.1, AC009216.8, AC011498.4, AC017241.1, AC027118.2, AC026497.1, AC009850.9, AC014014.1, AC017674.1, AC012600.4, AC012515.11, AC010189.4, AC008129.10, AC007834.20, AC023501.7, AC012293.9, AC044820.2, AC068126.2, AC068588.1, AC068557.1, AC027764.2, AC062037.2, AC024948.2, AC055811.1, AC024474.2, AC021467.2, AC027267.1, AC026244.1, AC010121.6, AC015867.2, AC016439.4, AC016753.4, AC011575.3, AC012600.3, AC013934.1, AC013499.2, AC011135.2, AL138753.3, AL136990.14, AL136439.2, AL138757.4, AL137025.2, AL138955.1, AL136104.3, AL022335.6, AP001979.1,

SEQ ID NO.179

NGO-Br-63

MK467/T7 3'

- 5 NM_014731.1, AB011124.1, AC019209.3, AC005829.1, AF045453.1, AL135999.2, AL132719.2, Z98946.15, AL021326.1, AC010385.3, AC007115.1, AC002477.1, NM_012654.1, AF179633.1, AL121809.4, AL035460.15, M85300.1, D14905.1, D14904.1, AW134487.1, AW005916.1, AI918105.1, AI369140.1, AI362807.1, AI536952.1, AA233070.1, AI800560.1, AI570845.1, AI084111.1, AI805727.1, AI566887.1, AI885796.1, AW205146.1, AA631005.1, AW088686.1, Z38359.1, AI570882.1, AI889744.1, F03249.1, T23438.1, AI093242.1, AI151303.1, H64737.1, T91286.1, 10 AA682753.1, AW057576.1, AW752274.1, AA577015.1, AA319634.1, H65227.1, AW246038.1, AA862950.1, AI573262.1, AA639497.1, AI148651.1, AI129016.1, R44479.1, AW874175.1, AI849112.1, AA118865.1, W53946.1, AW611372.1, AW359586.1, W96834.1, AA339527.1, AA320970.1, AA317924.1, AW523114.1, AI229250.1, AI229142.1, AA943809.1, AW658594.1, AW655764.1, AW426231.1, AW359271.1, AI863241.1, AI007273.1, AA832546.1, AA619805.1, AA571164.1, AA422555.1, AA260212.1, AA259669.1, AA240477.1, W16289.1, H51681.1, AL121891.18, AC008133.2, 15 AC021420.3, AC025898.2, AC009608.2, AC024225.8, AC024224.6, AC025194.2, AC016018.7, AL355482.1, AC024105.7, AC023504.4, AC064837.2, AC025772.3, AC012636.3, AC034138.2, AC021355.3, AC027688.2, AC023819.3, AC015478.3, AC016868.4, AC009962.3, AC012505.3, AL354652.3, AL355884.2, AC009453.7, AC046135.4, AC068633.3, AC026084.2, AC026285.4, AC026792.2, AC011356.3, AC024230.3, AC024537.2, AC027216.2, AC027526.2, AC026423.3, AC027685.2, AC015928.4, AC011033.3, AC011957.2, AC016180.5, 20 AC011213.4, AC023920.2, AC016483.6, AC023291.2, AC005052.1, AL356154.2, AL355590.2, AL354726.2, AL355476.1, AL353589.1, AL157375.1, AP001855.1, AP000752.1, AP000721.1,

SEQ ID NO.180

NGO-Br-64

MK731/T3 5'

- 25 NM_014963.1, AB023180.1, AC005390.1, AF060974.1, AC007246.3, AL049754.1, AE001274.1, AJ242840.1, AJ242839.1, Y15791.1, AE003835.1, AE003596.1, AC005290.3, AF117761.1, AF117760.1, NM_000506.2, AC007655.1, U73167.1, U90094.1, M24461.1, AL133224.2, AL121756.14, U50596.1, U00012.1, AL022374.1, X82071.1, AB001030.1, V00595.1, J00307.1, M33031.1, D17389.1, X54794.1, M60789.1, Y10403.1, AW410223.1, AW468990.1, AI827893.1, 30 AW081199.1, AA977476.1, AL045506.1, AL079747.1, AW206971.1, AW073064.1, AI559848.1, AI760801.1, AI430503.1, AA245512.1, AA245370.1, W62920.1, AW729115.1, AW668796.1, AW431830.1, AW348976.1, AW649811.1, AW623969.1, AW056157.1, AI987383.1, AI941796.1, AI896465.1, AI691275.1, AI670672.1, AI465663.1, AI456906.1, AI397644.1, AI054620.1, AA855993.1, C32683.1, AA354150.1, AA334812.1, AA286992.1, H69659.1, H59101.1, AC011474.2, AC020781.4, AC020582.3, AC068633.3, AC032027.2, AC048370.2, AC012334.2, AC008713.5, 35 AC016573.4, AC025868.2, AC023826.2, AC018445.3, AC019356.3, AC027817.1, AC012286.2, AC007524.2, AC026086.2, AC023356.4, AC011951.3, AC015930.3, AC012568.3, AC012374.9, AC024610.1, AC010011.3, AC012454.3, AC013279.3, AC013750.4, AC020372.1, AC013563.2, AC017853.1, AC007471.3, AC007597.2, AC007503.1, AL356138.3, AL138720.5, AL137162.5, AL137225.11, AL162499.3, AP001337.1,

40 SEQ ID NO.181

NGO-Br-64

MK731/T7 3')

- AC005390.1, NM_014963.1, AB023180.1, AC002351.1, Z82215.1, AE003544.1, NM_004474.1, NM_000758.1, AC005950.1, U37501.1, AF042832.1, AC004511.1, AC003675.1, AL163299.2, AC001228.1, AL050318.12, Z85994.1, 45 AJ006345.1, M13207.1, AP001754.1, AP001062.1, X03021.1, M11220.1, M10663.1, M28860.1, M28859.1, AC068783.2, AE002501.1, AC007537.3, AC005261.1, AL162756.2, AL122127.3, X97051.1, X17215.1, X57133.1, X16489.1, U18978.1, AB019441.1, X13972.1, M37277.1, AI200815.1, AI417909.1, AI459189.1, AI560887.1, AW270083.1, AI564758.1, AI745070.1, AI355293.1, AI815176.1, AL047897.1, AL047898.1, AW474741.1, AI469279.1, AI359252.1, AA722975.1, AA444008.1, AI220310.1, AI624704.1, AI289062.1, AI623674.1, AL045507.2, AA456471.1, Z25344.1, 50 AA444037.1, AA427461.1, R96945.1, AW472864.1, AA654248.1, AA456804.1, AA427462.1, AA954685.1, AI932512.1, AA485597.1, AI433817.1, AA485433.1, AA454577.1, AA457134.1, T30158.1, AA476273.1, AW138346.1, AA464482.1, T95376.1, T95296.1, AA299621.1, AA293227.1, AI866076.1, AI801586.1, AA884991.1, AA435961.1, AW013846.1, AW410224.1, AI391545.1, AA971658.1, AA932895.1, AW431713.1, AW547208.1, AW345308.1, AI085206.1, AI022933.1, AI912784.1, AI677936.1, AI655452.1, AA096946.1, T29160.1, AW749596.1, AW213795.1, AW207707.1, 55 AW005369.1, AV131761.1, AV062291.1, AI695173.1, AI524311.1, AI508690.1, AI462638.1, AI417791.1, AI232789.1, AI072326.1, AA288479.1, AA135536.1, W73276.1, W03892.1, D51085.1, T33074.1, AL162423.2, AC016525.3, AC018930.3, AC010033.7, AC034216.3, AC026699.2, AC009175.3, AC010590.4, AC011361.3, AC021424.3, AC013791.3, AC011182.3, AC018891.2, AC009899.5, AC023171.1, AC022754.1, AC013287.6, AC016743.3, AC021389.1, AC014953.1, AC003656.1, AP001356.1, AC016968.11, AC015545.10, AC024097.8, AC022296.8, 60 AC037471.2, AC025468.3, AC025460.3, AC024075.3, AC010378.3, AC008681.5, AC024293.2, AC023484.2, AC021328.3, AC019345.3, AC022051.3, AC018427.3, AC021200.4, AC011281.3, AC027171.1, AC024951.9, AC021585.3, AC017096.2, AC011140.3, AC009575.4, AC016968.10, AC015545.9, AC016757.3, AC010136.3, AC013567.2, AC009647.2, AC010782.1, AL035662.50, AL136079.3, AL157939.3, AL158817.2, AL158143.1,

SEQ ID NO.182

NGO-Br-65

MK385/T3 5'

- 5 AF086824.1, U39904.1, AF039218.1, AF070066.1, AC004811.2, AC002563.1, NM_015239.1, AK001544.1, AC007023.3, AC007078.3, AC000039.3, AC006480.3, AC005488.2, AC005088.2, AF030453.1, AL121823.12, AL161571.2, AL022326.1, AL078579.1, L09233.1, AE003628.1, AC005537.2, AC005036.1, AC007038.3, AC007451.1, AC006254.10, AF063424.1, AF092090.1, AC005359.1, AC000378.1, AL161513.2, AL035703.20, Z75543.1, AL035681.13, Z93020.1, X59046.1, X65624.1, AB037724.1, M22462.1, AW449442.1, AW444459.1, AI826767.1, AI674481.1, AA570498.1, H62116.1, AW760341.1, AW733957.1, AW598733.1, AW459885.1, AU082470.1, AV403875.1, AW325533.1, 10 AW325530.1, AW162177.1, AW149411.1, AW076876.1, AW076660.1, AI924223.1, AI510359.1, AA968035.1, AA508904.1, AA508038.1, AA236748.1, AA177241.1, AA140828.1, AA116487.1, AA107365.1, W62286.1, H16776.1, T18197.1, AC026363.3, AC026765.5, AL157828.5, AC012032.11, AC023923.2, AL159156.4, AL157362.2, AC019315.2, AL139429.4, AC019071.3, AC025232.3, AC023593.3, AC018720.3, AC012406.3, AC023811.7, AC005236.3, AC004980.2, AC007674.2, AC026507.1, AC016294.2, AC022253.2, AL139182.14, AL137118.8, AL162387.3, 15 AL161642.3, AL049770.1, AP001809.1, AC009774.4, AC021064.7, AC024505.3, AC023493.6, AC026418.2, AC024991.2, AC068482.1, AC027104.2, AC023170.3, AC019063.3, AC019043.3, AC027184.2, AC058808.1, AC026043.3, AC018513.3, AC026002.2, AC019356.3, AC016875.3, AC011952.4, AC009933.5, AC020796.2, AC018887.4, AC022245.3, AC016513.2, AC011009.4, AC022182.3, AC012306.3, AC016245.3, AC020201.1, AC016521.1, AF162757.1, AL133268.6, AL121955.9, AL136114.2, AL136159.4, AL353762.3, AL354720.3, AL355526.2, 20 AL161908.3, AL160400.3, AL138896.2, AL137838.2, AL133167.1, AL138689.1,

SEQ ID NO.183

NGO-Br-65

MK385/T7 3'

- 25 AC002563.1, AB023166.1, U75698.1, U93872.1, AP000542.1, AE003597.1, AC004506.1, AC004695.1, AL049781.4, AL034404.1, X58358.1, AP001819.1, AI861788.1, H10788.1, AW386741.1, AW581596.1, AW386738.1, AA308642.1, N57796.1, AI933041.1, AI984971.1, T91324.1, W42440.1, AI933217.1, N57810.1, AI933106.1, R50756.1, R44891.1, H79564.1, H63135.1, AA353105.1, AA224531.1, AI861826.1, AI245941.1, AW054833.1, AA778789.1, AI806134.1, AW483290.1, AW416772.1, AI936328.1, AA379967.1, AA677294.1, AW047976.1, AW047308.1, AW046893.1, 30 AA617920.1, AA546601.1, AW046868.1, AA822334.1, W78614.1, AI183534.1, AW525869.1, AW665288.1, AA957183.1, AI807388.1, AI228556.1, AI698168.1, AI102448.1, AA955912.1, AI017868.1, AI767064.1, AW797442.1, AW859870.1, AW248416.1, AW117872.1, AC026363.3, AC023264.2, AC069045.1, AC027398.2, AC009268.2, AC024485.2, AC022188.3, AC024111.6, AC011138.2, AC024217.6, AC022132.4, AC024927.2, AC023641.2, AC034147.4, AC013447.3, AC025690.3, AC019311.4, AC023974.2, AC023205.2, AC022460.2, AC018349.2, 35 AC017535.1, AC010689.2, AC004064.1, AL118502.34, AL139241.4, AL138693.6, AL161939.2, AL157716.2, AC001235.1, AP000452.2, AP001833.1,

SEQ ID NO.184

NGO-Br-66

MK805/T3 5'

- 40 U73200.1, AB000214.1, AC003080.1, AC002395.1, AC005244.1, Z68279.1, AC007327.1, AC005817.7, AC007665.24, AC008266.3, AE003615.1, AE003580.1, NM_010559.1, AC004615.1, AF140707.1, NM_003688.1, AF130357.1, AC004893.1, AC005839.1, AF111102.1, AC005807.1, AC005855.1, U58494.1, AC005356.1, AC003052.1, AC005211.1, AC004598.1, M17551.1, AF035582.1, AF032119.1, AJ403418.1, AF027865.1, X97915.1, AC002094.1, AJ290445.1, 45 AL021127.2, AL080241.14, Z83844.5, AL031347.1, U70381.1, U70380.1, U26425.1, X51976.1, X98188.1, X01709.1, X91192.1, AB029009.1, M27972.1, M18252.1, M36323.1, L35243.1, AB011297.1, AB011096.1, U08129.1, AL048447.2, AA378192.1, AA312335.1, AW501959.1, AA675911.1, AA015476.1, AA220385.1, AA681477.1, AW321789.1, AW701965.1, AW171289.1, AW140423.1, AI618679.1, AI617588.1, AI545690.1, AI416377.1, AW727131.1, AI878211.1, AA867310.1, AW822989.1, AW822908.1, AW140419.1, AW107372.1, AI876330.1, AI876315.1, AI787888.1, 50 AI673281.1, AI661565.1, AI647986.1, AI596598.1, AI593550.1, AI563647.1, AI448821.1, AI429489.1, AI416269.1, AI316550.1, AI286579.1, AI272572.1, AI272468.1, AI272432.1, AI265094.1, AI265081.1, AI265039.1, AI265016.1, AI227615.1, AI098293.1, AI097946.1, AU017425.1, AU016228.1, AU014817.1, AA983005.1, AA981167.1, AA930951.1, AA920957.1, AA920358.1, AA920053.1, AA919936.1, AA896813.1, AA896091.1, AA896033.1, AA896016.1, AA867305.1, AA797842.1, AA791920.1, AA734060.1, AA672803.1, AA656916.1, AA647396.1, AA561026.1, 55 AA432827.1, AA415676.1, AA239702.1, AA197111.1, AA118415.1, AA104979.1, AA104928.1, AA045964.1, AA014354.1, W38611.1, H93255.1, H89667.1, R15163.1, AC069071.2, AC018473.10, AC007775.2, AC025911.2, AC026386.4, AC024042.3, AC005805.1, AC002405.1, AC055890.2, AC021494.3, AC022701.1, AL355994.1, AL121750.3, AP000780.1,

60 SEQ ID NO.185

NGO-Br-66

MK805/T7 3'

- AB020671.1, D23673.1, D26154.1, U73200.1, AD001527.1, AC003003.1, AF048729.1, AL353012.1, AL096799.4, AJ011517.1, U66909.1, AE003569.1, AC007243.3, AC005071.2, NC_001224.1, AC007284.4, AC007514.5, AC002401.1,

- AF055066.1, AL163218.2, AJ011856.1, Z82195.1, AL031985.10, V00695.1, L36887.1, AP000521.1, AB023058.1, AC007040.2, AC005060.2, AC005353.1, Z98551.1, AL035475.6, AL031390.4, AC009233.3, AC020717.3, AF185568.1, U82670.2, AE003491.1, AC004553.1, AC002540.1, AF030694.2, AF214529.1, AC004992.1, AC004998.2, AC004999.1, AC007077.2, AC007402.3, AF006055.1, AC005081.2, AF052006.1, AC004814.2, AC006275.1, AE001368.1, AC000084.1, AC005031.1, U80017.1, AF045555.1, AC003968.1, AL033528.19, AL033385.1, AL034548.25, AL121601.13, AL031117.1, Z84486.1, Z93018.1, AL008734.10, Z84718.2, Z83841.1, Z92542.2, AL009181.1, U46165.1, AL008983.1, L36890.1, AP000211.1, AP000150.1, AP000138.1, AP000563.1, AP000224.1, AP000133.1, AP000086.1, AP000009.2, AB020863.1, AI742600.1, AW409781.1, AA487042.1, AI570591.1, AI052677.1, AW189149.1, AA732243.1, AI342608.1, AA813983.1, AI864433.1, AL121497.1, AI313170.1, AA535345.1, AI819339.1, AI140858.1, AA463855.1, AA622061.1, AW071972.1, AI039825.1, AI739551.1, AI681889.1, N63033.1, AI916806.1, AI189978.1, AA812039.1, AW009437.1, AI926737.1, AA551298.1, AA128822.1, AI222960.1, AI656010.1, AI147461.1, AI367859.1, AA732922.1, AI335920.1, AA405100.1, AL039337.2, AA602783.1, AI138662.1, AI128055.1, AI288513.1, AI192368.1, AA514278.1, AW009113.1, AI222961.1, AI929221.1, AA128823.1, W95443.1, AI804032.1, R53599.1, AA625309.1, AI308061.1, AI308050.1, AA604594.1, AI929221.1, N68947.1, AI570799.1, AW021963.1, AW419279.1, N34337.1, AI681778.1, T70294.1, AA628356.1, AA040382.1, H66939.1, AA497027.1, AW816672.1, AI332322.1, AA758762.1, R83381.1, AA026077.1, AA349890.1, AI301205.1, AI825535.1, R92218.1, AA829906.1, AA626936.1, W95788.1, AA861469.1, AI085101.1, AA576806.1, N51568.1, AA761610.1, AA040476.1, T77759.1, AA923625.1, AI090324.1, AA410392.1, R86315.1, AI125301.1, AA911222.1, H44545.1, T47795.1, AW630895.1, AI039856.1, AI344296.1, AI978577.1, H42397.1, T77760.1, AA928570.1, AC007775.2, AC015847.1, AC069071.2, AC015849.2, AC018473.10, AC024725.2, AC024710.2, AC055811.1, AC011374.4, AC016098.3, AC005308.6, AC006286.13, AL354739.3, AL122018.22, AL162491.3, AC016928.10, AC025511.2, AC011461.2, AC005073.2, AC012198.3, AC019092.2, AC007926.6, AC007862.4, AC010999.2, AC015652.6, AC021574.3, AC025994.2, AC021786.2, AC025025.2, AC005140.6, AC004153.5, AC023441.2, AC020966.1, AC013409.3, AC005139.3, AL162417.1, AC036200.2, AC010397.5, AC008742.6, AC008813.4, AC027733.2, AC009977.3, AC026379.3, AC026549.2, AC024986.2, AC005505.6, AC015623.3, AC016071.2, AC005504.3, AC004710.3, AL122035.2, AP001392.1, AP001104.1, AC069126.1, AC005842.6, AC069111.1, AC013553.10, AC062030.2, AC027632.4, AC068850.1, AC022150.4, AC016586.4, AC022147.4, AC009143.4, AC027548.2, AC067898.1, AC016385.3, AC025481.2, AC025928.2, AC027272.2, AC027586.1, AC010787.3, AC024969.2, AC012428.4, AC017030.4, AC021305.3, AC025337.1, AC022928.1, AC018879.3, AC011694.2, AL355385.4, AL109825.17, AL161911.3, AL157831.2, AL121747.21, AL109815.2, AL096782.3,

SEQ ID NO. 186

NGO-Br-67

MK495/T3 5'

- U13369.1, X13993.1, AA161421.1, AA214215.1, AA166833.1, AA166827.1, AA085249.1, AC025630.1, AC010554.1, AC011630.2, AL355134.1, AL158197.6, AC026915.1, AC068881.1, AC023572.3, AC018688.4, AC064866.2, AC064825.3, AC010970.2,

SEQ ID NO. 187

NGO-Br-67

MK495/T7 3'

- U20938.1, NM_000110.2, U09178.1, AB003063.1, U20981.1, U09179.1, D85035.1, U39742.1, U56248.1, AF220294.1, AE003647.1, AE003413.1, AE002206.1, AC007501.2, AC004535.1, AC004945.1, AC006977.3, AE001615.1, AC004962.1, AC002981.1, AC002546.1, AC002436.1, AL050342.42, AL139074.2, U88171.1, U39654.1, AP000003.1, AI752078.1, AI786904.1, AI746780.1, W49558.1, AI119026.1, W03174.1, AW630700.1, AI931647.1, AU076411.1, AW175385.1, AW174937.1, D36086.1, AW829780.1, AW829729.1, AW829453.1, AW828679.1, AW828317.1, AW421789.1, AI765768.1, AW859693.1, AW531377.1, AV008918.1, AI599543.1, AA926321.1, AA818512.1, AA891593.1, AA851914.1, AA886930.1, R04419.1, AL354881.3, AL162575.4, AC006448.10, AC008603.4, AL137159.1, AC008961.4, AC008561.3, AC021003.4, AL356266.2, AL133548.6, AP002006.1, AC068969.1, AC055784.2, AC036131.2, AC011333.4, AC034128.2, AC009579.3, AC027374.2, AC060828.3, AC025091.3, AC067805.1, AC046147.2, AC027618.2, AC015953.3, AC024606.2, AC025821.2, AC016310.5, AC011155.4, AC023814.2, AC023246.2, AC022206.2, AC025338.1, AC015567.3, AC019239.3, AC007490.3, AC019133.3, AC020173.1, AC006846.1, AL355493.2, AL355498.2, AL158210.6, AL356101.1, AL353759.3, AL161740.4, AL139243.3, AL139244.2, AL138920.2, AL139000.2, AP001934.1, AP001484.1,

SEQ ID NO.188

NGO-Br-69

MK319/T3 5'

- NM_007186.1, AF049105.1, AL121586.28, AF022655.1, NM_008383.1, U33198.1, AE003526.1, AC006933.3, AC006486.1, U34932.1, AC004877.1, AF072845.1, AC005602.1, AD000864.1, AD000833.1, L08845.1, AE003795.1, U94409.1, AI124555.1, AW060335.1, AA647911.1, AW732245.1, AW590218.1, AW340426.1, AI989500.1, AI983119.1, AI808699.1, AI654406.1, AI653050.1, AI650974.1, AI638614.1, AI637922.1, AA977540.1, AW626159.1, AW622831.1, AW622685.1, AJ397298.1, AW504867.1, AW399321.1, AW405716.1, AW096606.1, AW094388.1, AW094030.1, AI912988.1, AI886821.1, AI823876.1, AI782590.1, AI780656.1, AI775035.1, AI771616.1, AI695784.1,

- AI539054.1, AI488077.1, AI486997.1, AI435874.1, AI391305.1, AI382942.1, AI288287.1, AI277512.1, D89319.1, AA824970.1, AA824942.1, C23550.1, AA243659.1, AA131248.1, AA130548.1, C01658.1, W18282.1, L44352.1, D51291.1, R51070.1, T23439.1, AL139226.14, AC010751.3, AC010688.4, AC014935.1, AC010690.1, AC023065.3, AC021858.2, AL158835.3, AL133230.20, AL353653.5, AL139330.5, AL135907.3, AL353609.2, AC069242.1, AC025177.3, AC025531.2, AC011432.2, AC012277.2, AC023303.2, AL157888.2, AL139237.4,

SEQ ID NO.189

NGO-Br-69

MK319/T7 3'

- 10 NM_007186.1, AF049105.1, AL121586.28, AF022655.1, NM_008383.1, U33198.1, AC004691.1, AE003666.1, AC002503.1, M34989.1, X14428.1, AE003817.1, AE003513.1, AC004931.1, AC005977.3, AC005245.1, AL163304.2, AJ004834.1, AL009174.1, AP001759.1, AP001101.1, X75910.1, NM_000449.1, AF257304.1, AF257303.1, AC006533.7, AF206287.1, NM_009307.1, AC007463.3, AE001862.1, AF092918.1, AC003689.1, AC004134.1, AF020554.1, AL161540.2, AL161539.2, AL050135.1, U60780.1, AL031686.2, Z97337.2, Z99122.1, U22062.1, X80301.1, X85786.1, M86250.1, D37793.1, L03208.1, D43752.1, Z92952.1, D85027.1, AL037087.2, AI872306.1, AI811998.1, AI401068.1, AA613882.1, AI687495.1, AI224019.1, AA970425.1, AW083819.1, AA595119.1, AW084657.1, AI817733.1, AI419425.1, AI240622.1, R87989.1, AI204529.1, AI000880.1, AA848087.1, Z40915.1, AA502324.1, AW078517.1, AI699218.1, AA729465.1, T85911.1, R88035.1, AW504249.1, AW133062.1, AW435751.1, AW346610.1, AI534994.1, AI534415.1, AI530805.1, AI519460.1, AI512712.1, AI456969.1, AI455689.1, AI404669.1, AI388686.1, AI388197.1, AI388073.1, AI387697.1, AI387259.1, AI386601.1, AI192646.1, AI135562.1, AI135091.1, AI107565.1, AI063523.1, AI063307.1, AA942336.1, AA941421.1, AA201182.1, AA392346.1, W82939.1, AW784983.1, AW607628.1, AW454537.1, AW029340.1, AW024754.1, AI991341.1, AI937337.1, AI863172.1, AI717513.1, F28098.1, AI523953.1, AI343828.1, AI340266.1, AI032053.1, AI024499.1, AA991616.1, AA937835.1, AA889325.1, AA872357.1, AA812821.1, AA805252.1, AA746136.1, AA722399.1, AA660763.1, AA586676.1, AA532648.1, AA527348.1, AA523469.1, AA504479.1, AA417368.1, AA405813.1, AA262932.1, AA228934.1, AA055130.1, N30852.1, H94195.1, D63281.1, R72540.1, AL139226.14, AL122019.21, AC027740.2, AC022067.2, AC021359.2, AC017441.1, AL162382.2, AP000491.1, AC010759.2, AC046181.1, AC026053.2, AC022262.3, AC024341.2, AC020964.1, AC015349.1, AC020328.1, AC010671.7, AF161326.1, AL162271.2, AC020923.4, AC008906.3, AC008790.4, AC011459.2, AC009544.4, AC053476.1, AC019325.3, AC016841.2, AC011568.3, AC009565.7, AC022047.4, AC021225.3, AC012354.3, AL162234.3, AL157949.2, AL138699.1, AP000451.2, AP001384.1, AP001163.1, AP000666.1,

SEQ ID NO.190

NGO-Br-70

MK061/T3 5'

- 35 Z36816.1, AC008469.4, U91320.1, AL117630.1, Z82205.1, Z50112.1, X82322.1, AB018295.1, AF142100.1, AC008498.3, AE002153.1, AC004830.1, AC004738.1, Z78419.1, AL034397.1, X63598.1, L14017.1, Y13096.1, Y13095.1, X54660.1, Y14051.1, D86934.1, AB033763.2, L14020.1, AL046916.1, AW732487.1, AA088822.1, H50443.1, T65364.1, AA112796.1, F11994.1, R11879.1, AW414271.1, AW414220.1, AA075824.1, AA363903.1, AW786911.1, AA896188.1, AW403711.1, H19785.1, AI197257.1, T65515.1, AW401567.1, AL047058.1, R55598.1, AW143393.1, AW375060.1, AI591958.1, F11904.1, AA742633.1, AA517314.1, W85360.1, T08516.1, AA184178.1, D28616.1, AA000364.1, AW796180.1, AW401580.1, T16871.1, AA739011.1, AI153477.1, W21846.1, AW785749.1, AA053446.1, D21680.1, AW390748.1, AA032616.1, AW401807.1, AW801635.1, AA027649.1, Z45691.1, F08352.1, AI410833.1, AW557036.1, AA895817.1, AW546958.1, AW575180.1, AW640041.1, AW555199.1, AJ397620.1, AA018126.1, AJ397023.1, R09436.1, AW522370.1, AJ395743.1, AJ392332.1, AW269432.1, AW169948.1, AI914378.1, AL046089.1, AV106169.1, AI371352.1, AA922035.1, AA707531.1, N91137.1, R45445.1, AW815118.1, AW163019.1, AI522333.1, AA965117.1, AA317592.1, H10898.1, R16064.1, AC023861.2, AC025415.3, AC067823.2, AC026400.2, AC008785.3, AC020710.4, AC024452.2, AC026821.2, AC021956.3, AC023442.2, AL355499.5, AC023449.3, AC036143.2, AC025544.3, AC011509.5, AC008691.4, AC023020.3, AC048481.1, AC024053.2, AC008703.3, AC027678.1, AC023812.3, AC015900.2, AC009637.3, AC025221.2, AC025565.2, AC019141.3, AC018421.3, AC021603.2, AC023380.1, AC022390.1, AL356215.1, AL355972.2, AL139276.2, AL136989.4, AL161742.3, AL353713.1, AL158204.2, AL158143.1, AL137845.1,

SEQ ID NO.191

NGO-Br-70

MK061/T7 3'

- 55 AF035296.1, AC010889.2, AF038149.1, Z70685.1, AE003463.1, AC006317.3, AF200688.1, AC008041.5, AC005684.1, AC004601.1, AL133451.1, AL050347.1, X55146.1, Z73987.1, AW471383.1, AW294879.1, AI827389.1, AI433239.1, AW575180.1, AW574507.1, AI936491.1, AI803377.1, AW575276.1, AW574501.1, AW574595.1, AW081903.1, AI017541.1, AW575023.1, AW474843.1, AW269983.1, AI143057.1, AW662466.1, AW149715.1, AI818173.1, AW027629.1, AI129967.1, AI084109.1, AA629401.1, AJ032340.1, AA775878.1, AI734859.1, AI688609.1, AA134114.1, AA088684.1, AI537873.1, AW474193.1, AA709474.1, AW087318.1, AA052969.1, T17399.1, AW244157.1, AI198524.1, AA455953.1, AA662286.1, T65434.1, N23103.1, AI500354.1, T77285.1, R48306.1, T87060.1, AW079744.1, T16870.1, AA242771.1, AA364661.1, AA725410.1, AA888835.1, AW183474.1, R48408.1, R55361.1, AI952437.1, AI383126.1, AA772585.1, R17756.1, R53154.1, AI468078.1, T83615.1, AA740428.1, AA989632.1, AA776777.1, AW088969.1,

- AA970686.1, AW467672.1, F09551.1, R84473.1, AA053446.1, AW839837.1, AW801635.1, R40543.1, AA242901.1, AW375060.1, W21846.1, AW295371.1, AA485133.1, AA281393.1, AW834883.1, AW426950.1, AW335961.1, AI953843.1, AI935134.1, AI817633.1, AI808163.1, AA924764.1, AI370430.1, AA232269.1, AA224090.1, AP001028.3, AC003094.1, AC025920.8, AC024162.2, AC021006.3, AC020773.3, AC026197.1, AC026181.1, AC020755.2, AC024159.1, AC068063.2, AC026416.2, AC020942.4, AC067757.1, AC008162.2, AC046179.1, AC027654.1, AC019099.3, AC024944.2, AC016453.4, AC013350.6, AC024511.2, AC013816.3, AC023176.3, AC016525.3, AC024911.1, AC023157.4, AC010734.3, AC012167.4, AC008131.11, AC020499.1, AC017700.1, AC006100.1, AL356370.1, AL118519.20, AL138762.5, AL137853.7, AL133388.3, AL354680.4, AL160157.3, AL138848.3, AL353733.1, AL162430.1, AL157826.2, ,
- 10 SEQ ID NO.192
NGO-Br-70
MK231/T3 5'
- 15 Z36816.1, AC006075.1, Z54328.1, AC008469.4, U91320.1, AC003034.1, AF165142.1, AC004987.2, AL137290.1, AL117630.1, Z83849.1, Z93242.1, Z82205.1, Z50112.1, X82322.1, AB018295.1, AF142100.1, AC005137.1, AE002153.1, U89337.1, AC005940.3, AC004738.1, AE000895.1, AL163229.2, AL034397.1, X63598.1, L14017.1, Y13096.1, Y13095.1, X54660.1, Y14051.1, AP001684.1, D86934.1, AB033763.2, AP000705.2, Y11769.1, L14020.1, AL046916.1, AW732487.1, H50443.1, AA088822.1, T65364.1, AA112796.1, F11994.1, R11879.1, AA075824.1, AW403711.1, T65515.1, AW414271.1, AW414220.1, AW786911.1, AA363903.1, AA896188.1, AW401567.1, AL047058.1, R55598.1, H19785.1, AI197257.1, F11904.1, AW143393.1, AW401580.1, AW796180.1, AA517314.1, W85360.1, AA742633.1, AI591958.1, T08516.1, AW375060.1, AW401807.1, AA184178.1, D28616.1, AA000364.1, T16871.1, F08352.1, Z45691.1, AW785749.1, D21680.1, AW390748.1, AA739011.1, AI153477.1, AA032616.1, AA027649.1, AA018126.1, AW403200.1, AW402516.1, W21846.1, AA053446.1, AW402128.1, AI410833.1, AW557036.1, AA895817.1, AW546958.1, AW640041.1, AW555199.1, AJ397620.1, AI254622.1, T31811.1, AJ397023.1, AJ395743.1, AJ392332.1, 25 AW269432.1, AW169948.1, AI914378.1, AL046089.1, AV106169.1, AI371352.1, AA922035.1, AA707531.1, N91137.1, R45445.1, AW815118.1, AW163019.1, AI592661.1, AI522333.1, AI341327.1, AA317592.1, AA184644.1, H10898.1, R16064.1, AC027678.1, AC022390.1, AC023861.2, AC011591.4, AC027683.1, AC015844.4, AC015875.1, AL157397.2, AP001926.1, AP001284.1, AP000764.1, AP000614.3, AC025415.3, AC067823.2, AC019331.3, AC026400.2, AC010324.4, AC020710.4, AC022916.2, AC024452.2, AC027437.2, AC027069.2, AC026008.2, AC022696.3, 30 AC021956.3, AC023954.2, AC023442.2, AC023241.2, AL355860.1,
- SEQ ID NO.193
NGO-Br-70
MK464/T3 5'
- 35 Z36816.1, AK000595.1, Z54328.1, AC006960.1, AC007540.3, Z82205.1, Z50112.1, X82322.1, AF142100.1, AC002380.1, AE002153.1, AC004738.1, AC005371.1, AJ251829.1, Z85996.1, AL034397.1, X63598.1, L14017.1, Y13096.1, Y13095.1, X54660.1, Y14051.1, D86934.1, AB033763.2, L14020.1, AL046916.1, AA075824.1, AW403711.1, H50443.1, T65364.1, AW401567.1, T65515.1, AL047058.1, R55598.1, F11904.1, F11994.1, AW401580.1, AW796180.1, AW732487.1, AW401807.1, AA088822.1, Z45691.1, AW786911.1, AI197257.1, AA896188.1, AW403200.1, AW402516.1, 40 AA018126.1, R11879.1, T16871.1, T08516.1, AA517314.1, W85360.1, H19785.1, AA112796.1, T31811.1, AW414220.1, AW405526.1, AW414271.1, AW143393.1, AA363903.1, AW402128.1, AA027649.1, AA742633.1, AW785749.1, AI592661.1, F08352.1, AI591958.1, D21680.1, AW390748.1, AW402023.1, AA184644.1, AA184178.1, D76728.1, D28616.1, AA000364.1, AW640041.1, AJ397620.1, AJ397023.1, AV106169.1, AW815118.1, AW163019.1, AW159142.1, AW159141.1, AW159140.1, AW158139.1, AW158059.1, AI657929.1, AA317592.1, H10898.1, R16064.1, AC023861.2, 45 AC025415.3, AC067823.2, AC020710.4, AC024452.2, AC011052.4, AC021956.3, AC023442.2,
- SEQ ID NO.194
NGO-Br-70
MK464/T7 3'
- 50 AF035296.1, AE003725.1, AC007053.15, U96104.1, U58920.1, AF038149.1, Z70685.1, D87992.1, AC006317.3, AC008041.5, AC005684.1, AC004601.1, AL133451.1, AL050347.1, X55146.1, Z73987.1, AW575180.1, AA775878.1, AW575276.1, AW574595.1, AW575023.1, AW574501.1, AW574507.1, AW294879.1, AI827389.1, AA629401.1, AW471383.1, AI433239.1, AI936491.1, AI803377.1, AW149715.1, AW081903.1, AI017541.1, AW474843.1, AW269983.1, AW027629.1, AI143057.1, AW662466.1, AI818173.1, AI129967.1, AI084109.1, AI032340.1, AI734859.1, 55 AI688609.1, AI134114.1, AA088684.1, AI537873.1, AW474193.1, AA709474.1, AW087318.1, AA052969.1, T77285.1, T17399.1, AW244157.1, R53154.1, AI198524.1, AA455953.1, AA662286.1, R48408.1, N23103.1, T65434.1, AI500354.1, AA053446.1, AW801635.1, AW079744.1, R48306.1, T16870.1, T87060.1, AA364661.1, T83615.1, AA242771.1, AA725410.1, AA888835.1, AW183474.1, AI952437.1, AI383126.1, R55361.1, AA772585.1, AW839837.1, R17756.1, AI468078.1, AW375060.1, AW088969.1, AA740428.1, AA989632.1, AA776777.1, W21846.1, AA970686.1, F09551.1, 60 AW467672.1, R84473.1, AA242901.1, D30911.1, R40543.1, AW479983.1, AW834883.1, AW826181.1, AV417825.1, AW557036.1, AW555199.1, AW546958.1, AW527142.1, AW491879.1, AW426950.1, AW335961.1, AI229288.1, AI103583.1, AI155354.1, AI153477.1, AA895817.1, AA739011.1, AA290498.1, AA000364.1, AP001028.3, AC025920.8, AC024162.2, AC021006.3, AC020773.3, AC026197.1, AC026181.1, AC020755.2, AC024159.1, AC017539.1, AC006589.3, AC008141.2, AC068063.2, AC067757.1, AC046179.1, AC027654.1, AC019099.3, AC024944.2,

AC016453.4, AC013350.6, AC024511.2, AC013816.3, AC023176.3, AC016525.3, AC024911.1, AC023157.4, AC010734.3, AC008131.11, AC017700.1, AL356370.1, AL118519.20, AL137853.7, AL133388.3, AL354680.4, AL138848.3, AL353733.1, AL162430.1, AL157826.2,

5 SEQ ID NO.195

NGO-Br-71

MK137/T3 5'

AB025608.1, AB009048.1, D45408.1, AB023029.1, AC005922.1, U64851.1, U92032.1, AJ001535.1, U66525.1, AB008265.1, AP000495.1, AC007187.4, AE003492.1, AC010125.3, AC002088.1, AC003071.1, AE001774.1, 10 AC005509.1, AC005900.1, AE001119.1, AC004063.1, AF040653.1, AL353995.1, AL031466.1, AL132715.2, AL161666.2, U28760.1, AL109609.5, AL031579.1, Z66567.1, Z82211.1, Z99129.1, AL021918.1, AL022159.1, AJ001088.1, AL041831.1, AA911802.1, AI791494.1, AI791283.1, AW639607.1, AW540750.1, AI553588.1, AI194910.1, AW565485.1, AW470837.1, AW440357.1, AW106522.1, AV201819.1, AL037101.1, AV091786.1, AI444814.1, AI114364.1, AI002480.1, AA002743.1, AL355146.4, AL161434.3, AL132673.16, AL356292.1, AC027069.2, 15 AC067734.3, AL161788.4, AC058786.7, AC025936.2, AC046186.2, AC009944.3, AC008459.4, AC026989.2, AC025669.2, AC026505.3, AC026390.1, AC024422.2, AC021696.3, AC018826.3, AC012525.6, AL157785.2, AL355332.1, AC062004.2, AC013244.8, AC007943.2, AC027679.1, AC010429.4, AC027741.2, AC026557.2, AC012349.3, AC020732.3, AC027625.2, AC051630.1, AC026958.2, AC021514.3, AC012148.2, AC022580.2, AC009680.5, AC010993.10, AC010994.9, AC010730.4, AC010101.4, AC012195.2, AC014437.1, AC010843.8, 20 AC018408.1, AC011673.2, AC011114.1, AC010132.2, AC007555.1, AC006799.1, AL356357.1, AL356009.2, AL121954.4, AL139278.2, AL354920.1, AL139397.2, AL162719.1, AL138724.2, AP001954.1, AP001823.1,

SEQ ID NO.196

NGO-Br-71

25 MK137/T7 3'

AC006014.2, AC004705.2, AL035652.5, AC044786.2, AE002147.1, AC004848.1, AC007735.2, AC004907.2, AF107885.2, U67494.1, AL161588.2, AL031986.1, AL022373.1, AI732538.1, AI652638.1, AA505930.1, AA991355.1, AW235448.1, AL041832.1, AI791494.1, AI791283.1, AL041831.1, AV254980.1, AW552644.1, AV267495.1, AV264008.1, AV260689.1, AV259564.1, AV258534.1, AV208825.1, AV260910.1, AV264098.1, AW552124.1, 30 AW317034.1, AA391903.1, AA536375.1, AA536264.1, AV210836.1, AW692176.1, AW438480.1, AJ388903.1, AW210311.1, AI643503.1, AI545190.1, AI394892.1, AI141264.1, AA497287.1, AA404284.1, AA256257.1, AW567217.1, AW361948.1, AV267670.1, AU077746.1, AI906249.1, AI901829.1, AV034590.1, AI621492.1, AI551985.1, AI395360.1, AI179945.1, AU030825.1, AA906203.1, AA894271.1, AA852029.1, AA673655.1, C62664.1, C61515.1, AA445695.1, AA418204.1, AA141341.1, AA104978.1, H11780.1, R13493.1, T81922.1, Z44433.1, AL356292.1, AL355146.4, 35 AL161434.3, AL132673.16, AL136305.5, AC007943.2, AC011078.2, AL133508.2, AL138763.2, Z93245.1, AC011585.3, AC018976.2, AC011939.2, AC014847.1, AC022442.3, AC009820.3, AC026491.3, AC022467.4, AC016221.4, AC021619.3, AL137017.5, AL121715.2, AL133322.3,

SEQ ID NO.197

40 NGO-Br-72

MK419/T3 5'

AK000528.1, NM_016123.1, AF155118.1, AL161587.2, M63234.1, AL031135.1, AC005868.1, AL096699.11, X98048.1, NC_001148.1, AF249887.1, AC002392.2, AE003724.1, AF030694.2, NM_004690.1, AC007313.3, AF164041.1, AC006559.6, AC007102.4, AF104413.1, AF104414.1, AE001409.1, AF015463.1, AC005220.1, U67476.1, AL161573.2, 45 AL161572.2, Z68136.2, AL049662.1, AL121783.1, S46763.1, AL021749.1, AL034558.2, U45981.1, Z70720.1, Z73565.1, Z29667.1, L34028.1, L34027.1, D10606.1, AB011474.1, AB026649.1, M84660.1, M74445.1, U07163.1, H53674.1, AI967314.1, AW560842.1, AW761247.1, AI794934.1, AI812788.1, AI774138.1, AI772185.1, AW876515.1, AW756795.1, AW329262.2, AW329038.2, AW649958.1, AW568064.1, AW496536.1, AW348715.1, AW334566.1, AW094252.1, AI960995.1, AI920205.1, C95693.1, AI594372.1, AA592233.1, H36649.1, T92029.1, T18143.1, AC016143.5, 50 AC021719.3, AC025567.6, AC026763.5, AC010161.5, AL354696.1, AC022507.12, AC023928.3, AC009671.3, AC024954.2, AL354815.1, AL121880.15, AC024886.6, AC022072.8, AC031992.2, AC024244.4, AC067883.1, AC057605.1, AC055596.1, AC055595.1, AC049865.1, AC049836.1, AC048201.1, AC048200.1, AC027086.2, AC021723.3, AC021849.3, AC013809.3, AC019131.3, AC011308.3, AC013549.2, AC006091.9, AC017374.1, AL353592.1,

55

SEQ ID NO.198

NGO-Br-72

MK419/T7 3'

AK000528.1, NM_016123.1, AF155118.1, AC000118.1, AC004033.3, AC004232.1, AC009509.7, AL049839.3, 60 AC008521.5, AL021546.1, AC003002.1, AC000378.1, AL096791.12, AC007227.3, AF051976.2, AC005859.1, AC002565.1, AL132639.2, AC005581.1, AL035400.13, AP000180.1, AP000104.1, Z85987.13, AC005695.1, AC005563.1, AL049643.12, AC005821.1, AC005088.2, AC005031.1, AL135749.2, AL035249.6, AC004805.1, U52111.1, AL138976.3, AL121985.13, AC005914.1, AL035588.21, AC005081.2, AC005519.2, AC007993.15, AC005486.2, AL031848.11, AC004223.1, AF001550.1, AL022318.2, Z98742.5, U62292.1, D84394.1, AP000313.1, AL163305.2, AL121988.10,

- AP001760.1, AF030876.1, AC005288.1, AC003663.1, AL121586.28, AC004858.2, AF001549.1, Z98200.8, AC002072.1, AC004887.2, AC002299.1, AC005874.3, AF134471.1, AC004477.1, AC005730.1, AC006061.1, AL021939.1, AJ010770.1, AC011462.4, U47924.1, AL035458.35, AL021937.1, AC008101.15, AC009247.11, AC004771.1, AL031133.1, AL049766.14, AC006115.1, AC002369.1, AL133500.2, AP000168.1, AP000053.1, AP000121.1, AC000134.14, AC005803.1, AC005514.1, AL031281.6, AC004745.1, AL035422.12, AC003007.1, Z95152.1, AC004983.2, AL163282.2, AL163267.2, AP000045.1, AC005745.4, AC011508.4, AL023879.1, AL022399.2, AA114131.1, H78605.1, H78687.1, AA084609.1, H07953.1, AA630854.1, AW023111.1, AA501614.1, T74524.1, AA468505.1, AA614254.1, AI889579.1, AA515939.1, AA515728.1, AA612727.1, N64587.1, AW674631.1, AW069227.1, AI679002.1, AI634187.1, AI457313.1, AA536040.1, AA485328.1, AI925869.1, AA622801.1, AA602906.1, AA228368.1, W02749.1, R98218.1, AI653776.1, AI244157.1, AI708005.1, AI421257.1, AW082104.1, AI962030.1, AA715173.1, AA715075.1, AA664126.1, AA297666.1, AL134940.1, AI733856.1, AA613761.1, AA447247.1, AA347969.1, AA284247.1, C15363.1, T54783.1, AW151824.1, AI290405.1, AA864603.1, T49633.1, AW151201.1, AW090754.1, AI933714.1, AW304536.1, AI446336.1, AI278972.1, AA573213.1, AA456924.1, AA303054.1, R93919.1, AW341978.1, AL118612.1, AA552989.1, AW131356.1, AI754105.1, AA502991.1, T47936.1, AI733523.1, AI310343.1, AA669054.1, AA563770.1, AW844636.1, AW770827.1, AI669421.1, AA847499.1, AW576251.1, AW500684.1, AW192599.1, AI755214.1, AI754567.1, AI569100.1, AI249688.1, AI187148.1, AI080307.1, AI038304.1, AA584862.1, AW188742.1, AI077941.1, AA535216.1, T47324.1, AI817230.1, AI525100.1, AI560085.1, AW510513.1, R66121.1, AI904811.1, AA779075.1, AL043144.2, AA225519.1, AC021719.3, AC016143.5, AL355386.1, AC025262.5, AL356280.2, AL162411.1, AC008760.4, AC016953.5, AC010807.4, AL139252.2, AC026868.2, AC009470.3, AL353743.1, AC002993.1, AC009124.4, AC018942.2, AC022826.3, AC023329.2, AL158196.4, AC025278.2, AC021258.3, AC025395.2, AL158165.3, AL034372.30, AL109806.13, AC037464.2, AC011484.2, AC019194.2, AC016888.4, AL160010.3, AC016073.2, AC034198.2, AC027631.2, AL139807.5, AC007621.13, AC008812.6, AL162611.4, AC005995.2, AL121943.14, AC012014.5, AL355490.3, AC008731.4, AL354864.1, AC019071.3, AC026469.3, AL354720.3, AL158014.4, AC026790.2, AP002016.1, AC008749.4, AC021852.3, AC012236.3, AL121845.18, AL163051.1, AC061979.2, AC012291.3, AC026160.1, AC024380.2, AC018808.3, AL158827.4, AC016554.5, AC022554.2, AC006393.6, AC005867.1, AL162584.2, AL161615.2, AL138788.1, AC010607.4, AC026286.2, AC026817.1, AP001177.1, AC025060.3, AC015714.4, AC011247.3, AL121834.8, AL136450.1, AC013564.3, AC012451.3, AC021510.2, AC016485.2, AL137186.4, AL162595.5, AL137247.3, AL137856.2, AC025695.3, AL158152.3, AC068485.1, AC008555.3, AC020697.3, AC010149.4, AL139255.1, AC011501.5, AC008774.3, AC027551.2, AP001501.1, AC007366.3, AC041047.3, AL136139.5, AP001198.1, AC022410.3,

SEQ ID NO.199

NGO-Br-73

MK642/T3 5'

- AF147338.1, AK000060.1, AE003569.1, AF111426.1, AC007048.4, AC005385.3, U60334.1, AF020802.1, AL163269.2, Z95889.1, Z83317.1, AP001724.1, AP000687.1, AJ229041.1, AC008526.5, AC000122.1, AC005901.1, AL117327.5, AP000377.1, AE003526.1, AC007216.2, AC005249.1, U95742.1, AC006933.3, AC004512.1, AL133419.15, AI692537.1, AW243461.1, AW235223.1, AI671570.1, AW653857.1, AW274251.1, T58078.1, T58198.1, AW485453.1, AW428440.1, AA918819.1, AA017211.1, AA247593.1, AV347965.1, AV103024.1, T27488.1, AV242595.1, AV341902.1, AV346780.1, T11529.1, AV245244.1, AV229602.1, AU030011.1, AW575669.1, AW557886.1, AW529718.1, AW212594.1, AV376787.1, AV374992.1, AV367312.1, AV340052.1, AV273236.1, AV265359.1, AV250828.1, AV221007.1, AV219070.1, AV218774.1, AV206725.1, AW066980.1, AI847479.1, AI837994.1, AI835991.1, AV159366.1, AV169546.1, AV152290.1, AV142949.1, AV141913.1, AV130057.1, AV126713.1, AV117344.1, AV115850.1, AV102420.1, AV095928.1, AV075293.1, AV063673.1, AV057658.1, AV056084.1, AV056034.1, AI747610.1, AV038768.1, AV030316.1, AV004917.1, AI574942.1, AI550786.1, AI463222.1, AI462153.1, C78201.1, AA423250.1, AA259531.1, AC015955.4, AP001033.3, AC017914.1, AC012303.2, AL354863.4, AL139010.6, AC027201.2, AC012893.1, AL161612.4, AL022285.6, Z93065.1, AC017070.3, AC055820.2, AC026195.2, AC016205.4, AC011178.3, AC012584.5, AC017432.1, AL160257.3, AC008784.5, AC010323.4, AC034299.2, AC034282.2, AC016893.3, AC032000.1, AC024010.2, AC023809.6, AC022375.1, AL138904.2, AL354990.1,

SEQ ID NO.200

NGO-Br-73

MK642/T7 3'

- AF147338.1, AK000060.1, X80821.1, U60334.1, AE003480.1, AC000122.1, M96441.1, AC005901.1, AC000044.2, AC000034.2, AC004984.1, L28955.1, AL133367.2, AL080079.1, Z80901.1, AL033377.2, AI692537.1, AW653857.1, AA918819.1, T58078.1, T58198.1, AV349661.1, AV349644.1, AV350717.1, AV328677.1, AW070252.1, AW775904.1, AW792828.1, AW274009.1, AW193700.1, AL121308.1, AW023476.1, AI910455.1, AI765240.1, AI567672.1, AI376609.1, AI351633.1, AI291783.1, AI291446.1, AA652658.1, AA570928.1, AA496039.1, H93102.1, R86033.1, R77622.1, R68550.1, AW774292.1, AW413948.1, AW155190.1, AW029172.1, AW009281.1, AU069485.1, AU030011.1, AI182684.1, AI122141.1, AI096187.1, AA839637.1, AA762941.1, AA691770.1, C72277.1, AA548171.1, AA451530.1, AA423704.1, W29889.1, H44377.1, T11529.1, AC015955.4, AP001033.3, AC021893.10, AC027514.2, AL139010.6, AP001460.2, AC026658.2, AC027061.2, AF235092.1, AC015631.3, AC023680.2, AC010000.2, AC015395.1, AL355377.2, AC024702.3, AC016493.3, AC024681.2, AC024087.3, AC011940.3, AC022734.2, AC011916.1, AC010942.1, AC005000.1, AL161904.2, AL139300.2,

-115-

SEQ ID NO. 201

NGO-Br-74

MK761/T3 5'

- 5 AE003523.1, AC006257.1, AC005330.1, AL355927.1, U56728.1, AL049766.14, AB037825.1, AK000573.1, AE003832.1, AE003801.1, AE003785.1, AC002087.1, NM_002172.1, AC004829.2, AC005887.3, U29244.1, AC004293.1, X74470.1, Z11532.1, X72306.1, V00542.1, AA765066.1, R57163.1, AA896010.1, AA178333.1, C80989.1, AW105563.1, AA930992.1, C80990.1, C81381.1, AA612483.1, AA383435.1, AW326797.1, AW447131.1, AA681894.1, AW104025.1, Z36392.1, Z36470.1, AW413469.1, AA684257.1, AW149818.1, AL265028.1, AW781170.1, AI907775.1, AA735139.1, 10 AA371572.1, AA313662.1, AA299963.1, AA148581.1, AA135264.1, AW774261.1, AW609685.1, AW300461.1, AI397692.1, AI069165.1, AI068528.1, AA841557.1, AA755125.1, AA623736.1, AC008795.5, AC008855.4, AC01145.3, AC012122.2, AC055879.2, AC069189.1, AC017022.3, AC022187.2, AC013500.3, AC019563.1, AL162579.4, AC026334.3, AC069079.1, AC069026.1, AC027328.2, AC010337.3, AC010472.4, AC008549.4, AC011448.2, AC026393.2, AC011289.3, AC027094.2, AC025974.2, AC025956.2, AC022823.3, AC017010.2, AC015904.3, 15 AC013370.5, AC007477.5, AC020693.3, AC022302.3, AC007413.4, AC007330.5, AC017049.3, AC022176.1, AC019249.3, AF209070.1, AC018198.1, AC017513.1, AC015178.1, AL353664.3, AL354675.2, AL353690.1, AP001372.1, AP001367.1, AP001103.2, AP001085.2, AP001030.2,

SEQ ID NO.202

20 NGO-Br-74

MK761/T7 3'

- AC025098.4, AC005560.2, AC027661.1, AC011806.1, AC006257.1, AC005330.1, AL355927.1, U56728.1, AL049766.14, AB037825.1, AK000573.1, AE003801.1, AE003478.1, NM_006496.1, NM_002172.1, AC005887.3, AC009465.5, U29244.1, AC005317.1, AC004293.1, AL023518.2, X74470.1, Z11532.1, V00542.1, X54048.1, AK001973.1, 25 AK001746.1, M27543.1, AB014467.1, J03198.1, AA765066.1, R57163.1, AW105563.1, C80989.1, C80990.1, C81381.1, AA896010.1, AA178333.1, AA930992.1, AA612483.1, AA383435.1, AW104025.1, AA681894.1, AW326797.1, AW447131.1, Z36392.1, Z36470.1, AW413469.1, AA684257.1, AL265028.1, AW149818.1, AI453042.1, AW781170.1, AV349095.1, AV248065.1, AI907775.1, AA735139.1, AA371572.1, AA313662.1, AA299963.1, AA148581.1, AA135264.1, AV211122.1, AI829193.1, AV172729.1, AI766084.1, AI620180.1, AI400167.1, AI397692.1, AI356812.1, 30 AI337030.1, AI269102.1, AI261301.1, AI092059.1, AI033551.1, AI033398.1, AA954839.1, AA838238.1, AA766120.1, AA755125.1, AA736929.1, AA706621.1, AA704130.1, AA652992.1, C72329.1, AA587349.1, AA490356.1, AA235987.1, AA085406.1, AC008795.5, AC008855.4, AC01145.3, AC012122.2, AC022061.2, AC016691.4, AC022960.2, AC009831.3, AC055879.2, AC027133.1, AC017022.3, AC019563.1, AL162579.4, AC027328.2, AC015904.3, AC024016.2, AL355310.3, AL353664.3, AL354675.2, AL139802.3,

35 SEQ ID NO.203

NGO-Br-75

MK344/T3 5'

- AL157792.2, AL033380.11, U55042.1, X64070.1, AC006607.1, AC006576.15, AF070718.1, AC004703.1, AL122003.17, 40 AB015752.1, AC011309.4, AF030876.1, NM_013369.1, U82695.2, AF031075.1, AF194032.1, AF081058.1, AF081057.1, AF081056.1, AF081055.1, AF058419.1, U68299.1, U52112.1, AL163298.2, AL080286.16, AL096677.18, L06231.1, X53705.1, AP001753.1, AP001059.1, X81326.1, X53709.1, X53708.1, D86115.1, AW650954.1, AL119238.1, AW030498.1, AI661495.1, AA831895.1, AW393793.1, AW393785.1, AW213405.1, AV230556.1, AW124066.1, AI931357.1, AV124496.1, AI631758.1, AI585396.1, AA918201.1, AA890172.1, AA882048.1, AA757981.1, AA538210.1, 45 AA474203.1, AA402070.1, AA199109.1, AA053059.1, R82169.1, R23708.1, AC063960.2, AC012053.2, AC020661.4, AC023137.2, AC026045.3, AC034236.1, AC016530.3, AC019068.3, AC015557.1, AL138781.3, AL162151.2, AC062006.2, AC044906.2, AC036174.2, AC021165.3, AC023133.2, AC009677.3, AC021462.3, AL353803.1, AL160268.3,

50 SEQ ID NO.204

NGO-Br-75

MK344/T7 3'

- AL049749.2, Z83733.1, AE003545.1, U97009.1, AC005512.1, Z78018.1, AB036794.1, AC008701.5, AC006319.3, AC004160.1, AC005026.1, AL049859.7, Z69637.1, AL035686.12, AE003804.1, AE003275.1, NC_002387.1, U17009.2, 55 AC002066.1, AJ133269.1, AL030995.1, AI964952.1, AW847510.1, AW453459.1, AW125886.1, AI562053.1, AI180354.1, AI130241.1, AW840570.1, AW840396.1, AW795642.1, AW600573.1, AW588022.1, AW455711.1, AW331252.1, AW306566.1, AI913878.1, AI813344.1, AI767557.1, AI593529.1, AA888474.1, AA603364.1, AA601251.1, AA550370.1, AA428312.1, AA305564.1, D78836.1, Z45190.1, AC063960.2, AC006447.17, AC011085.4, AC023285.2, AP001027.1, AL355358.1, AC025684.2, AC021877.4, AC011243.3, AL160291.2, AC006404.20, AC015424.1, AC019870.1, 60 AC020079.1, AC007835.5, AC010565.3, AC010690.1, AC068007.1, AC062025.1, AC009578.3, AC023820.2, AC015567.3, AL109965.22, AL132671.19, AC069237.1, AC044882.2, AC068593.1, AC064847.1, AC023136.3, AC021555.3, AC026242.3, AC013685.3, AC016808.2, AC017040.3, AC013278.1, AP002000.1, AP001931.1,

SEQ ID NO.205

NGO-Br-76
MK415/T3 5'

- 5 AB033888.1, NM_009236.1, L35032.1, AF047389.1, AF047043.1, AF017182.1, U66141.1, AJ001029.1, NM_000346.1, AF116571.1, NM_006941.1, NM_005686.1, AF149301.1, AC007461.8, AF006501.4, AF098915.1, AF083105.1, AF029696.1, AL031587.3, S74504.1, Z46629.1, AJ001183.1, L29086.1, U08223.2, NM_007084.1, NM_009238.1, NM_009233.1, NM_009234.1, NM_005986.1, AF107044.1, AF061784.1, AF009414.1, AL163672.1, AX001335.1, AX001334.1, U12533.1, AJ004858.1, X96997.1, X70298.1, X94126.1, AB014474.1, D61688.1, M90534.1, D83649.1, AB012236.1, Y13436.1, AA764352.1, AW321606.1, AL043036.2, AL120408.1, AA172336.1, AW533152.1, AW532037.1, AW532030.1, AW529354.1, AW414006.1, AW251615.1, AW060475.1, AI884987.1, AI816765.1, 10 AV116901.1, AI600115.1, AI594348.1, AI569726.1, AA965274.1, AI416080.1, AI406268.1, AI327463.1, AI176078.1, AI137787.1, AA734962.1, AA616534.1, AA521730.1, AA040785.1, AW822773.1, AW506135.1, AW417535.1, AW046996.1, AW015864.1, AI566947.1, AI552551.1, AI359981.1, AL355803.2, AC024914.17, AL137061.2,

SEQ ID NO. 206

- 15 NGO-St-114 5' combined;

- AC005618.1, X97999.1, NM_005642.1, U18062.1, Z65840.1, NM_011901.1, AF144562.1, Z65839.1, AC004540.1, AL137039.1, U20660.1, AE003630.1, U15947.1, AL132889.2, AL132885.1, AE003646.1, AE003605.1, AE003412.1, AF146393.1, AC004058.1, U32788.1, AC004056.1, AL355094.2, AJ131018.1, Z97180.1, AP001821.1, AC005825.3, AC006804.3, AE003778.1, AE003576.1, AE003510.1, AF136829.1, AF081203.1, AC004992.1, AF195611.1, AF195610.1, 20 AC006961.16, AC006581.16, AC005414.2, U68299.1, AF016687.1, U23527.1, L78833.1, U18349.1, AC004267.1, AF047659.1, U09744.1, AL117206.1, AL137080.2, Z81467.1, Z81028.1, Z82180.19, Z77652.2, Z75892.1, AL050305.9, Z77249.1, Z97629.1, AJ250862.1, U55366.1, X06535.1, U40028.1, AP001331.1, AP001111.1, AB029433.1, AB003324.1, D00170.1, Y17816.1, AU077198.1, AW673639.1, AA315968.1, AW029214.1, AA622246.1, D59188.1, AI904582.1, AW877796.1, AA595371.1, AA278660.1, AW877790.1, AA894917.1, AA252724.1, AA328618.1, AW402842.1, 25 AW362899.1, H14854.1, AW394189.1, AA312894.1, AW365030.1, T72766.1, AW582369.1, T65190.1, T52076.1, AW609538.1, AW366774.1, AA372836.1, AW380678.1, AA460590.1, F11914.1, AA383821.1, T47333.1, AA336307.1, AW403760.1, AA337398.1, AI951709.1, T34968.1, AA346865.1, AL119477.1, AW816164.1, AA348197.1, AA619797.1, T05543.1, AI158644.1, T83104.1, C03576.1, C03455.1, T86869.1, AV121343.1, AA572579.1, AA095559.1, AA517694.1, AA920998.1, AV205440.1, AA763469.1, AV212370.1, AI117791.1, AV213552.1, AV212700.1, C89279.1, H21207.1, 30 AV216550.1, AV100198.1, AV218081.1, AV214781.1, AV199703.1, AI722257.1, AA336858.1, AA102949.1, AA182987.1, W26005.1, AW645787.1, AW638295.1, AW199696.1, R52386.1, AW563125.1, AW563124.1, AW506736.1, AW506735.1, AW506714.1, AW506713.1, AW433456.1, AW330840.1, AW056105.1, AI987345.1, AW728753.1, AI519245.1, AI511851.1, AI456317.1, AI455940.1, AA264246.1, AI756661.1, AI755675.1, AC008579.2, AC020971.1, AC025193.1, AC021705.4, AC025256.4, AC068708.2, AC020898.3, AC020907.3, AC009035.5, AC026886.2, 35 AC021271.4, AC025944.3, AC025945.2, AC026220.2, AC007186.8, AC019704.1, AC015613.1, AC007913.1, AL158151.5, AL157888.2, AL136135.2, AL133263.2, Z98857.36, AC026124.3, AC027751.2, AC026384.2, AC024050.6, AC019207.3, AC020725.3, AC019835.1, AC014673.1, AC008189.2, AL109836.17, AP001894.1, AP001863.1, AP001548.1, AP001544.1, AP001493.1, AP001282.1, AP000906.2,

- 40 SEQ ID NO.207

NGO-St-114
YS071/T3 5'

- NM_005642.1, AC005618.1, U18062.1, X97999.1, NM_011901.1, AF144562.1, Z65840.1, AE003630.1, U15947.1, AL132889.2, AL132885.1, AF146393.1, AC004058.1, AJ131018.1, AP001821.1, AE003778.1, AE003576.1, AC004992.1, 45 AC005414.2, AF016687.1, L78833.1, AC004267.1, AF047659.1, Z81028.1, U55366.1, U40028.1, AW029214.1, AU077198.1, AW877796.1, AW877790.1, AA595371.1, AA252724.1, AA894917.1, AA622246.1, AA312894.1, AA328618.1, AA460590.1, AW403760.1, T47333.1, AI904582.1, T72766.1, AA278660.1, AA372836.1, F11914.1, T34968.1, T65190.1, AW673639.1, H14854.1, T05543.1, AA383821.1, AI158644.1, AA315968.1, AA572579.1, AW402842.1, AA517694.1, AW362899.1, AW582369.1, AV121343.1, AA920998.1, AW816164.1, AW394189.1, 50 AV205440.1, C89279.1, AV213552.1, AV212370.1, AW609538.1, AV212700.1, AW365030.1, AA619797.1, AW380678.1, C03576.1, AV216550.1, AV100198.1, AI722257.1, AA182987.1, AV218081.1, AV214781.1, AL119477.1, D59188.1, AW645787.1, AW638295.1, AW199703.1, AW199696.1, AW728753.1, AI519245.1, AI511851.1, AI456317.1, AI455940.1, AA264246.1, AI471179.1, AW375040.1, AW375037.1, AW021363.1, AI976597.1, AV049065.1, C54464.1, C54153.1, C51985.1, AA426143.1, AA406093.1, C11684.1, R74232.1, D27736.1, AC008579.2, AC020971.1, 55 AC025193.1, AC020907.3, AC007186.8, AC019704.1, AL136135.2, AL133263.2, Z98857.36, AC026124.3, AP001863.1, AC068193.4, AC036188.2, AC024947.2, AC025766.3, AC010623.3, AC016558.3, AC008534.3, AC036127.2, AC068579.1, AC009142.4, AC011724.2, AC024698.4, AC022198.2, AC021719.3, AC022788.2, AC010764.3, AC009695.4, AC025532.2, AC021157.3, AC016890.4, AC022273.2, AC016685.4, AC011266.3, AC023349.2, AC018492.3, AC012101.3, AC024158.1, AC012448.3, AC010741.3, AC012387.4, AC017805.1, AC014787.1, 60 AC006937.5, AC006905.1, AL356435.1, AL109955.13, AL135939.9, AL133542.3, AL161790.3, AL162418.2, AL159176.3, AP001993.1,

SEQ ID NO. 208
NGO-St-114

YS071/T7 3'

NM_005642.1, AC005618.1, U18062.1, X97999.1, NM_011901.1, AF144562.1, AL009178.4, AB016897.1, AL109801.13, AE003618.1, AC007504.3, AC007172.6, AC005834.1, AB007651.1, AE003764.1, AE003738.1, AL078581.11, AL031259.1, Z81455.2, Z82900.1, AB025604.1, Z30211.1, AC012082.6, AC004747.2, AC004521.2, AC024750.1, AF233591.1, AC012099.4, AC003012.1, AC005076.2, AC007269.2, AF121898.1, AC006075.1, AC004583.1, AF042091.1, AL163282.2, AL117191.4, AL121716.16, AL161585.2, AL121754.18, AL008723.8, AL021182.1, AL031429.11, AL035593.11, AL023094.2, U37796.1, X04112.1, X15215.1, AI052691.1, AI346408.1, AW304965.1, AI709369.1, AW190867.1, AW192823.1, AI818211.1, AI434577.1, AW264130.1, AA613880.1, AA507377.1, AA417113.1, AI675129.1, AI371764.1, AI285611.1, AI125952.1, AW069225.1, AI376092.1, W65333.1, AI804531.1, AI366201.1, AI940448.1, AW860175.1, AW604918.1, AA326994.1, AA461518.1, AA063580.1, AA825152.1, AA604623.1, AI278875.1, AA947107.1, AA417019.1, W39724.1, AI274749.1, W15503.1, AA776228.1, AW512466.1, W61316.1, AI090392.1, AI356847.1, AW607519.1, AA975911.1, AA037065.1, AA838760.1, AW089083.1, AA635906.1, AA824551.1, AA602587.1, AW265444.1, AA188912.1, T90567.1, AW519252.1, AW150510.1, R73733.1, AA508614.1, W56065.1, T86870.1, AL118821.1, AA508722.1, AA886319.1, AA577447.1, AA380499.1, AA314905.1, AA854628.1, AA412648.1, H84875.1, AW614384.1, F09561.1, AA326994.1, AA037079.1, AA380870.1, R30839.1, AI287373.1, AI654286.1, R27607.1, T65121.1, H85281.1, N87733.1, AA715623.1, AA946962.1, AA460590.1, AA628285.1, C02002.1, AA894943.1, AA876963.1, AI431981.1, AA585211.1, AI216614.1, AA381394.1, AA278612.1, AA585402.1, AW463162.1, D80075.1, R52386.1, AA036649.1, AA671025.1, AA369696.1, AW057744.1, T86869.1, AA794137.1, AW414681.1, AC020971.1, AC025419.6, AC021297.2, AC020004.1, AC064829.3, AC009954.3, AC011791.3, AC013328.5, AC007819.7, AC009807.3, AC016991.2, AC009345.6, AC008043.3, AC018408.1, AC017738.1, AC018228.1, AL138817.5, AL356212.1, AL133518.3, AL136980.3, AL139294.1, AL031011.20, AP000708.1, Z82169.1, Z95393.1,

SEQ ID NO.209

25 NGO-St-114

YS081/T3 5'

AC005618.1, X97999.1, NM_005642.1, U18062.1, Z65840.1, Z65839.1, AC004540.1, AL137039.1, AE003630.1, AL132889.2, AL132885.1, AE003646.1, AE003605.1, AE003412.1, AC004058.1, AC004056.1, Z97180.1, AP001821.1, AC006804.3, AE003778.1, AE003576.1, AE003510.1, AF136829.1, AC006961.16, AC006581.16, AE001546.1, U68299.1, U18349.1, AC004267.1, AF047659.1, U09744.1, Z77249.1, U55366.1, X06535.1, AP001111.1, AB029433.1, Z95704.1, AB003324.1, D00170.1, Y17816.1, AU077198.1, AW673639.1, AA315968.1, D59188.1, T52076.1, AA312894.1, AW366774.1, AA336307.1, AA337398.1, AI951709.1, AA460590.1, AL119477.1, AA348197.1, T86869.1, AA095559.1, AW029214.1, AW877796.1, AW877790.1, AA595371.1, AA252724.1, AA894917.1, AW563125.1, AW563124.1, AW506736.1, AW506735.1, AW506714.1, AW506713.1, AW433456.1, AW330840.1, AW056105.1, AI987345.1, AI519245.1, AI511851.1, AI456317.1, AI455940.1, AA264246.1, AW649858.1, AW622907.1, AW217541.1, AW217534.1, AI239260.1, C93674.1, AW787238.1, AW787237.1, AW597401.1, AW565183.1, AW352495.1, AW331243.1, AW286148.1, AI668513.2, AW021363.1, AI976597.1, AI966918.1, AI966929.1, AI964567.1, AV155610.1, AI756661.1, AI755675.1, AV049065.1, AI746131.1, AI711682.1, AI677124.1, AI667849.1, AI665080.1, AI637127.1, AI549172.1, AI461446.1, AI461444.1, AA979929.1, AA979727.1, C72737.1, AA426143.1, AA406093.1, AA123407.1, C19565.1, R74232.1, T18355.1, AC008579.2, AC021705.4, AC007186.8, AC019704.1, AC007913.1, AL158151.5, Z98857.36, AC025179.3, AC008814.3, AC026384.2, AC024050.6, AC019207.3, AC020725.3, AC019835.1, AC014673.1, AC008189.2, AL109836.17, AL161444.2, AP001894.1, AP001863.1, AP001548.1, AP001544.1, AP001493.1, AP001282.1, AP000906.2, AC068193.4, AC012386.9, AC006513.25, AC068979.2, AC036188.2, AC008533.5, AC011367.5, AC011371.4, AC009142.4, AC025796.2, AC021409.3, AC010764.3, AC021373.3, AC011693.4, AC016685.4, AC018862.3, AC018994.3, AC012109.2, AC010741.3, AC012726.1, AC017805.1, AC014787.1, AC006937.5, AC006871.1, AC006803.2, AL354880.3, AL109955.13, AL139119.5, AL135939.9, AL355804.2, AL354674.2, AL161790.3, AL159176.3, AL157770.2, AP001993.1, AP001806.1, AP001457.1, AP000881.1, AP000826.1, AP000646.1, AP000621.1,

50 SEQ ID NO.210

NGO-ST-114

YS081/T7 3'

NM_005642.1, AC005618.1, U18062.1, X97999.1, NM_011901.1, AF144562.1, AE003618.1, AC004927.2, AC007172.6, AC005834.1, AE003738.1, AF165124.1, AL163258.2, AL078581.11, AL031259.1, AL109801.13, Z81455.2, L77246.1, AP001713.1, AP000178.1, AP000033.1, AP000266.1, AP000102.1, Z99115.1, M15318.1, AC004747.2, AE002267.1, AC004828.2, AE001658.1, AC004583.1, AF042091.1, AL163282.2, AL109985.2, AL049569.13, U37796.1, X76272.1, X04112.1, X15215.1, AB018107.1, AI434577.1, AI371764.1, AA947107.1, AW519252.1, AA776228.1, AW512466.1, AW304965.1, AW264130.1, AI376092.1, AI274749.1, AI090392.1, AI052691.1, AA824551.1, AA635906.1, AA604623.1, AA507377.1, AA417019.1, AA188912.1, AA063580.1, W61316.1, AI346408.1, AA825152.1, AW069225.1, AA037065.1, AI675129.1, AI285611.1, AI278875.1, AI125952.1, AA975911.1, AA613880.1, AA602587.1, AA461518.1, W15503.1, AW089083.1, AW190867.1, T90567.1, W56065.1, AW265444.1, AI356847.1, T86870.1, AA838760.1, AI818211.1, AI366201.1, AA417113.1, AW192823.1, AI709369.1, AW150510.1, AA508614.1, AA886319.1, AA577447.1, AW607519.1, AA380499.1, AA854628.1, H84875.1, AA508722.1, AW614384.1, F09561.1, AI940448.1, AW860175.1, AW604918.1, W65333.1, W39724.1, AA314905.1, AA326994.1, AI804531.1, R73733.1,

AA412648.1, AI287373.1, AL118821.1, R27607.1, AA037079.1, T65121.1, AI654286.1, AA380870.1, N87733.1, AA715623.1, AA946962.1, C02002.1, AA628285.1, H85281.1, AA460590.1, AA894943.1, AA876963.1, AA585211.1, AI216614.1, R30839.1, AA278612.1, AA585402.1, D80075.1, AA036649.1, AW057744.1, AA794137.1, AA671025.1, AI431981.1, AA381394.1, AA794920.1, AW463162.1, AI607308.1, AA691044.1, AW414681.1, AC020971.1, AC025419.6, AC020004.1, AC064829.3, AC064826.2, AC034126.2, AC016547.5, AC008835.3, AC026466.3, AC009954.3, AC024883.3, AC011791.3, AC016991.2, AC008043.3, AC018408.1, AC017738.1, AL133518.3, AL133472.3, AL031011.20, Z95393.1, AC007834.20, AC007623.20, AC009757.7, AC021171.3, AC010644.5, AC010590.4, AC008825.3, AC027749.2, AC024483.2, AC015533.4, AC027630.4, AC024466.3, AC018737.2, AC024399.2, AC009554.4, AC026890.1, AC026021.1, AC016063.4, AC011781.4, AC016357.6, AC022518.2, AC013478.3, AC015826.2, AL356212.1, AL137140.5, AL136359.4, AL161900.3, AL122125.1, AL139294.1, AP001872.1,

SEQ ID NO.211

NGO-St-114

YS1615/T3 5'

X97999.1, AC005618.1, NM_005642.1, U18062.1, NM_011901.1, AF144562.1, U20660.1, U15947.1, AL132889.2, AL132885.1, AF146393.1, AC004058.1, AJ131018.1, AP001821.1, AE003778.1, AE003576.1, AC004992.1, AF195611.1, AF195610.1, AC005414.2, AF016687.1, L78833.1, AC004267.1, AF047659.1, AL117206.1, Z81467.1, Z81028.1, Z82180.19, Z77652.2, Z75892.1, AL050305.9, Z97629.1, U55366.1, U40028.1, AW029214.1, AA622246.1, AI904582.1, AW877796.1, AA595371.1, AW877790.1, AA278660.1, AA894917.1, AA252724.1, AA328618.1, AW402842.1, AW362899.1, H14854.1, T72766.1, AW394189.1, T65190.1, AW365030.1, AA372836.1, AW582369.1, F11914.1, AU077198.1, AW609538.1, AW380678.1, AA383821.1, T47333.1, AW403760.1, T34968.1, AA460590.1, AA312894.1, AW816164.1, AA346865.1, AA619797.1, T05543.1, AI158644.1, AV121343.1, AA572579.1, C03576.1, AA517694.1, T83104.1, C03455.1, AA920998.1, AV205440.1, AV212370.1, AV213552.1, AV212700.1, C89279.1, AA763469.1, H21207.1, AV216550.1, AI117791.1, AV100198.1, AV218081.1, AV214781.1, AW199703.1, AI722257.1, AA182987.1, AA336858.1, AW645787.1, AW638295.1, AW199696.1, AW728753.1, AA102949.1, AI471179.1, AW375040.1, AW375037.1, AV049065.1, C54464.1, C54153.1, C51985.1, C49917.1, C11684.1, D27736.1, AC008579.2, AC020971.1, AC025193.1, AC025256.4, AC020898.3, AC020907.3, AC009035.5, AC015613.1, AL136135.2, AL133263.2, Z98857.36, AC026124.3, AC027751.2, AP001863.1, AC068193.4, AC036188.2, AC024947.2, AC025972.2, AC041033.2, AC026404.4, AC025766.3, AC024583.3, AC010243.3, AC010273.3, AC010302.3, AC010623.3, AC016558.3, AC008534.3, AC036127.2, AC068579.1, AC009171.4, AC009142.4, AC013670.3, AC017106.3, AC018686.4, AC011724.2, AC024698.4, AC022198.2, AC021719.3, AC019033.4, AC022788.2, AC023629.2, AC010764.3, AC021828.2, AC009695.4, AC025532.2, AC021157.3, AC016890.4, AC022273.2, AC016685.4, AC011266.3, AC023349.2, AC018492.3, AC012101.3, AC024158.1, AC012448.3, AC010741.3, AC012387.4, AC017805.1, AC014787.1, AC006937.5, AC006905.1, AC006704.1, AL356435.1, AL355593.3, AL133542.3, AL161790.3, AL162418.2, AL159176.3, Z92842.1, Z92863.2, AP001993.1,

SEQ ID NO.212

NGO-ST-114

YS1615/T7 3'

AC005618.1, NM_005642.1, U18062.1, X97999.1, NM_011901.1, AF144562.1, AL009178.4, AB016897.1, AE003618.1, AC007504.3, AB007651.1, AE003764.1, AE003738.1, AF165124.1, AL078581.11, AL031259.1, Z81455.2, Z82900.1, L77246.1, AB025604.1, Z99115.1, M15318.1, Z30211.1, AC012082.6, AC004521.2, AC024750.1, AE003600.1, AF233591.1, AE001658.1, AF121898.1, AF022814.1, AF042091.1, AF005383.1, AL117191.4, AL121716.16, AC002077.1, AL021182.1, AL031429.11, X76272.1, X04112.1, X15215.1, AI052691.1, AI346408.1, AW304965.1, AW190867.1, AI709369.1, AW192823.1, AI818211.1, AI434577.1, AW264130.1, AA507377.1, AA613880.1, AA417113.1, AI675129.1, AI371764.1, AI285611.1, AI125952.1, AI376092.1, AW069225.1, AI366201.1, AI804531.1, AA063580.1, AA461518.1, W65333.1, AA825152.1, AA604623.1, AA947107.1, AI278875.1, AA417019.1, AI274749.1, W15503.1, AA776228.1, AW512466.1, W61316.1, AI090392.1, AI940448.1, W39724.1, AI356847.1, AW860175.1, AW604918.1, AA975911.1, AA037065.1, AA838760.1, AA635906.1, AW089083.1, AA824551.1, AA602587.1, AW265444.1, AA188912.1, AW519252.1, T90567.1, AW150510.1, AA508614.1, W56065.1, AW607519.1, T86870.1, R73733.1, AL118821.1, AA886319.1, AA508722.1, AA577447.1, AA380499.1, AA854628.1, H84875.1, AW614384.1, F09561.1, AI287373.1, AA314905.1, AA326994.1, R30839.1, R27607.1, T65121.1, AA412648.1, AI654286.1, N87733.1, AA715623.1, AA037079.1, AA946962.1, AA380870.1, C02002.1, AA628285.1, AA894943.1, AA876963.1, AI431981.1, AA460590.1, H85281.1, AA585211.1, AI216614.1, AA278612.1, AA585402.1, D80075.1, AW057744.1, AA381394.1, AA036649.1, AA794137.1, AA691044.1, AA671025.1, AA794920.1, AW414681.1, AW463162.1, AA549454.1, AC020971.1, AC025419.6, AC064829.3, AC064826.2, AC008835.3, AC013328.5, AC009807.3, AC018408.1, AC017738.1, AC018228.1, AL138817.5, AL133472.3, AL136980.3, Z82169.1, AC009757.7, AC060773.2, AC036223.2, AC008825.3, AC027438.2, AC015679.3, AC015964.2, AC021450.3, AC011218.4, AC022625.1, AC006719.1, AL163153.1,

SEQ ID NO.213

NGO-St-114

YS1631/T7 3'

NM_005642.1, AC005618.1, U18062.1, X97999.1, NM_011901.1, AF144562.1, AL009178.4, AB016897.1, AE003618.1,

- AC007504.3, AB007651.1, AE003738.1, AF165124.1, AL078581.11, AL031259.1, AL109801.13, Z81455.2, Z82900.1, L77246.1, AB025604.1, Z99115.1, M15318.1, Z30211.1, AC012082.6, AC004521.2, AC024750.1, AC012099.4, AL121716.16, AL021182.1, AP001037.1, AI052691.1, AW304965.1, AI709369.1, AI346408.1, AW190867.1, AW192823.1, AI818211.1, AI434577.1, AW264130.1, AA507377.1, AA613880.1, AA417113.1, AI675129.1, AI371764.1, AI285611.1, AI125952.1, AI376092.1, AW069225.1, AI366201.1, AI804531.1, AA461518.1, AA063580.1, W65333.1, AA825152.1, AA604623.1, AA947107.1, AI278875.1, AA417019.1, AI274749.1, W15503.1, AA776228.1, AW512466.1, W61316.1, AI090392.1, AI356847.1, W39724.1, AA975911.1, AA037065.1, AI940448.1, AW860175.1, AW604918.1, AA838760.1, AW089083.1, AA635906.1, AA824551.1, AA602587.1, AW265444.1, AA188912.1, AW519252.1, T90567.1, AW150510.1, AA508614.1, W56065.1, T86870.1, AL118821.1, R73733.1, AA508722.1, AA886319.1, AW607519.1, AA577447.1, AA380499.1, AA854628.1, H84875.1, AW614384.1, F09561.1, AI287373.1, R30839.1, AA326994.1, R27607.1, T65121.1, AA314905.1, AI654286.1, N87733.1, AA412648.1, AA715623.1, AA946962.1, AA628285.1, C02002.1, AA037079.1, AA380870.1, AA894943.1, AA876963.1, AI431981.1, AA585211.1, AI216614.1, AA460590.1, H85281.1, AA278612.1, AA585402.1, D80075.1, AW057744.1, AA794137.1, AA691044.1, AA671025.1, AA794920.1, AW414681.1, AA381394.1, AA036649.1, AI859319.1, AW463162.1, AC020971.1, AC025419.6, AC064829.3, AC064826.2, AC034126.2, AC008835.3, AC013328.5, AC009807.3, AC018228.1, AL133472.3, AL136980.3, AC023599.7, AC068540.2, AC009757.7, AC060773.2, AC036223.2, AC008825.3, AC026083.3, AC027438.2, AC015679.3, AC015964.2, AC011218.4, AC024065.2, AC011647.3, AC013478.3, AC006719.1, AL135842.4,
- 20 SEQ ID NO. 214
NGO-St-114
YS1682/T3 5'
- AC005618.1, X97999.1, NM_005642.1, U18062.1, Z65840.1, Z65839.1, AC004540.1, AL137039.1, AE003630.1, AE003646.1, AE003605.1, AE003412.1, AC004058.1, AC004056.1, AL132889.2, Z97180.1, AL132885.1, AP001821.1, AC004005.2, AC006804.3, AE003778.1, AE003510.1, AF136829.1, AC006961.16, AC006581.16, U68299.1, U18349.1, AF047659.1, U09744.1, Z77249.1, U55366.1, X06535.1, AP001111.1, AB029433.1, AB003324.1, D00170.1, Y17816.1, AU077198.1, AW673639.1, AA315968.1, D59188.1, T52076.1, AW366774.1, AA336307.1, AA337398.1, AA312894.1, AI951709.1, AL119477.1, AA348197.1, AA460590.1, T86869.1, AA095559.1, AW029214.1, AA252724.1, AW877796.1, AW877790.1, AW563125.1, AW563124.1, AW506736.1, AW506735.1, AW506714.1, AW506713.1, AW433456.1, AW330840.1, AW056105.1, AI987345.1, AI519245.1, AI511851.1, AI456317.1, AI455940.1, AA264246.1, AW649858.1, AI239260.1, C93674.1, AW787238.1, AW787237.1, AW597401.1, AW565183.1, AW352495.1, AW331243.1, AW286148.1, AI668513.2, AW021363.1, AI976597.1, AI966918.1, AI966929.1, AI964567.1, AI857189.1, AI755661.1, AI755675.1, AV049065.1, AI746131.1, AI711682.1, AI677124.1, AI667849.1, AI665080.1, AI637127.1, AI549172.1, AI461446.1, AI461444.1, AA979929.1, AA979727.1, C72737.1, AA426143.1, AA406093.1, C19565.1, R74232.1, T18355.1, AC008579.2, AC021705.4, AC007186.8, AC019704.1, AC007913.1, AL158151.5, AC068193.4, AC026384.2, AC024050.6, AC019207.3, AC020725.3, AC019835.1, AC014673.1, AC008189.2, AL109836.17, AL159176.3, Z98857.36, AP001894.1, AP001863.1, AP001548.1, AP001544.1, AP001493.1, AP001282.1, AP000906.2, AC012386.9, AC006513.25, AC068979.2, AC036188.2, AC009142.4, AC025796.2, AC021409.3, AC021373.3, AC016685.4, AC012109.2, AC012726.1, AC014787.1, AC006871.1, AC006803.2, AL354880.3, AL109955.13, AL135939.9, AL355472.2, AL355804.2, AL354674.2, AL157770.2, AP001993.1, AP001806.1, AP000881.1, AP000826.1, AP000646.1, AP000621.1,
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- SEQ ID NO. 215
NGO-St-114
YS1743/T3 5'
- AC005618.1, X97999.1, NM_005642.1, U18062.1, Z65840.1, Z65839.1, AC004540.1, AL137039.1, AE003630.1, AC000003.1, AE003646.1, AE003605.1, AE003412.1, AC004254.1, AC004056.1, AL035448.28, Z97180.1, AC006804.3, AE003758.1, AE003634.1, AE003597.1, AE003510.1, AC007029.3, AF136829.1, AC000064.1, AC002458.1, NM_004703.1, AC006961.16, AC006581.16, AC007566.1, AC006240.1, U68299.1, AC004148.1, AC005547.1, U18349.1, U73644.1, U09744.1, AL132889.2, Z77249.1, AL132885.1, X06535.1, X77723.1, X91141.1, AP001111.1, AB029433.1, AB003324.1, D00170.1, Y17816.1, AU077198.1, AW673639.1, AA315968.1, D59188.1, T52076.1, AW366774.1, AA336307.1, AA337398.1, AI951709.1, AA312894.1, AL119477.1, AA348197.1, AA460590.1, T86869.1, AA095559.1, AW563125.1, AW563124.1, AW506736.1, AW506735.1, AW506714.1, AW506713.1, AW433456.1, AW330840.1, AW056105.1, AI987345.1, AI976597.1, AI519245.1, AI511851.1, AI456317.1, AI455940.1, AA264246.1, AW649858.1, AI239260.1, C93674.1, AW787238.1, AW787237.1, AW597401.1, AW565183.1, AW374004.1, AW352495.1, AW331243.1, AW286148.1, AI668513.2, AL120839.1, AW021363.1, AI966918.1, AI966929.1, AI964567.1, AI912789.1, AI857189.1, AI755661.1, AI755675.1, AV049065.1, AI746131.1, AI711682.1, AI677124.1, AI667849.1, AI665080.1, AI637127.1, AI549172.1, AI461446.1, AI461444.1, AA979929.1, AA979727.1, C72737.1, AA426143.1, AA406093.1, AA203657.1, C19565.1, R74232.1, F06378.1, T18355.1, AC008579.2, AC021705.4, AC015898.4, AC026989.2, AC020553.3, AC015900.2, AC011789.4, AC022373.1, AC007186.8, AC019704.1, AC007913.1, AL158151.5, AL157785.2, AL355332.1, AC026728.3, AC026712.3, AC026384.2, AC024050.6, AC019207.3, AC020725.3, AC023953.2, AC009593.4, AC019835.1, AC014673.1, AC008189.2, AC008159.1, AL109836.17, AP001894.1, AP001548.1, AP001544.1, AP001493.1, AP001282.1, AP000906.2, AC012386.9, AC006513.25, AC068979.2, AC063921.4, AC055875.2, AC034211.3, AC008066.3,
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AC020740.4, AC025942.2, AC025796.2, AC021409.3, AC022788.2, AC025525.2, AC025532.2, AC021373.3, AC022247.2, AC017029.4, AC016685.4, AC011566.3, AC012109.2, AC015727.3, AC010741.3, AC009981.5, AC019821.1, AC007984.3, AC012726.1, AF212833.1, AC017607.1, AC014838.1, AC009366.6, AC006871.1, AC006803.2, AL354880.3, AL109955.13, AL135939.9, AL355804.2, AL354674.2, AL161790.3, AL157770.2, Z98857.36, AP001993.1, AP001806.1, AP000881.1, AP000826.1, AP000646.1, AP000621.1,

SEQ ID NO.216

NGO-St-114

YS1751/T7 3'

10 NM_005642.1, AC005618.1, U18062.1, X97999.1, NM_011901.1, AF144562.1, AL121748.6, AL031259.1, Z81455.2, AL009178.4, AB016897.1, AC010227.5, AC008893.4, AC008000.7, AC007172.6, AC004583.1, AF042091.1, AL355094.2, AL163282.2, AL031683.1, X15215.1, AB005246.1, AB005230.1, AW304965.1, AI052691.1, AW190867.1, AI709369.1, AW192823.1, AI346408.1, AI818211.1, AI434577.1, AW264130.1, AA613880.1, AA507377.1, AA417113.1, AI804531.1, AI371764.1, AI285611.1, AI675129.1, AI125952.1, AW069225.1, AI376092.1, AI366201.1, AA947107.1, 15 AA461518.1, AA063580.1, AA825152.1, AA776228.1, AA604623.1, AI278875.1, AI274749.1, AA417019.1, W65333.1, W15503.1, AW512466.1, W61316.1, AI090392.1, AI356847.1, AA975911.1, W39724.1, AA037065.1, AW265444.1, AW089083.1, AA838760.1, AA635906.1, AA824551.1, AA602587.1, AI940448.1, AA188912.1, AW519252.1, AW860175.1, AW604918.1, T90567.1, AW150510.1, W56065.1, T86870.1, AA508614.1, AL118821.1, R73733.1, AA508722.1, AA886319.1, AA577447.1, AA380499.1, AA854628.1, AW614384.1, AW607519.1, H84875.1, F09561.1, 20 AI654286.1, AI287373.1, R30839.1, AA326994.1, T65121.1, R27607.1, AA314905.1, AA946962.1, N87733.1, AA715623.1, AA412648.1, AA628285.1, C02002.1, AA037079.1, AA894943.1, AA876963.1, AI431981.1, AA380870.1, AI216614.1, AA585211.1, AA278612.1, AA585402.1, AA460590.1, H85281.1, AW057744.1, D80075.1, AA794137.1, AA691044.1, AA671025.1, AA794920.1, AW414681.1, AC025419.6, AC015533.4, AC009954.3, AC016357.6, AC021952.4, AL133518.3, AL353600.1, AL031011.20, Z95393.1, AC012600.4, AC012515.11, AC007834.20, 25 AC007623.20, AC021171.3, AC026459.2, AC008952.4, AC010626.4, AC068206.1, AC027630.4, AC044795.2, AC024399.2, AC012600.3, AC016275.2, AC015826.2, AC009615.2, AC004555.2, AL356212.1, AL137140.5, AL136980.3, AL161900.3, AL139294.1,

SEQ ID NO. 217

30 NGO-St-114

YS1771/T3 5'

AC005618.1, X97999.1, NM_005642.1, U18062.1, Z65840.1, Z65839.1, AC004540.1, AL137039.1, AE003630.1, AL132889.2, AL132885.1, AE003646.1, AE003605.1, AE003412.1, AC004058.1, AC004056.1, Z97180.1, AP001821.1, AC006804.3, AE003510.1, AF136829.1, AC006961.16, AC006581.16, U68299.1, U18349.1, U09744.1, Z77249.1, 35 X06535.1, AP001111.1, AB029433.1, AB003324.1, D00170.1, Y17816.1, AU077198.1, AW673639.1, AA315968.1, D59188.1, T52076.1, AA312894.1, AW366774.1, AA336307.1, AA337398.1, AA460590.1, AI951709.1, AL119477.1, AA348197.1, T86869.1, AA095559.1, AW029214.1, AW877796.1, AW877790.1, AA595371.1, AA252724.1, AA894917.1, AW563125.1, AW563124.1, AW506736.1, AW506735.1, AW506714.1, AW506713.1, AW433456.1, AW330840.1, AW056105.1, AI987345.1, AI519245.1, AI511851.1, AI456317.1, AI455940.1, AA264246.1, AW649858.1, 40 AI239260.1, C93674.1, AW787238.1, AW787237.1, AW597401.1, AW565183.1, AW352495.1, AW331243.1, AW286148.1, AI668513.2, AW021363.1, AI976597.1, AI966918.1, AI966929.1, AI964567.1, AI756661.1, AI755675.1, AV049065.1, AI746131.1, AI711682.1, AI677124.1, AI667849.1, AI665080.1, AI637127.1, AI549172.1, AI461446.1, AI461444.1, AA979929.1, AA979727.1, C72737.1, AA426143.1, AA406093.1, C19565.1, R74232.1, T18355.1, AC008579.2, AC021705.4, AC007186.8, AC019704.1, AC007913.1, AL158151.5, Z98857.36, AC026384.2, AC024050.6, 45 AC019207.3, AC020725.3, AC019835.1, AC014673.1, AC008189.2, AL109836.17, AP001894.1, AP001863.1, AP001548.1, AP001544.1, AP001493.1, AP001282.1, AP000906.2, AC012386.9, AC006513.25, AC068979.2, AC009142.4, AC022198.2, AC025796.2, AC021719.3, AC021409.3, AC022788.2, AC021782.2, AC025321.2, AC010929.2, AC025532.2, AC021373.3, AC016685.4, AC012109.2, AC018879.3, AC010741.3, AC012726.1, AC006871.1, AC006803.2, AL354880.3, AL109955.13, AL135939.9, AL355804.2, AL354674.2, AL161790.3, 50 AL157770.2, AP001993.1, AP001806.1, AP000881.1, AP000826.1, AP000646.1, AP000621.1,

SEQ ID NO.218

NGO-St-114

YS181/T3 5'

55 AC005618.1, X97999.1, NM_005642.1, U18062.1, Z65839.1, Z65840.1, AC006804.3, AE003512.1, AC002052.8, AC006961.16, AW673639.1, D59188.1, AA315968.1, AU077198.1, T52076.1, AW366774.1, AA348197.1, AA337398.1, AA336307.1, AI951709.1, T86869.1, AA095559.1, AL119477.1, AA312894.1, AI239260.1, AA516747.1, AC008579.2, AC007913.1, AL158151.5, AC017003.2, AC012386.9, AC068979.2, AC026101.6, AC016639.5, AC016632.4, AC034249.1, AC021373.3, AC017624.1, AC010671.7, AC006871.1, AC006803.2, AP001806.1, AP000881.1, 60 AP000826.1, AP000646.1,

SEQ ID NO. 219

NGO-St-114

YS191/T7 3'

5 AC005618.1, NM_005642.1, U18062.1, X97999.1, NM_011901.1, AF144562.1, AL009178.4, AB016897.1, AE003618.1, AC007504.3, AB007651.1, AE003764.1, AE003738.1, AF165124.1, AL163258.2, AL078581.11, AL031259.1, Z81455.2, Z82900.1, L77246.1, AP001713.1, AP000178.1, AP000033.1, AB025604.1, AP000266.1, AP000102.1, Z99115.1, M15318.1, Z30211.1, AC012082.6, AC004521.2, AC024750.1, AL121716.16, AL109801.13, AL008723.8, AL021182.1, AB018107.1, AB005246.1, AI052691.1, AI346408.1, AW304965.1, AW190867.1, AI709369.1, AW192823.1, AI434577.1, AI818211.1, AW264130.1, AA613880.1, AA507377.1, AA417113.1, AI675129.1, AI371764.1, AI285611.1, AI125952.1, W65333.1, AI376092.1, AW069225.1, AI366201.1, AI804531.1, AA461518.1, AA063580.1, AA825152.1, AA604623.1, AW860175.1, AW604918.1, AI940448.1, AI278875.1, AA947107.1, W39724.1, AA417019.1, AI274749.1, W15503.1, AA776228.1, AW512466.1, W61316.1, AI090392.1, AI356847.1, AA975911.1, AA037065.1, AA838760.1, AW089083.1, 10 AW607519.1, AA635906.1, AA824551.1, AA602587.1, AW265444.1, AA188912.1, AW519252.1, T90567.1, AW150510.1, R73733.1, AA508614.1, W56065.1, T86870.1, AL118821.1, AA508722.1, AA886319.1, AA577447.1, AA380499.1, AA854628.1, H84875.1, AA314905.1, AW614384.1, F09561.1, AA326994.1, AA412648.1, AI287373.1, R30839.1, AA037079.1, R27607.1, AA380870.1, T65121.1, AI654286.1, N87733.1, AA715623.1, AA946962.1, H85281.1, AA460590.1, AA628285.1, C02002.1, AA894943.1, AA876963.1, AI431981.1, AA585211.1, AI216614.1, AA278612.1, 15 AA585402.1, AA671025.1, D80075.1, AW463162.1, AA381394.1, AA036649.1, AA794137.1, AW057744.1, R52386.1, AA794920.1, AA549454.1, AV100160.1, AC020971.1, AC025419.6, AC064829.3, AC064826.2, AC008835.3, AC013328.5, AC009807.3, AC017738.1, AC018228.1, AL133472.3, AL136980.3, AL353600.1, Z82169.1, AC009757.7, AC060773.2, AC036223.2, AC008825.3, AC027438.2, AC015679.3, AC013782.3, AC016693.4, AC024065.2, AC011647.3, AC013478.3, AC006719.1,

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SEQ ID NO. 220

NGO-St-114

YS274/T7 3'

25 NM_005642.1, AC005618.1, U18062.1, X97999.1, NM_011901.1, AF144562.1, AE003618.1, AC007172.6, AC005834.1, AE003738.1, AF165124.1, AL163258.2, AL078581.11, AL031259.1, Z81455.2, AP001713.1, AP000178.1, AP000033.1, AP000266.1, AP000102.1, AC004747.2, AC004583.1, AF042091.1, AL163282.2, AL163277.2, AL132879.2, X76272.1, X04112.1, AP001732.1, X15215.1, AP001037.1, AB018107.1, AI434577.1, AI371764.1, AA947107.1, AW519252.1, AA776228.1, AW512466.1, AW304965.1, AW264130.1, AI376092.1, AI274749.1, AI090392.1, AI052691.1, AA824551.1, AA635906.1, AA604623.1, AA507377.1, AA417019.1, AA188912.1, AA063580.1, W61316.1, 30 AW069225.1, AI346408.1, AA825152.1, AI675129.1, AI278875.1, AI125952.1, AA975911.1, AA613880.1, AA602587.1, AA461518.1, AA037065.1, AI285611.1, AW089083.1, AW190867.1, W15503.1, T90567.1, W56065.1, AW265444.1, AI356847.1, T86870.1, AI366201.1, AA838760.1, AA417113.1, AI818211.1, AW192823.1, AI709369.1, AW607519.1, AW150510.1, AA508614.1, AA886319.1, AA577447.1, AA380499.1, AA854628.1, AW860175.1, AW604918.1, H84875.1, AA508722.1, AW614384.1, AI940448.1, AA412648.1, F09561.1, AA314905.1, W39724.1, W65333.1, 35 AA326994.1, AI804531.1, R73733.1, AA037079.1, AI287373.1, AL118821.1, AA380870.1, R27607.1, T65121.1, AI654286.1, N87733.1, AA715623.1, AA946962.1, H85281.1, AA628285.1, C02002.1, AA460590.1, AA894943.1, AA876963.1, AA585211.1, AI216614.1, R30839.1, AA278612.1, AA585402.1, AA381394.1, AW463162.1, D80075.1, AA671025.1, AA794137.1, AA036649.1, AW057744.1, AI431981.1, R52386.1, AA794920.1, AA369696.1, AA549454.1, AC020971.1, AC025419.6, AC020004.1, AC064829.3, AC016547.5, AC008835.3, AC009954.3, AC011791.3, 40 AC016991.2, AC008043.3, AC018408.1, AC017738.1, AL133518.3, AL031011.20, Z95393.1, AC007834.20, AC007623.20, AC067724.3, AC009757.7, AC021171.3, AC064826.2, AC027235.2, AC010515.5, AC008825.3, AC027749.2, AC024483.2, AC015533.4, AC027630.4, AC025229.3, AC046169.1, AC044876.1, AC018737.2, AC024399.2, AC026890.1, AC022020.3, AC024424.2, AC016063.4, AC019157.4, AC011781.4, AC016357.6, AC022518.2, AC013478.3, AC015826.2, AL355305.2, AL139258.3, AL137140.5, AL161900.3, 45 AL122125.1, AL139294.1, AL022594.18, AP001872.1,

SEQ ID NO.221

NGO-St-114

YS303/T7 3'

50 NM_005642.1, AC005618.1, U18062.1, X97999.1, NM_011901.1, AF144562.1, AC007172.6, AL121748.6, Z81455.2, Z82900.1, AC004521.2, AC012099.4, AC004583.1, AF042091.1, AL163282.2, Z92812.1, X15215.1, AI052691.1, AW304965.1, AI709369.1, AW190867.1, AI346408.1, AW192823.1, AI818211.1, AW264130.1, AA613880.1, AA507377.1, AI434577.1, AI675129.1, AA417113.1, AI371764.1, AI285611.1, AI125952.1, AI804531.1, AW069225.1, AI376092.1, AI366201.1, AA461518.1, AA825152.1, AA604623.1, AI278875.1, AA947107.1, AA063580.1, AI274749.1, 55 AA776228.1, AA417019.1, W15503.1, W65333.1, AW512466.1, AI356847.1, W61316.1, AI090392.1, AA975911.1, AA037065.1, W39724.1, AW089083.1, AA635906.1, AA838760.1, AW265444.1, AA824551.1, AA602587.1, AI940448.1, AA188912.1, AW860175.1, AW604918.1, AW519252.1, T90567.1, AW150510.1, AA508614.1, W56065.1, T86870.1, AL118821.1, AA508722.1, AA886319.1, AA577447.1, R73733.1, AA380499.1, AA854628.1, AW614384.1, AW607519.1, H84875.1, F09561.1, AI654286.1, AI287373.1, R30839.1, AA326994.1, R27607.1, T65121.1, AA946962.1, AA314905.1, 60 AA715623.1, N87733.1, AA412648.1, AA628285.1, C02002.1, AA894943.1, AA876963.1, AI431981.1, AA380870.1, AA037079.1, AI216614.1, AA585211.1, H85281.1, AA460590.1, AA278612.1, AA585402.1, AW057744.1, D80075.1, AW414681.1, AA794137.1, AA671025.1, AA691044.1, AA794920.1, AA036649.1, AW280434.1, AI162830.1, AC020971.1, AC015533.4, AC016357.6, AL138817.5, AL133518.3, AL353600.1, AL031011.20, Z82169.1, Z95393.1,

-122-

SEQ ID NO.222

NGO-St-114

YS305/T7 3'

- 5 NM_005642.1, AC005618.1, U18062.1, X97999.1, Z81455.2, AL078462.9, AL034349.3, X15215.1, AJ052691.1, AW304965.1, AI709369.1, AW190867.1, AJ18211.1, AJ346408.1, AW192823.1, AJ804531.1, AI434577.1, AW264130.1, AA613880.1, AA507377.1, AA417113.1, AI675129.1, AJ371764.1, AJ125952.1, AJ285611.1, AW069225.1, AJ376092.1, AJ366201.1, AA461518.1, W65333.1, AA825152.1, AA604623.1, AJ278875.1, AA947107.1, AA417019.1, AJ274749.1, AA776228.1, AA063580.1, W15503.1, AW512466.1, AI090392.1, W61316.1, W39724.1, AJ356847.1, AA975911.1, AW089083.1, AJ940448.1, AA635906.1, AA037065.1, AW265444.1, AA824551.1, AA602587.1, AA838760.1, 10 AW519252.1, AA188912.1, W56065.1, T86870.1, AW860175.1, AW604918.1, T90567.1, AA886319.1, AA577447.1, AW150510.1, AA854628.1, AA508614.1, R73733.1, AW614384.1, AA380499.1, F09561.1, AW607519.1, AA508722.1, AJ654286.1, AL118821.1, H84875.1, AA326994.1, AJ287373.1, AA946962.1, AA314905.1, T65121.1, R27607.1, AA412648.1, AA628285.1, C02002.1, R30839.1, N87733.1, AA715623.1, AJ216614.1, AA894943.1, AA876963.1, AA380870.1, AA037079.1, AA585211.1, AA278612.1, AA585402.1, AA460590.1, H85281.1, AW057744.1, AI431981.1, 15 D80075.1, AA036649.1, AL031011.20, Z95393.1, AC018923.5, AC036181.2, AC068931.1, AC009440.2, AC027630.4, AC009554.4, AC006286.13, AC011996.3, AC010890.3, AC009528.7, AC007913.1, AL158151.5, AL161785.4,

SEQ ID NO.223

NGO-St-115

20 YS1641/T7 3'

- L34543.1, L07872.1, L34544.1, NM_015874.1, L08904.1, D14041.1, S63463.1, X17459.1, M81871.1, U60093.1, U60094.1, M81877.1, M81876.1, AE003830.1, AC006578.5, AC005974.1, AC002416.1, AL021578.1, AB024964.1, AB026048.1, AC012397.31, AC012147.7, AC009396.5, AC007270.2, AC007314.3, AF049850.1, AF016494.1, AL032655.1, U23177.1, D25323.1, D90170.1, D90168.1, M64933.1, AJ627646.1, AA641661.1, AJ401150.1, 25 AW090508.1, AA701607.1, AJ962712.1, AJ953614.1, AW131544.1, AJ829826.1, AW302357.1, AA042864.1, AA640106.1, AJ984992.1, AA903408.1, AA483607.1, AA501219.1, AA069672.1, AW249681.1, AW235086.1, AJ381502.1, AJ619912.1, AJ291840.1, AJ023923.1, T67414.1, AJ580826.1, AJ375729.1, AJ565611.1, AJ334962.1, AJ334964.1, AJ669755.1, N95392.1, AW425207.1, AW815621.1, AW005947.1, AJ982567.1, AJ144435.1, AA171398.1, AA788576.1, F33435.1, AJ631440.1, AA669918.1, AW815443.1, AW391454.1, AA101255.1, AA676341.1, AW815833.1, 30 AA169326.1, AW815622.1, AW391447.1, AW815635.1, U69195.1, AA101351.1, AA908462.1, AA126685.1, AW815508.1, AW815506.1, AW249892.1, AW815512.1, AW609613.1, AA044415.1, AA678797.1, AW381515.1, AW474060.1, AW801962.1, AW381537.1, R12509.1, AA156824.1, AW379059.1, AW371260.1, AJ720441.1, AW189578.1, T23713.1, AW371378.1, AW381482.1, AW381510.1, AW381496.1, AA705248.1, R19314.1, T70135.1, AW462450.1, AW381476.1, F05151.1, AJ206928.1, AW381459.1, AW843169.1, AW610177.1, AW393428.1, 35 AW016196.1, AW009270.1, AA092442.1, AW371229.1, AJ658933.1, AJ919572.1, AW384329.1, AJ708578.1, AJ435870.1, AJ274998.1, AA969666.1, AA235124.1, W25228.1, AC006391.7, AC016175.1, AL356136.1, AC009423.2, AC017078.3, AC027239.2, AC024155.2, AC021304.2, AL354733.4, AL135938.7, AL353743.1, AP001998.1, AC022816.9, AC021256.4, AC024322.2, AC017144.1, AL162420.3, AC009192.60, AC068789.3, AC051628.10, AC018995.4, AC012480.4, AC035149.2, AC016591.4, AC040893.1, AC023199.2, AC026808.1, AC022926.2, 40 AC015797.2, AC013664.1, AL356260.1, AL118513.14, AL354999.1, AL160035.3, AL159978.2, AL022597.5, AP001532.1, AP001400.1, AP000590.3, Z92865.1, AL022596.1,

SEQ ID NO. 224

NGO-St-115

45 YS1693/T7 3'

- L34543.1, L07872.1, L34544.1, NM_015874.1, L08904.1, D14041.1, S63463.1, X17459.1, M81871.1, U60093.1, U60094.1, M81877.1, M81876.1, AE003830.1, AC005974.1, AL021578.1, AB024964.1, AB026048.1, AC012397.31, AC012147.7, AC007270.2, AF049850.1, AF016494.1, X56462.1, D25323.1, D90170.1, D90168.1, M64933.1, X59856.1, AA641661.1, AJ627646.1, AJ962712.1, AA701607.1, AW090508.1, AJ401150.1, AW131544.1, AJ953614.1, AJ829826.1, 50 AW302357.1, AA042864.1, AA640106.1, AJ984992.1, AA903408.1, AA483607.1, AA069672.1, AW249681.1, AW235086.1, AJ381502.1, AJ619912.1, AJ291840.1, AJ023923.1, AA501219.1, T67414.1, AJ580826.1, AJ375729.1, AJ565611.1, AJ334962.1, AJ334964.1, AJ669755.1, N95392.1, AW815621.1, AW005947.1, AJ982567.1, AJ144435.1, AA171398.1, AA788576.1, AW425207.1, F33435.1, AJ631440.1, AA669918.1, AW815443.1, AW391454.1, AA101255.1, AA676341.1, AW815833.1, AA169326.1, AW815622.1, AW391447.1, AW815635.1, U69195.1, AA101351.1, AA908462.1, AA126685.1, AW815508.1, AW815506.1, AW249892.1, AW815512.1, AW609613.1, AA044415.1, AA678797.1, AW381515.1, AW474060.1, AW381537.1, R12509.1, AA156824.1, AW379059.1, AW371260.1, AJ720441.1, AW189578.1, T23713.1, AW371378.1, AW381482.1, AW381510.1, AW801962.1, AW381496.1, AA705248.1, R19314.1, T70135.1, AW381476.1, F05151.1, AJ206928.1, AW462450.1, AW381459.1, AW843169.1, AW610177.1, AW393428.1, AW016196.1, AW009270.1, AA092442.1, AW371229.1, AJ658933.1, AJ919572.1, AW384329.1, AJ708578.1, 60 AW384329.1, AJ708578.1, T79039.1, AW381472.1, F37823.1, AA705236.1, AA895510.1, AC006391.7, AC016175.1, AL356136.1, AC017078.3, AL135938.7, AC016389.2, AC021003.4, AC017144.1, AC016337.1, AL356266.2, AL162420.3, AL161719.6, AL161899.2, AC009192.60, AC068789.3, AC051628.10, AC012480.4, AC022926.2, AC015797.2, AC013664.1, AL137250.3, AL356258.2, AL356260.1, AL354999.1, AL160035.3, AL159978.2, AP001532.1, AP001400.1, AP000590.3,

SEQ ID NO.225

NGO-St-115

YS1713/T7 3'

- 5 L34543.1, L07872.1, L34544.1, NM_015874.1, L08904.1, D14041.1, S63463.1, X17459.1, M81871.1, U60093.1, U60094.1, M81877.1, M81876.1, L07873.1, AE003830.1, AC005974.1, AL096770.14, AL021578.1, AB024964.1, AB026048.1, AC012397.31, AC010329.3, AC012147.7, AE003603.1, AE002611.1, AC004506.1, AC007270.2, AJ239329.2, D25323.1, AA641561.1, AW090508.1, AI627646.1, AI962712.1, AI953614.1, AI401150.1, AW131544.1, AA701607.1, AW302357.1, AI829826.1, AA501219.1, AI984992.1, AA042864.1, AA640106.1, AA903408.1, 10 AA483607.1, AA069672.1, AW249681.1, AW235086.1, AI381502.1, AI619912.1, AI291840.1, AI023923.1, T67414.1, AI580826.1, AI375729.1, AI565611.1, AW425207.1, AI334962.1, AI334964.1, AI669755.1, N95392.1, AW005947.1, AI982567.1, AI144435.1, AA171398.1, AA788576.1, AW815621.1, F33435.1, AI631440.1, AA101255.1, AA676341.1, AA669918.1, AW815443.1, AA169326.1, AW391454.1, AW815833.1, AA101351.1, U69195.1, AA908462.1, AW815622.1, AW391447.1, AW815635.1, AW801962.1, AW249892.1, AA126685.1, AA044415.1, AW815508.1, 15 AW815506.1, AW815512.1, AW609613.1, AA678797.1, AW462450.1, AW381515.1, AW474060.1, AW381537.1, AA156824.1, AW379059.1, AW371260.1, AI720441.1, R12509.1, AW189578.1, AW371378.1, AW381482.1, AW381510.1, AW381496.1, T23713.1, T70135.1, AW381476.1, AA705248.1, R19314.1, F05151.1, AW381459.1, AI206928.1, AW843169.1, AW009270.1, H19326.1, AW016196.1, R45471.1, AW084668.1, AI916589.1, AI435870.1, AI274998.1, AI095803.1, AA235124.1, AA234950.1, W25228.1, AA092442.1, AI352024.1, AW384329.1, AC006391.7, 20 AC016175.1, AL356136.1, AL353636.2, AL135938.7, AL158822.4, AC017144.1, AL162420.3, AC069151.1, AC009192.60, AC068789.3, AC041003.2, AC012480.4, AC053495.3, AC020603.3, AC020726.3, AC012297.3, AC018491.7, AC007532.7, AC013956.1, AC015797.2, AC013664.1, AC013097.1, AL356435.1, AL354999.1, AL162418.2, AL160035.3, AL159978.2, AL163639.1, AL139023.1, AP001532.1, AP001400.1, AP000590.3,

25 SEQ ID NO.226

NGO-St-115

YS1732/T7 3'

- L34543.1, L07872.1, L34544.1, NM_015874.1, L08904.1, D14041.1, S63463.1, X17459.1, M81871.1, U60093.1, U60094.1, AE003830.1, AC005974.1, AC007270.2, AF049850.1, AF016494.1, AL117207.1, D90170.1, D90168.1, 30 M64933.1, AI627646.1, AI401150.1, AA701607.1, AA641661.1, AI962712.1, AI829826.1, AW131544.1, AI953614.1, AW302357.1, AA042864.1, AW090508.1, AA640106.1, AI984992.1, AA903408.1, AA483607.1, AI291840.1, AW249681.1, AW235086.1, AI381502.1, AI619912.1, AI580826.1, AI375729.1, AA069672.1, AI334962.1, AI334964.1, T67414.1, AI669755.1, AI565611.1, N95392.1, AW005947.1, AI144435.1, AI023923.1, AI982567.1, AA788576.1, F33435.1, AW815621.1, AA501219.1, AA171398.1, AI631440.1, AA101255.1, AA676341.1, AA169326.1, AW815443.1, 35 AW391454.1, AW815833.1, AA669918.1, AA101351.1, AA908462.1, AW815635.1, AW815622.1, AW391447.1, AW425207.1, AW249892.1, AA678797.1, AW815508.1, AA044415.1, AW815506.1, AW815512.1, AW609613.1, AA126685.1, U69195.1, AW381515.1, AW189578.1, AW474060.1, AW381537.1, AA156824.1, AA705248.1, AW379059.1, AW371260.1, AI720441.1, AW371378.1, R19314.1, AW381482.1, AW381510.1, T23713.1, AW381496.1, R12509.1, AI206928.1, F05151.1, AW381476.1, AW610177.1, AW393428.1, AW016196.1, AW381459.1, AW843169.1, 40 AI658933.1, AW009270.1, AI919572.1, AW371229.1, T70135.1, AA092442.1, AW801962.1, AW462450.1, AI708578.1, AW384329.1, AW381472.1, AA895510.1, T79039.1, AI401152.1, F37823.1, AC006391.7, AC016175.1, AL356136.1, AC017144.1, AL162420.3, AC068789.3, AC012480.4, AC022263.4, AC021643.7, AC016390.3, AC013664.1, AL354999.1, AL031113.1, AL160035.3, AL159978.2, AL021574.2, AP000590.3, AL020985.1, AL021568.1,

45 SEQ ID NO.227

NGO-St-115

YS1792/T7 3'

- L34543.1, L07872.1, L34544.1, NM_015874.1, L08904.1, D14041.1, S63463.1, X17459.1, M81871.1, U60093.1, U60094.1, M81877.1, M81876.1, AC007270.2, AF049850.1, AF016494.1, D25323.1, D90170.1, D90168.1, M64933.1, 50 AI627646.1, AI401150.1, AA701607.1, AA641661.1, AI962712.1, AI829826.1, AW131544.1, AA640106.1, AI953614.1, AA042864.1, AW302357.1, AW090508.1, AI984992.1, AA483607.1, AA903408.1, AW249681.1, AW235086.1, AI381502.1, AI291840.1, AI619912.1, AI580826.1, AA069672.1, T67414.1, AI375729.1, AI023923.1, AI334964.1, AI565611.1, AI334962.1, AI669755.1, N95392.1, AW005947.1, AI144435.1, AI982567.1, AW815621.1, AA788576.1, F33435.1, AA501219.1, AA171398.1, AI631440.1, AA101255.1, AA676341.1, AA669918.1, AW815833.1, AW815443.1, 55 AA169326.1, AW391454.1, AA101351.1, AA908462.1, AW815622.1, AW425207.1, AW391447.1, AW815635.1, AW249892.1, AA678797.1, AW815508.1, AA044415.1, AW815506.1, AW815512.1, AW609613.1, AA126685.1, AW381515.1, U69195.1, AW474060.1, AW381537.1, AW189578.1, AA156824.1, AI720441.1, AW379059.1, AW371260.1, AW371378.1, AA705248.1, AW381496.1, AW381482.1, AW381510.1, R12509.1, T23713.1, AW381476.1, R19314.1, AI206928.1, F05151.1, AW381459.1, AW843169.1, AW610177.1, AW393428.1, AW016196.1, AW009270.1, 60 T70135.1, AI658933.1, AA092442.1, AW371229.1, AI919572.1, AW801962.1, AW462450.1, AI708578.1, AW384329.1, AW381472.1, F37823.1, AA895510.1, AA705236.1, T79039.1, AC006391.7, AC016175.1, AL356136.1, AC010633.4, AC015575.5, AC011760.8, AL162420.3, AC068789.3, AC012480.4, AC019214.2, AL354999.1, AL160035.3, AL159978.2, AP000590.3,

SEQ ID NO.228

NGO-St-115

YS1801/T3,

- 5 L07872.1, L34544.1, L34543.1, NM_015874.1, L08904.1, D14041.1, S63463.1, X17459.1, M81871.1, L07873.1, U60094.1, U60093.1, X59130.1, X59129.1, M81869.1, M81874.1, M81870.1, AB003695.1, M81873.1, M81872.1, M81875.1, AF085173.1, AE003646.1, AE003411.1, AF047659.1, AC011288.3, AC002338.2, AC007729.2, AE003662.1, AC006978.2, AC007082.4, AC006263.1, AF003130.1, Y08501.1, U80814.1, X66728.1, X65871.1, AJ007973.1, X58393.1, M94383.1, AE002611.1, AF223391.1, AC024864.1, AC024206.1, AC012329.3, AF104919.1, AL355836.1, AL157756.2, AL161587.2, AL161492.2, AL132964.2, AL137898.1, AL132962.1, AL035581.1, Z93385.1, Z81086.1, 10 AL035445.4, U70855.1, X96762.1, AL031135.1, U69195.1, AW462450.1, AL325751.1, AA935398.1, AW084668.1, AI916589.1, AW801962.1, T79039.1, T70135.1, AA501219.1, W25228.1, AI435870.1, AI274998.1, AI095803.1, AA235124.1, AA234950.1, R37405.1, AA081973.1, AA101254.1, H19326.1, AW239382.1, AW090508.1, R16902.1, F04242.1, AA969666.1, R45471.1, AA232981.1, AI352024.1, AW384329.1, T19153.1, AA233367.1, AI953614.1, R44578.1, F01398.1, AA641661.1, T23712.1, AW384317.1, AA101350.1, AI962712.1, AW425207.1, AW249681.1, 15 AI627646.1, AI401150.1, AA171575.1, AW131544.1, R19314.1, AA817421.1, AI142713.1, AA736032.1, R71133.1, AW760949.1, AJ394324.1, AW418568.1, AW221760.1, AW093987.1, AW043304.1, AI995809.1, AV200012.1, AV198387.1, AV191304.1, AI779257.1, C65393.1, D73771.1, D69291.1, D68255.1, D37730.1, AL356136.1, AC006391.7, AC019747.1, AC015644.3, AC015641.3, AC068980.2, AC021871.8, AC063967.1, AC024734.3, AC024447.2, AC006927.22, AC017011.3, AC010780.3, AC025099.1, AC010147.4, AC013569.3, AC017470.1, 20 AC006714.2, AL353636.2, AL158822.4, AP001377.1, AC012598.9, AC055764.3, AC067725.2, AC025573.4, AC024560.5, AC036183.2, AC055790.2, AC069123.1, AC069026.1, AC013610.2, AC068491.1, AC024084.2, AC008751.4, AC008749.4, AC005077.2, AC008267.3, AC027094.2, AC034098.1, AC025889.2, AC016462.3, AC027268.1, AC025317.2, AC018681.5, AC023815.2, AC018491.7, AC013504.2, AC013097.1, AC006904.2, AC006900.1, AC006719.1, AL138904.2, AL354990.1, AP000904.2, AP001455.1, AP000706.1, AL009206.1,

25 SEQ ID NO.229
NGO-St-115
YS1801/T7 3'

- 30 L34543.1, L07872.1, L34544.1, NM_015874.1, L08904.1, D14041.1, S63463.1, X17459.1, M81871.1, U60093.1, U60094.1, M81877.1, M81876.1, AE003627.1, AC005734.1, AE003830.1, AC005974.1, AL021578.1, AB024964.1, AB026048.1, AC012397.31, AC012147.7, AC006729.1, AE003603.1, AE003578.1, AC008261.3, AC017118.3, AC007270.2, AC005149.1, AF068710.1, AE000051.1, AJ239329.2, D25323.1, AW090508.1, AI627646.1, AA641661.1, AI962712.1, AI953614.1, AI401150.1, AW131544.1, AA701607.1, AW302357.1, AI829826.1, AA501219.1, AI984992.1, AA042864.1, AA640106.1, AA903408.1, AA483607.1, AA069672.1, AW249681.1, AW235086.1, AI381502.1, 35 AI619912.1, AI291840.1, AI023923.1, T67414.1, AI580826.1, AW425207.1, AI375729.1, AI565611.1, AI334962.1, AI334964.1, AI669755.1, N95392.1, AW005947.1, AI982567.1, AI144435.1, AA171398.1, AA788576.1, AW815621.1, F33435.1, AI631440.1, AA101255.1, AA676341.1, AA669918.1, AW815443.1, AA169326.1, AW391454.1, AW815833.1, AA101351.1, U69195.1, AA908462.1, AW815622.1, AW391447.1, AW815635.1, AW801962.1, AW249892.1, AI126685.1, AA044415.1, AW815508.1, AW815506.1, AW815512.1, AW609613.1, AA678797.1, AW462450.1, 40 AW381515.1, AW474060.1, AW381537.1, AA156824.1, AW379059.1, AW371260.1, AI720441.1, R12509.1, AW189578.1, AW371378.1, AW381482.1, AW381510.1, AW381496.1, T23713.1, T70135.1, AW381476.1, AA705248.1, R19314.1, F05151.1, AW381459.1, AI206928.1, AW843169.1, AW009270.1, AW016196.1, AW084668.1, AI916589.1, AI435870.1, AI274998.1, AI095803.1, AA235124.1, AA234950.1, W25228.1, AA969666.1, AA092442.1, F04242.1, R45471.1, AW384329.1, AC006391.7, AC016175.1, AL356136.1, AC010631.4, AC025727.1, AC018490.4, AC020100.1, 45 AL135938.7, AC018869.3, AC017144.1, AL138767.6, AL162420.3, AC009192.60, AC068789.3, AC025573.4, AC036183.2, AC041003.2, AC012480.4, AC025763.2, AC021089.2, AC011454.3, AC010533.3, AC008785.3, AC064816.1, AC011124.3, AC055769.1, AC019311.4, AC027284.1, AC018411.3, AC019202.3, AC007532.7, AC013956.1, AC020022.1, AC015797.2, AC013664.1, AC010694.2, AC006754.1, AL139235.6, AL354999.1, AL160035.3, AL159978.2, AP001904.1, AP001532.1, AP001400.1, AP000590.3,

50 SEQ ID NO.230
NGO-St-115
YS276/T7 3'

- 55 L34543.1, L07872.1, L34544.1, NM_015874.1, L08904.1, D14041.1, S63463.1, X17459.1, M81871.1, U60094.1, U60093.1, M81877.1, L07873.1, AE003830.1, AC005974.1, AL021578.1, AB024964.1, AB026048.1, AC012397.31, AC012147.7, AE002611.1, AC007270.2, U64857.1, AF049850.1, AF016494.1, D90170.1, D90168.1, M64933.1, AA641661.1, AI627646.1, AW090508.1, AI962712.1, AI401150.1, AW131544.1, AA701607.1, AI953614.1, AI829826.1, AW302357.1, AA042864.1, AI984992.1, AA640106.1, AA903408.1, AA501219.1, AA483607.1, AA069672.1, AW249681.1, AW235086.1, AI381502.1, AI619912.1, AI291840.1, AI023923.1, T67414.1, AI580826.1, AI375729.1, 60 AI565611.1, AI334962.1, AI334964.1, AI669755.1, N95392.1, AW815621.1, AW425207.1, AW005947.1, AI982567.1, AI144435.1, AA171398.1, AA788576.1, F33435.1, AI631440.1, AW815443.1, AA669918.1, AW391454.1, AW815833.1, AA101255.1, AA676341.1, AA169326.1, AW815622.1, AW391447.1, AW815635.1, AA101351.1, AA908462.1, U69195.1, AA126685.1, AW815508.1, AW815506.1, AW815512.1, AW609613.1, AW249892.1, AA044415.1, AA678797.1, AW801962.1, AW381515.1, AW474060.1, R12509.1, AW381537.1, AA156824.1, AW379059.1, T23713.1,

AW371260.1, AI720441.1, AW189578.1, AW371378.1, AW381482.1, AW381510.1, AW381496.1, AW462450.1, AA705248.1, R19314.1, F05151.1, T70135.1, AW381476.1, AI206928.1, AW381459.1, AW843169.1, AW610177.1, AW393428.1, AW016196.1, AA092442.1, AW009270.1, AW371229.1, AI658933.1, AI919572.1, H19326.1, AW084668.1, AI916589.1, R16902.1, AA235124.1, AI708578.1, AW384329.1, AC006391.7, AC016175.1, AL356136.1, 5 AC017078.3, AL135938.7, AC017144.1, AL162420.3, AC009192.60, AC068789.3, AC051628.10, AC012480.4, AC053495.3, AC022926.2, AC018491.7, AC015797.2, AC013664.1, AC013097.1, AC006915.1, AL356260.1, AL354999.1, AL160035.3, AL159978.2, AP001532.1, AP001400.1, AP000590.3,

SEQ ID NO.231

10 NGO-St-115

YS302/T7 3'

L34543.1, L07872.1, L34544.1, NM_015874.1, L08904.1, D14041.1, S63463.1, X17459.1, M81871.1, U60093.1, U60094.1, M81877.1, M81876.1, AC008408.5, AC011422.2, AE003830.1, AC006356.3, AC005974.1, AL021578.1, AB024964.1, AB026048.1, AC012397.31, AC012147.7, AE003578.1, AC007115.1, AC007270.2, U66059.1, AF030179.1, 15 AC005149.1, AF049850.1, AF016494.1, AL133376.6, D25323.1, D90170.1, D90168.1, U07978.1, M64933.1, AI627646.1, AA641661.1, AW090508.1, AI401150.1, AI953614.1, AI962712.1, AW131544.1, AA701607.1, AI829826.1, AA042864.1, AW302357.1, AA640106.1, AI984992.1, AA903408.1, AA483607.1, AW249681.1, AW235086.1, AI381502.1, AA501219.1, AA069672.1, AI619912.1, AI291840.1, AI023923.1, T67414.1, AI580826.1, AI375729.1, AI565611.1, AI334962.1, AI334964.1, AI669755.1, N95392.1, AW005947.1, AI144435.1, AW815621.1, AI982567.1, AA788576.1, 20 AA171398.1, AW425207.1, F33435.1, AI631440.1, AA669918.1, AW815443.1, AA101255.1, AW391454.1, AA676341.1, AW815833.1, AA169326.1, AW815622.1, AA101351.1, AW391447.1, AW815635.1, AA908462.1, AA126685.1, AW815508.1, AW249892.1, AW815506.1, AW815512.1, AW609613.1, U69195.1, AA044415.1, AA678797.1, AW381515.1, AW474060.1, AW381537.1, AA156824.1, R12509.1, AW801962.1, AW379059.1, AW371260.1, AI720441.1, AW189578.1, AW371378.1, T23713.1, AW381482.1, AW381510.1, AW381496.1, AA705248.1, R19314.1, 25 AW381476.1, F05151.1, AW462450.1, AI206928.1, T70135.1, AW381459.1, AW843169.1, AW009270.1, AA092442.1, AW610177.1, AW393428.1, AW016196.1, AW371229.1, AI658933.1, AI919572.1, R16902.1, H19326.1, AI708578.1, AA235124.1, AA969666.1, AW384329.1, R45471.1, AC006391.7, AC016175.1, AL356136.1, AC011340.3, AC017144.1, AL162420.3, AC009192.60, AC068789.3, AC012480.4, AC027785.2, AC025508.2, AC012346.3, AC027284.1, AC009659.3, AC021978.4, AC013448.3, AC020022.1, AC015797.2, AC010694.2, AL137160.4, AL354999.1, 30 AL160035.3, AL159978.2, AP001532.1, AP001400.1, AP000590.3,

SEQ ID NO.232

NGO-St-115

YS323/T7 3'

L34543.1, L07872.1, L34544.1, NM_015874.1, L08904.1, D14041.1, S63463.1, X17459.1, M81871.1, U60093.1, U60094.1, M81877.1, M81876.1, AE003830.1, AC005974.1, AC007270.2, AF049850.1, AF016494.1, D25323.1, D90170.1, D90168.1, M64933.1, AA641661.1, AI627646.1, AA701607.1, AI962712.1, AW131544.1, AI401150.1, AW090508.1, AI953614.1, AI829826.1, AA042864.1, AW302357.1, AA640106.1, AI984992.1, AA903408.1, AW249681.1, AW235086.1, AI381502.1, AI619912.1, AI291840.1, AA483607.1, AI580826.1, AA069672.1, AI375729.1, 40 AA501219.1, T67414.1, AI565611.1, AI023923.1, AI334962.1, AI334964.1, AI669755.1, N95392.1, AI982567.1, AW005947.1, AI144435.1, AW815621.1, AA788576.1, F33435.1, AA171398.1, AI631440.1, AW815443.1, AA101255.1, AA676341.1, AW391454.1, AW425207.1, AW815833.1, AA169326.1, AA669918.1, AW815622.1, AW815635.1, AW391447.1, AA101351.1, AA908462.1, AW815508.1, AW815506.1, AW249892.1, AW815512.1, AW609613.1, U69195.1, AA126685.1, AA044415.1, AA678797.1, AW381515.1, AW189578.1, AW474060.1, AW381537.1, 45 AA156824.1, R12509.1, AW379059.1, AW371260.1, AI720441.1, AA705248.1, AW371378.1, T23713.1, AW381482.1, AW381510.1, AW381496.1, F05151.1, AW381476.1, AI206928.1, R19314.1, AW801962.1, AW381459.1, T70135.1, AW843169.1, AW610177.1, AW393428.1, AW016196.1, AI658933.1, AA092442.1, AW462450.1, AW009270.1, AI919572.1, AW371229.1, AW384329.1, AI708578.1, AW381472.1, AA895510.1, F37823.1, R45471.1, R16902.1, AC006391.7, AC016175.1, AL356136.1, AC017144.1, AL162420.3, AC068789.3, AC012480.4, AC013664.1, 50 AL354999.1, AL160035.3, AL159978.2, AP000590.3,

SEQ ID NO.233

NGO-St-115

YS372/T7 3'

L34543.1, L07872.1, L34544.1, NM_015874.1, L08904.1, D14041.1, S63463.1, X17459.1, M81871.1, U60093.1, U60094.1, M81877.1, M81876.1, AE003830.1, AC005974.1, AC012397.31, AC007270.2, AF049850.1, AF016494.1, D25323.1, D90170.1, D90168.1, M64933.1, AA641661.1, AI627646.1, AA701607.1, AI962712.1, AW131544.1, AW090508.1, AI953614.1, AI401150.1, AI829826.1, AA042864.1, AW302357.1, AA640106.1, AI984992.1, AA903408.1, AA483607.1, AW249681.1, AW235086.1, AI381502.1, AA069672.1, AI619912.1, AI291840.1, AI580826.1, T67414.1, 60 AI023923.1, AA501219.1, AI375729.1, AI565611.1, AI334962.1, AI334964.1, AI669755.1, N95392.1, AW005947.1, AI144435.1, AI982567.1, AW815621.1, AA788576.1, F33435.1, AA171398.1, AW425207.1, AI631440.1, AA101255.1, AW815443.1, AA676341.1, AW391454.1, AA669918.1, AA169326.1, AW815833.1, AW815622.1, AA101351.1, AW391447.1, AW815635.1, AA908462.1, U69195.1, AW815508.1, AW249892.1, AW815506.1, AW815512.1, AA126685.1, AW609613.1, AA044415.1, AA678797.1, AW381515.1, AW474060.1, AW381537.1, AW189578.1,

5 R12509.1, AA156824.1, AW379059.1, AW371260.1, A1720441.1, AW371378.1, AA705248.1, T23713.1, AW381482.1, AW381510.1, AW381496.1, AW381476.1, R19314.1, T70135.1, F05151.1, A1206928.1, AW801962.1, AW381459.1, AW843169.1, AW462450.1, AW610177.1, AW393428.1, AW016196.1, AW009270.1, AA092442.1, AW371229.1, A1658933.1, A1919572.1, AW384329.1, A1708578.1, AW381472.1, F37823.1, T79039.1, AA895510.1, AA705236.1, AC006391.7, AC016175.1, AL356136.1, AC017144.1, AL162420.3, AC009192.60, AC068789.3, AC012480.4, AC010552.3, AC023549.2, AC022931.3, AC022391.2, AL354999.1, AL160035.3, AL159978.2, AP001005.1, AP000590.3,

SEQ ID NO.234

10 NGO-St-115

YS406/T7 3'

15 L34543.1, L07872.1, L34544.1, NM_015874.1, L08904.1, D14041.1, S63463.1, X17459.1, M81871.1, U60093.1, U60094.1, M81877.1, AE003830.1, AC005974.1, AC007270.2, AF049850.1, AF016494.1, AF035530.1, D25323.1, D90170.1, D90168.1, M64933.1, AA701607.1, AA641661.1, A1627646.1, A1962712.1, A1401150.1, AW131544.1, AW090508.1, A1953614.1, A1829826.1, AA042864.1, AW302357.1, AA640106.1, A1984992.1, AA903408.1, AW249681.1, AW235086.1, A1381502.1, AA483607.1, A1619912.1, A1291840.1, AA069672.1, A1580826.1, T67414.1, A1375729.1, A1023923.1, A1565611.1, A1334962.1, A1334964.1, AA501219.1, A1669755.1, N95392.1, AW005947.1, A1144435.1, A1982567.1, AW815621.1, AA788576.1, F33435.1, AA171398.1, A1631440.1, AA101255.1, AA676341.1, AW815443.1, AA169326.1, AW425207.1, AA669918.1, AW391454.1, AW815833.1, AA101351.1, AW815622.1, 20 AA908462.1, AW815635.1, AW391447.1, AW249892.1, AW815508.1, AA044415.1, AW815506.1, AA678797.1, AA126685.1, AW815512.1, AW609613.1, U69195.1, AW381515.1, AW474060.1, AW381537.1, AW189578.1, AA156824.1, AW379059.1, AW371260.1, A1720441.1, AW371378.1, AW381482.1, AW381510.1, AW381496.1, R12509.1, AA705248.1, T23713.1, AW381476.1, A1206928.1, F05151.1, AW381459.1, R19314.1, AW843169.1, T70135.1, AW801962.1, AW610177.1, AW393428.1, AW016196.1, AW462450.1, A1658933.1, AW009270.1, 25 AA092442.1, AW371229.1, A1919572.1, A1708578.1, AW384329.1, AW381472.1, F37823.1, A1274998.1, AA235124.1, W25228.1, AC006391.7, AC016175.1, AL356136.1, AC022173.4, AC009377.5, AC017144.1, AL162420.3,

SEQ ID NO.235

NGO-St-116

30 YS1651/T3 5'

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SEQ ID NO.236

NGO-St-116

YS1651/T7 3'

-127-

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SEQ ID NO.237

NGO-St-116

30 YS1701/T3 5'

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SEQ ID NO.238

NGO-St-116

YS1701/T7 3'

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YS1731/T7 3'

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YS1784/T7 3'

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SEQ ID NO.241

NGO-St-116

20 YS1796/T7 3'

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SEQ ID NO.242

NGO-St-116

50 YS353/T7 3'

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- AA479788.1, AA130632.1, AW516994.1, AW513837.1, AJ744383.1, AA970442.1, AA196514.1, AI168478.1, AW085863.1, AI573195.1, AA219578.1, AA164508.1, AW236411.1, AW192162.1, AW572335.1, AA133938.1, AW674312.1, AC010746.3, AC024884.6, AC027473.2, AC032001.2, AL136079.3, AL138760.4, AC026299.2, AL354869.1, AF252831.1, AF252830.1, AF202031.1, AF189745.1, AC063980.1, AC008821.4, AC008840.3, AC008511.4, AL137180.3, AL160258.3, AF260011.1, AC026746.3, AC016645.3, AC026750.2, AC026809.1, AC016517.4, AP001561.1, AP000641.1, AP000799.1, AC006909.1, AC055839.2, AC026610.2, AC021592.3, AC018406.2, AC021065.3, AL137072.1, AC009822.3, AC026803.2, AC068191.1, AC027003.2, AC016458.2, AC018740.2, AC005308.6, AC011578.3, AC011267.2, AC012670.2, AC016998.1, AC009232.2, AL356112.2, AL109808.2,
- 10 SEQ ID NO.243
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- 35 SEQ ID NO.244
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- 60 SEQ ID NO.245
NGO-St-117
YS025/T7 3'

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- 25 SEQ ID NO.246
NGO-St-117
YS062/T3 5'
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- 50 SEQ ID NO.247
NGO-St-117
YS062/T7 3'
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- 55
- 60

AI371256.1, AA733183.1, AA531124.1, AA365494.1, F30300.1, AI370734.1, T90909.1, Z25096.1, AA027130.1, AA115569.1, T71475.1, AI432578.1, AW088726.1, AA721771.1, AA115089.1, T49643.1, R00622.1, T83325.1, AA426250.1, N93780.1, T83700.1, AA393863.1, AA282967.1, AI872750.1, R00626.1, AI471045.1, AW750808.1, AW369701.1, R08138.1, N74066.1, AI370415.1, AA658299.1, T55344.1, AA003997.1, AW744236.1, AW742885.1, 5 AA250467.1, AW557746.1, AW208617.1, AA968175.1, AW322345.1, AI500088.1, AA260498.1, AA848318.1, AA958697.1, AI877303.1, AA397074.1, AA008542.1, AA036229.1, AW456866.1, AI931743.1, AA253686.1, AW743789.1, AI411403.1, AL033383.25, AL136309.3, AL355594.3, AC021873.7, AC068763.2, AC022912.3, AC034235.2, AC025224.3, AC025502.2, AC024325.2, AC019078.3, AL137142.8, AL133407.4, AL139254.3, AL354955.1, AP000916.2, AP001804.1, AC055832.2, AC004166.10, AC020947.5, AC010246.4, AC010348.3, 10 AC009061.8, AC067929.1, AC025127.2, AC005073.2, AC007003.2, AC004867.2, AC027394.2, AC012350.3, AC010947.3, AC025740.1, AC018553.2, AC013532.2, AL355552.1, AL139294.1,

SEQ ID NO.248

NGO-St-117

15 YS286/T7 3'

NM_006117.1, AF153612.1, AF069301.1, AF257175.1, AF244138.1, NM_011868.1, AF153613.1, AP000689.1, AB003151.1, U11419.1, NM_012574.1, NM_008171.1, NM_000834.2, AC005232.1, AC011915.3, U88963.1, AF111103.1, AC005304.1, U11287.1, U90278.1, M91562.1, D10651.1, AE003498.1, AC007000.2, AC004843.1, AC006014.2, AC005488.2, AC004878.2, AC007786.1, AC002082.1, AC005071.2, AC006504.1, AC005355.1, 20 AC005273.1, U72724.1, U17243.1, AL121767.3, AL133233.2, AB022216.1, AC011525.4, AF024504.2, AC004953.1, AC007773.1, AC006487.7, AC005796.1, AL352976.2, AJ239322.3, Z75955.1, AP001342.1, AP001135.2, AI870279.1, AI807002.1, AL036852.1, AI564314.1, AI565595.1, W67775.1, AW270727.1, AI610377.1, AW662848.1, AA617696.1, AA934587.1, AI096931.1, AA628682.1, AW731836.1, AA913577.1, AI391743.1, AW474447.1, AI363079.1, AI336097.1, AI432577.1, AI352108.1, AI352327.1, AA969876.1, AA995606.1, W74527.1, AA622402.1, AI085901.1, AA027090.1, 25 AI307399.1, AI287814.1, AA620556.1, W79046.1, AW194674.1, AW182085.1, AA085733.1, AA187157.1, AI625204.1, AI031865.1, AW591699.1, AA897169.1, AA972318.1, AI349588.1, AI674578.1, AI659404.1, AA365494.1, AW302400.1, F36532.1, AI371256.1, AA733183.1, AA531124.1, AA027130.1, AA115569.1, F30300.1, AI370734.1, T90909.1, Z25096.1, T71475.1, AI432578.1, AA426250.1, AW088726.1, T83700.1, AA393863.1, AA721771.1, AA115089.1, T49643.1, AA282967.1, R00622.1, T83325.1, N93780.1, AW750808.1, AI872750.1, R00626.1, R08138.1, AI471045.1, 30 AW369701.1, N74066.1, AI370415.1, AA658299.1, AA003997.1, AW744236.1, AA250467.1, T55344.1, AA848318.1, AA968175.1, AW742885.1, AW322345.1, AW208617.1, AW557746.1, AI877303.1, AI500088.1, AA260498.1, AA958697.1, AA397074.1, AA008542.1, AA036229.1, AW456866.1, AI931743.1, AA253686.1, AI411403.1, W67774.1, AL033383.25, AL136309.3, AL355594.3, AC021873.7, AC068763.2, AC022912.3, AC034235.2, AC025224.3, AC025502.2, AC024325.2, AC019078.3, AL133293.18, AL137142.8, AL133407.4, AL139254.3, AL354955.1, 35 AP000916.2, AP001804.1, AC055832.2, AC004166.10, AC020947.5, AC010246.4, AC010348.3, AC061712.2, AC009061.8, AC005073.2, AC007003.2, AC010139.3, AC004867.2, AC027394.2, AC012350.3, AC011039.4, AC010947.3, AC025740.1, AC013532.2, AC005143.1, AL355487.1,

SEQ ID NO.249

40 NGO-St-118

YS1802/T7 3'

NM_001655.1, X81198.1, AF111103.1, AF111102.1, S74341.1, AF151870.1, NM_016049.1, AE003475.1, AL136295.2, U32692.1, AF019376.1, Z70680.1, AE003528.1, AC004931.1, AE000604.1, AC006050.1, AL117667.2, AL096862.18, Z46793.1, AL035250.17, AL031224.1, Z99289.1, AL109798.19, AL112548.1, L29789.1, AA412680.1, AI755123.1, 45 AA102578.1, AA206349.1, AW055098.1, AA293170.1, AW439825.1, AW269634.1, AI076926.1, AI025067.1, AI700509.1, AI078164.1, AI697821.1, AA705915.1, AI160192.1, AI093354.1, AA165600.1, AA705055.1, AA527537.1, AA192464.1, AI653666.1, AI264667.1, AI650293.1, AI091869.1, AA506760.1, AI950897.1, AI380068.1, AI264617.1, AI125887.1, AA047461.1, AI890839.1, AI683902.1, N24749.1, N32156.1, AI302074.1, AA088764.1, N26132.1, AI040426.1, AI358017.1, AI141871.1, AW474078.1, AI523696.1, N32947.1, AA688242.1, AI961853.1, AI446329.1, 50 AI002397.1, AA993720.1, AA707731.1, AA422132.1, H99310.1, AI879755.1, AI918396.1, AA804436.1, AA928305.1, AW168784.1, AA719418.1, AI087106.1, AI024105.1, AW129693.1, W15326.1, H94333.1, AI962023.1, W42458.1, N21273.1, AW194030.1, AA856562.1, AI758429.1, AA243440.1, AA434593.1, W85810.1, AI079791.1, H99597.1, N67805.1, AA808672.1, AW303758.1, AI769314.1, R76982.1, AI754941.1, N42618.1, H98545.1, AA599213.1, AI832336.1, AA811624.1, H88780.1, AI886101.1, AI474209.1, H88997.1, N94593.1, AI888666.1, AA055972.1, 55 AA788790.1, AA491237.1, AI401139.1, H96031.1, T99642.1, AA598401.1, AA026110.1, Z40496.1, AI658990.1, AP000941.2, AP000846.1, AP000869.1, AC019068.3, AC019509.1, AC010015.3, AC036149.2, AC027187.2, AC025241.2, AC026015.2, AC027724.1, AC012532.3, AC015914.3, AC022658.3, AC024732.2, AC016276.2, AC002317.1, AL163952.1, AL135929.4, AC000380.1, AL135909.3, AC020636.4, AC023892.11, AC010856.3, AC055864.2, AC023156.3, AC068590.1, AC025079.3, AC021269.3, AC013670.3, AC021378.3, AC060765.1, AC058803.1, AC021150.5, AC013386.4, AC019162.3, AC027521.1, AC018425.3, AC012274.2, AC024231.3, 60 AC025978.1, AC013331.4, AC016418.4, AC023018.2, AC021567.2, AC011783.3, AC012436.4, AC020636.3, AC010066.5, AC011892.3, AC014423.1, AL121919.13, AL353638.2, AL160285.5, AL139284.3, AL356033.1, AL354000.2, AL354985.2, AL161451.4, AL157950.3, AL353774.1, AL160290.3, AL139003.1, AP001393.1,

SEQ ID NO.250

NGO-St-119

YS334/T3 5'

- 5 NM_003146.1, M86737.1, S50213.1, L08814.1, L08815.1, U84139.1, AB004793.1, AE003462.1, X68408.1, L08825.1, AL031904.1, AL035653.12, AC007058.2, U40759.1, NC_001145.1, AE002662.1, AE002914.1, AE003202.1, AE002711.1, AC007285.3, AL163298.2, AL163002.1, S74619.1, Z48622.1, AP001753.1, AB001517.1, AP001055.1, Z79396.1, AW247262.1, AA258912.1, AA443507.1, AA085435.1, AA312302.1, F07281.1, AA359039.1, D55248.1, D54571.1, D54563.1, D54952.1, D54973.1, AW802206.1, D53930.1, AA355756.1, AA404188.1, A1556014.1, AA104553.1, AL138347.1, AW489221.1, AA253486.1, AW320565.1, AA088369.1, H10266.1, AW401443.1, D77299.1, AW381661.1, 10 AA993395.1, AA464881.1, AA036329.1, A1913779.1, AA476079.1, AA306252.1, AA590151.1, AW748405.1, AW366265.1, AA130307.1, A1789443.1, AW378315.1, AW269617.1, AW370347.1, AW480897.1, AA497585.1, AW536819.1, AW536546.1, AU060291.1, AA162184.1, W07230.1, AP000781.2, AC020482.1, AC009182.3, AL139094.5, AC044849.2, AC020624.5, AC016588.5, AC010741.3, AL161790.3, AC068888.2, AC013552.4, AC022413.3, AC011472.5, AC068473.1, AC024176.4, AC019023.3, AC019286.4, AC024462.2, AC020561.2, AC016441.4, 15 AC022770.4, AC025303.1, AC006286.13, AC021638.5, AC018018.1, AC018205.1, AC003656.1, AL356318.1, AL355178.2, AL133463.8, AL160401.4, AL139816.4, AL158160.1, AL118500.5,

SEQ ID NO.251

NGO-St-119

20 YS334/T7 3'

- NM_003146.1, M86737.1, S50213.1, U84139.1, L08814.1, AC007967.3, AC017111.4, AC026237.4, AC005313.2, AF130357.1, AC004918.1, AF131217.2, AF165124.1, AL163247.2, AL021938.1, AL035534.1, AB037738.1, A1200891.1, A1832834.1, A1694393.1, A1597819.1, AA773470.1, AA640958.1, A1989881.1, A1954549.1, AA669346.1, AL043692.1, AA872063.1, AW771391.1, A1653466.1, AA488456.1, A1770053.1, A1719199.1, AA181676.1, A1768076.1, AW250844.1, 25 A1769368.1, A1326218.1, A1292284.1, AA102606.1, AW583325.1, AA630377.1, AW246563.1, A1803290.1, AW469194.1, AW072040.1, A1801767.1, AA129398.1, AA129437.1, N47701.1, AW055203.1, AA204842.1, AA403256.1, AW162590.1, AW873160.1, N47715.1, AA428207.1, A1802539.1, AW474265.1, AW517489.1, AA155636.1, AA187844.1, A1708178.1, A1298177.1, AA084865.1, AW196881.1, A1802262.1, AA223606.1, AA188417.1, AW182589.1, AW601976.1, A1125376.1, AA983384.1, A1669267.1, AA047175.1, A1369594.1, AA640599.1, 30 AA629829.1, AA506517.1, AA426576.1, A1034453.1, A1927125.1, A1198409.1, AA088196.1, AA644298.1, AA172185.1, A1024913.1, AA282185.1, AW772651.1, AA418911.1, AA679982.1, AA232539.1, AA928645.1, A1421368.1, AW516350.1, A1249088.1, AA770296.1, AL042406.1, A1913779.1, A102637.1, W92454.1, AW732257.1, AW194956.1, A1433062.1, AA203343.1, AA581113.1, T29388.1, AA258817.1, AA173277.1, AW873703.1, A1569301.1, AA522909.1, H10212.1, AW138326.1, A1630694.1, A1475149.1, AA367901.1, AP000781.2, AC068719.1, AL355364.3, AC021659.7, 35 AC008383.4, AC010757.2, AC009475.3, AC012291.3, AC027118.2, AC023547.2, AC026245.1, AC011808.3, AC007856.6, AC015665.2, AL136227.4, AL356094.1,

SEQ ID NO.252

NGO-St-120

40 YS357/T3 5'

- NM_013285.1, L05425.1, U69600.1, AL034379.8, AL021571.1, AB015478.1, X99436.1, AC024751.1, AC006920.10, NM_009722.1, NM_001681.1, AC006581.16, AJ223584.1, A131821.1, AL121578.1, AL008715.1, X52496.1, X02814.1, M23115.1, M23114.1, Z11500.1, J04703.1, AF235167.1, AE003511.1, AC002045.1, AC007216.2, U95742.1, AC002299.1, AF196970.1, AC007283.3, AF013149.1, AF152363.1, AC005844.7, AC005841.3, AF001549.1, 45 AC000385.1, AL049988.1, AL109865.36, Z50028.1, Z68325.1, Z82204.1, AL049849.1, S75106.1, AK000019.1, AB020863.1, X07653.1, AA373618.1, AW245855.1, AW161434.1, AW409934.1, AW163245.1, AA126101.1, AA690847.1, AW362598.1, AW377646.1, AA858436.1, AL024316.1, AW377648.1, AW427911.1, H35824.1, A112354.1, A1573674.1, AA684606.1, A1035443.1, AA316055.1, AA171883.1, AV125438.1, A1853194.1, AA308223.1, AW326870.1, AV125326.1, AA692026.1, AV138378.1, AA303227.1, AA581348.1, AW765532.1, AA989948.1, 50 C70491.1, AW773907.1, D23001.1, AV442312.1, AW650351.1, A1994797.1, A1488290.1, N38238.1, T80141.1, AW736578.1, A1077091.1, A1908898.1, A1847850.1, A1776439.1, A1467314.1, A1382397.1, A1290588.1, A1091365.1, AA414121.1, AA409715.1, AA038677.1, AW738493.1, A1709211.1, A1661426.1, A1482631.1, A1114591.1, D78236.1, AA742179.1, AA744826.1, AA663314.1, AA594218.1, AA452237.1, AA410224.1, AA298534.1, AA199847.1, H74324.1, R99587.1, AC023077.3, AC027731.2, AL355880.2, AC011124.3, AC018953.5, AC023502.3, AC026155.3, AC024905.7, 55 AC067611.1, AC064107.1, AC056245.1, AC033416.1, AC027813.1, AC021828.2, AL138975.1, AC026677.2, AC022164.4, AC022147.4, AC023398.2, AC027006.2, AC025043.3, AC017041.2, AC016838.3, AC023448.2, AC021481.3, AC019325.3, AC023958.2, AC025279.1, AC022408.3, AC016492.1, AP001767.1, AP001120.1,

SEQ ID NO.253

60 NGO-St-120

YS357/T7 3'

- NM_013285.1, L05425.1, AL034379.8, U69600.1, AC007020.4, AF085279.1, L39991.1, AF176688.1, AC006200.2, AE003829.1, NM_010393.1, NM_006574.1, NM_002824.1, AF126482.1, AF125444.1, AF059274.1, AF088905.1, AC005515.1, AF016684.1, AL121748.6, Z72514.1, U20374.1, U47326.1, X16423.1, X16203.1, X16197.1, U07055.1,

X64053.1, X16481.1, X65748.1, X00246.1, Y13586.1, Y10211.1, M24398.1, M27134.1, M23445.1, L29190.1, M27034.1, J00393.1, M63790.1, AC000365.1, NM_010398.1, AC007281.3, AF041855.1, AF057279.1, AF082510.1, U88154.1, U88153.1, U96752.1, U91424.1, Z68106.1, AL020997.1, AL110509.2, X16198.1, X16424.1, AB021155.1, M11284.1, L00606.1, AW157242.1, AA902387.1, AI925558.1, AI628921.1, AW070650.1, AA401208.1, AW409935.1, AW162279.1, 5 AA722289.1, AW172793.1, AA126418.1, AA780182.1, AA857353.1, AW804193.1, AW156969.1, AW183614.1, AI376281.1, AI826742.1, AA582490.1, AA446557.1, AW246802.1, AI474094.1, AA483614.1, AA934590.1, AA846248.1, AI253092.1, AA888018.1, AW804232.1, AI699045.1, AI954511.1, AA171554.1, AI867001.1, AI760439.1, AW804255.1, AI763044.1, AW804270.1, AI825244.1, AI671605.1, AA126000.1, AI702310.1, AA766044.1, AI798554.1, AW250835.1, W81287.1, AW768894.1, AA635139.1, AW002316.1, AW362969.1, AW118384.1, AA493881.1, AI470650.1, 10 AA659293.1, AA863491.1, AA196109.1, AA831455.1, AI244063.1, AA659297.1, N32569.1, AI245761.1, AA515590.1, AI909114.1, T27737.1, AA524198.1, AW607751.1, AI345764.1, AW301566.1, AI310849.1, AI310651.1, AW268086.1, AI589981.1, AA056760.1, AW268169.1, AA403201.1, AL135350.1, AA614309.1, AI907635.1, AW529039.1, AI112872.1, AI060050.1, AA546717.1, AW532741.1, AW557260.1, AV220510.1, AI646349.1, AI536459.1, AW653179.1, AI853259.1, AV090573.1, AI058723.1, AV310274.1, AV236721.1, AV236719.1, AV167761.1, 15 AW111676.1, AV311465.1, AV296078.1, AV225966.1, AA646750.1, AA472792.1, AA111295.1, AC027731.2, AL355880.2, AC023077.3, AC026348.3, AC068683.1, AC022553.2, AC023000.2, AC010058.5, AC013019.1, AC010195.7, AC026992.2, AC027820.2, AC021884.2, AC022388.2, AC022937.3, AC019056.4, AC017422.1, AC015232.1, AC007438.6, AC006086.7, AC006087.12, AC002490.1, AL159141.1, AC044907.2, AC022558.3, AC044814.2, AC025036.6, AC051623.1, AC012145.3, AC021523.3, AC021296.2, AC007477.5, AC021959.4, 20 AC006279.6, AC015535.4, AC020585.5, AC025110.1, AC010009.4, AC016767.3, AC019749.1, AC018050.1, AC016210.1, AC015148.1, AC009454.1, AL136090.10, AL135840.7, AL133341.9, AP001390.1, AP001120.1,

SEQ ID NO.254

NGO-St-121

25 YS363/T3 5'
AF098638.1, NM_004703.1, X77723.1, X91141.1, U70777.1, D85844.1, D86066.1, AB001750.1, D88828.1, D38038.1, Y08613.1, AF164343.1, AC000021.1, AB022176.1, AL031003.1, AC011309.4, AC002089.1, AC013454.4, AC003019.1, U58108.1, L78833.1, AF051934.1, AL163268.2, AC000119.1, AL022476.2, S86117.1, AJ229042.1, AB018418.1, AC010151.3, AC024080.2, AC008444.4, AC002340.2, AE003833.1, AE003798.1, AF035218.1, AC006249.1, 30 AC004657.1, AF027868.1, AL031661.28, AL161587.2, AL117188.1, AL049845.7, AL031431.8, AL022239.1, U22110.1, D90899.1, Z79479.1, AB020865.1, Z34519.1, Z99114.1, AW501546.1, W28259.1, W27092.1, AW371635.1, AL042125.1, AA611522.1, AA614931.1, AW748799.1, AA110819.1, Z28809.1, AW304131.1, AI371714.1, AW450989.1, AV162434.1, AI024379.1, AI288155.1, H24233.1, H16513.1, AW371421.1, AW496353.1, R40226.1, AA208526.1, AA075857.1, AA543909.1, AW501200.1, AW385206.1, AW760996.1, AW558606.1, AW558583.1, AW298142.1, AW294127.1, 35 AI874594.1, AI835959.1, AI788080.1, AV100560.1, AI537352.1, AI411951.1, AI410456.1, AA858493.1, AI309599.1, AI194657.1, AI182965.1, AI152676.1, AI144668.1, AI060676.1, AI046764.1, AA959394.1, AA940384.1, AA797665.1, AA763173.1, AA717573.1, AA710050.1, AA709538.1, AA561671.1, AA408328.1, AA285493.1, AA270256.1, AA241245.1, AA230889.1, AA213293.1, AA104682.1, AA104275.1, AA104274.1, AA087023.1, AA062156.1, AA061500.1, AA031128.1, AA028486.1, AA011772.1, W63860.1, W34388.1, W18032.1, W09805.1, AW694402.1, 40 AW691053.1, AV213344.1, AV007100.1, AA892832.1, AA489256.1, T76002.1, AC015727.3, AC006338.3, AC007248.2, AC007039.3, AC006990.3, AC006983.2, AC053490.1, AC006982.1, AC036236.1, AC026852.1, AC020855.2, AC021307.3, AC010089.2, AC024353.2, AC011753.2, AC020562.1, AC013575.1, AC011900.1, AL163760.1,

SEQ ID NO. 255

45 NGO-St-121

YS363/T7 3'

AC004148.1, AL157499.1, AL050211.1, AC009275.5, AC008154.6, AE003690.1, AE003653.1, AC005524.1, Z47358.1, X98238.1, AI972322.1, AA193309.1, AA528241.1, AW235706.1, AA527684.1, AI436191.1, AA890512.1, AW299850.1, AA767452.1, AI580941.1, AI056055.1, AI130923.1, AA283713.1, AI418205.1, AI056706.1, AI808670.1, AW137415.1, 50 AI400431.1, AW295892.1, AA846649.1, AA960854.1, AI222234.1, AI084465.1, AA479888.1, AA917434.1, AA960792.1, AA290870.1, AW089851.1, AI090024.1, AI078176.1, AA683232.1, AI023887.1, AA706411.1, AA040801.1, AI632800.1, AI367258.1, AA693619.1, W15394.1, T03894.1, AI955173.1, AI269900.1, AA218890.1, AI669191.1, AA760918.1, AI826582.1, AI910510.1, AW082288.1, N52967.1, Z39660.1, Z28661.1, W58520.1, AA954763.1, R50797.1, AA041239.1, H90518.1, AI349313.1, AI301633.1, AA412174.1, AI800039.1, F26651.1, AW235792.1, AA621533.1, AA194263.1, 55 AI932942.1, H09347.1, AI953061.1, R40788.1, AW752307.1, AA216603.1, AW351827.1, H73642.1, Z28597.1, AW137802.1, H51737.1, N45966.1, AW576920.1, Z20686.1, Z28596.1, Z24941.1, AA425331.1, N44279.1, AA766379.1, AI742337.1, AA426446.1, AI696486.1, Z72398.1, D20547.1, AA778438.1, AV331582.1, AW046470.1, AA472952.1, AA120705.1, AV357525.1, AA409778.1, AC016370.4, AC026940.2, AC026455.2, AC015932.4, AC019267.3, AC018853.3, AC009074.2, AC009201.3, AC022549.1, AC014455.1, AC017510.1, AC006491.23, AC011631.1, 60 AL157823.3, AP001847.1, Z92859.1,

SEQ ID NO.256

NGO-St-122

YS1742/T3 5'

NM_005089.1, D49677.1, U51224.1, D49676.1, AC004106.1, NM_009453.1, D45205.1, NM_011663.1, S69507.1, D26474.1, D17407.1, U92882.1, Z74476.1, AC002530.1, U80017.1, AL031767.13, AL133100.1, AL096854.5, Z99279.1, M83200.1, AP000002.1, AK000538.1, NC_001139.1, AC005250.1, AC003074.1, AC004451.1, AC004882.2, AC007402.3, AC009992.5, AC004947.2, AF098999.1, AL121754.18, U60414.1, U62631.1, U57971.1, AB013003.1, AB013004.1, 5 AP000173.1, AP000333.1, AW866867.1, AJ417175.1, AW371109.1, AW137848.1, AJ200960.1, N80309.1, AA845804.1, AA320008.1, AA028127.1, AA028151.1, AA814970.1, AA814962.1, AA920561.1, AA331011.1, AW364105.1, AI598939.1, AW144684.1, AW356771.1, AW805221.1, AJ472111.1, AW345188.1, AW535394.1, AI576737.1, AJ454541.1, AI112465.1, AA601026.1, AI112441.1, AI663887.1, AA388471.1, AW383892.1, AV357914.1, AW826265.1, AW613523.1, AW514825.1, AV331731.1, AW117909.1, AV149324.1, AV124185.1, AV036810.1, AA841469.1, 10 AA771282.1, AA507133.1, AA199064.1, Z74661.1, W27716.1, AV440680.1, AW671805.1, AW569275.1, AV359278.1, AV212567.1, AW039499.1, AI989107.1, AI946720.1, AI868501.1, AV117593.1, AI763597.1, AV062802.1, AI755024.1, AV032630.1, AI648156.1, AI594159.1, AI466310.1, AI452794.1, AI412501.1, AI381209.1, AI232722.1, AI101718.1, AI011347.1, AI266800.1, AI114436.1, AI058893.1, AA807323.1, AA763112.1, AA709977.1, AA600133.1, AA545349.1, AA519216.1, AA452591.1, AA424001.1, AA329479.1, AA326345.1, Z81248.1, AA078585.1, C07041.1, C06862.1, 15 C06853.1, H34402.1, AC008536.5, AC008461.4, AC008812.6, AC008763.4, AC017027.4, AC016287.3, AC011257.3, AL136314.4, AC025259.4, AC068227.1, AC020985.4, AC018429.3, AC019244.2, AL139113.4, AL137004.2, AC069141.1, AC063954.2, AC046141.3, AC007641.10, AC067960.2, AC018728.2, AC009245.8, AC027495.2, AC025669.2, AC044808.1, AC023841.2, AC023421.2, AC026513.2, AC015916.3, AC019049.2, AC016814.3, AC011985.3, AC018671.5, AC016503.2, AC021329.3, AC021563.1, AC011094.2, AL121983.7, AL157361.6, 20 AL139419.1, AP000654.1,

SEQ ID NO.257

NGO-St-122

YS1742/T7 3'

25 NM_005089.1, AC004106.1, D49677.1, U51224.1, D49676.1, NM_011663.1, NM_009453.1, S69507.1, D45205.1, D26474.1, D17407.1, AL031317.1, AL139078.2, AB026659.1, AW194326.1, AW089584.1, AI991464.1, AI828556.1, AA430135.1, AA723697.1, AI634052.1, AW237119.1, T67521.1, AA377829.1, AW515964.1, AA569819.1, T67543.1, AA601026.1, AA669459.1, AW609046.1, AI663908.1, AI663887.1, AI893901.1, AI636519.1, AI632192.1, H41170.1, AC008536.5, AC008461.4, AC008451.3, AC040954.1, AC007569.8, AC027671.2, AC016823.4, AC021594.3, 30 AL138881.4, AP001641.1,

SEQ ID NO.258

NGO-St-123

YS1702/T7 3'

35 U40705.1, AF043911.1, NM_003218.1, U74382.1, AF003001.1, AC006572.2, AL163204.2, NM_009352.1, U65586.1, X93511.1, U70993.1, L63545.1, AC004484.2, AC004617.1, U47029.1, D83257.1, Y17297.1, AC011738.4, AE003685.1, NM_009263.1, AL033534.1, Z47809.1, S78177.1, X13986.1, X51834.1, X16151.1, J04806.1, NC_001145.1, AC004667.2, AE003478.1, AE003432.1, AC002080.1, AC004964.2, AC007285.3, Z36238.1, Z48618.1, AL036326.1, AA467901.1, N68057.1, AW772242.1, AI394003.1, AA135978.1, AA135764.1, AA467846.1, T76958.1, AA463246.1, AW152089.1, 40 F13251.1, AW088675.1, R70911.1, AW860774.1, AA468251.1, AL046407.1, AI347136.1, AA317158.1, AI524143.1, Z45971.1, AI144010.1, AA207271.1, T63517.1, AI802125.1, AA468235.1, AI689994.1, AI680979.1, AW003979.1, AA529658.1, R68526.1, AI125634.1, AW197488.1, AI088591.1, AA204808.1, AI989793.1, Z19923.1, AI553354.1, R25990.1, AI313657.1, AI313655.1, AW367580.1, AI653818.1, AA982217.1, AW822952.1, AW413558.1, AW413468.1, AW412565.1, AW412480.1, AW411784.1, AW261735.1, AW260247.1, AW260085.1, AW259661.1, AW240668.1, 45 AW240555.1, AW215800.1, AW212687.1, AW209307.1, AW209207.1, AW209119.1, AW208838.1, AW113907.1, AI987812.1, AI929854.1, AI891858.1, AI875465.1, AI875197.1, AI847805.1, AI839505.1, AI802541.1, AI790405.1, AI788611.1, AV017671.1, AV001287.1, AI648742.1, AI647513.1, AI528600.1, AI325605.1, AI282135.1, AI182295.1, AI132382.1, AU021551.1, AI043071.1, AI043053.1, AI042865.1, AI035296.1, AA986704.1, AA980925.1, AA839469.1, AA798241.1, AA789592.1, AA591084.1, AA563324.1, AA537448.1, AA145872.1, AA122501.1, AA073811.1, W08572.1, 50 AL137013.3, AL050303.2, AC022893.2, AF164115.1, AC011941.4, AC012670.2, AL162851.3, AC068925.1, AC023087.3, AC011904.2, AC024067.3, AC024095.6, AC021771.2, AC018453.3, AC015364.1, AC017348.1, AC008172.1, AC055808.2, AC011346.3, AC017014.3, AC026903.2, AC016486.4, AC012288.2, AC012602.2, AC014153.1, AL139162.3, AL009027.1,

55 SEQ ID NO. 259

NGO-St-124

YS033/T3 5'

60 AF039690.1, AF161348.1, AC006041.2, AC004636.1, AE003598.1, AE003485.1, NM_007186.1, AC005694.3, AC005529.7, AC005527.3, AC006221.1, AC004755.1, AF049105.1, AF022655.1, AL121586.28, Z47074.1, AP000965.2, U48937.2, AE003029.1, AF163441.1, AF123008.1, AF123007.1, AF122994.1, AF092091.1, AL137686.1, Z82185.1, AL035070.3, AJ011930.1, AP001068.1, AP001067.1, M98498.1, W29097.1, AI092201.1, AA690806.1, AA155014.1, AV127431.1, AA089195.1, AI967815.1, AI865255.1, AV359357.1, AV328696.1, AV287587.1, AV313495.1, AV272703.1, AV233789.1, AV233050.1, AA143515.1, AW708128.1, AW368913.1, AV338709.1, AV332139.1, AV290604.1, AV323766.1, AV027087.1, AI240775.1, AI170252.1, AI038890.1, AW679928.1, AW584240.1,

-136-

AW581584.1, AW581582.1, AW573270.1, AW518642.1, AW516804.1, AW436684.1, AW369753.1, AW341252.1, AV354655.1, AW134807.1, AI969272.1, AI949771.1, AI948870.1, AI924168.1, AI914290.1, AI892918.1, AI871649.1, AI832248.1, AI830664.1, AI824895.1, AI819076.1, AI819130.1, AL037429.1, AI796870.1, AI769675.1, AI717994.1, AI708155.1, AI700048.1, AI697939.1, AI697687.1, AI689763.1, AI660476.1, AI655335.1, AU059236.1, AI621281.1, AI394537.1, AI379706.1, AI341342.1, AI304914.1, AI301627.1, AI300957.1, AI299037.1, AI299037.1, AI290292.1, AI224563.1, AI167134.1, AI146249.1, AI140672.1, AI089910.1, AI039908.1, AI016407.1, AA995707.1, AA973566.1, AA967806.1, AA938631.1, AA907234.1, AA780678.1, AA742364.1, AA682624.1, AA591111.1, AA452630.1, AA252245.1, AA252941.1, AA242923.1, AA153891.1, W65797.1, W05501.1, N70619.1, D81647.1, AC024509.2, AL355978.2, AC019168.3, AC023267.2, AC024691.2, AC009011.2, AC034307.2, AC022983.2, AC015865.1, AC013902.1, AC017166.1, AC006839.13, AL139226.14, AC035146.2, AC007640.2, AC012411.3, AC021822.3, AC013829.4, AC021670.2, AL162453.4,

SEQ ID NO. 260

NGO-St-124

15 YS033/T7 3'

AF039690.1, U79271.1, AL117525.1, AC009479.3, AC005358.1, AF136378.1, AC005081.2, AF045555.1, AL031650.21, AC006919.5, AC010967.2, AC008056.6, NM_012776.1, AC005386.1, NM_001619.2, U42580.2, AC007533.5, S81843.1, U08438.1, Z68282.1, AL121757.7, AL049544.4, AL031681.13, S48813.1, U39674.1, L23127.1, M34073.1, M80776.1, X61157.1, AB025639.1, M74822.1, M87854.1, X53421.1, AI735499.1, AW028371.1, AI445418.1, AI266387.1, AI288955.1, AW193663.1, AI298467.1, AI168222.1, AI148323.1, AI140814.1, AI089322.1, AA879456.1, AA843811.1, AA829894.1, AA102109.1, AA029201.1, W72147.1, N51485.1, AI808317.1, AI033069.1, AA161465.1, AA812519.1, N64528.1, H99906.1, AA886109.1, R71679.1, AI970343.1, AA744290.1, AW021346.1, AA099913.1, AW195719.1, AI267979.1, AA083859.1, AI038590.1, N51277.1, AA883684.1, R07471.1, H98684.1, R36854.1, F25334.1, R39448.1, AA083954.1, R54092.1, H09074.1, AA346369.1, AA910762.1, AW873705.1, N21975.1, D59844.1, AW195087.1, H11525.1, AA971254.1, W77907.1, W29097.1, AW057648.1, AL041060.1, AI659852.1, AA878973.1, AW392482.1, AI057361.1, AA715235.1, F35739.1, AW427844.1, AW022199.1, AI963422.1, AA860455.1, AA026096.1, AA026096.1, AI481147.1, N71178.1, AW413553.1, AW046739.1, AI529534.1, AI661769.1, AA269966.1, AI614472.1, AA026516.1, AI713205.1, AI575014.1, AI112396.1, AI073194.1, AI651890.1, AI575171.1, AA466212.1, AW181975.1, AI888595.1, AV162955.1, AI452798.1, AI167638.1, AW495689.1, AI397450.1, AW547034.1, AW479264.1, AC024079.2, AC022960.2, AL161723.3, AP001333.1, AC044855.2, AC060801.2, AC018648.2, AC068004.1, AC009623.3, AC013699.2, AC021912.3, AC018685.5, AC016675.4, AF202962.1, AL139349.16, AL132661.15, AL117190.2, AC010798.6, AC037488.2, AC036143.2, AC034212.3, AC008377.3, AC018640.1, AC009444.2, AC025803.2, AC021417.3, AC026750.2, AC024242.2, AC026809.1, AC022882.3, AC016721.4, AC024342.2, AC009923.3, AC022828.2, AC023002.1, AC011237.3, AC017078.3, AC011290.2, AL080314.29, AL163540.3, AL162632.1, AL353713.1, AL158068.4, AL159973.2, AL133501.1, AP001586.1, AP001023.1, AP000425.1,

SEQ ID NO.261

NGO-St-124

YS173/T3 5'

40 AF039690.1, AF161348.1, AC006615.1, AC006041.2, AC004636.1, AB006709.1, AE003598.1, AC005070.1, AC007632.4, AC005041.2, AC006221.1, Z47074.1, U48937.2, AC007019.4, AC011751.2, AF145727.1, AF164622.1, AF163441.1, AF204231.1, AC010870.4, AC005589.1, AC008072.3, AF092091.1, AF009623.1, AC004048.1, AC004257.1, AL163300.2, AL137686.1, U88309.1, AL021492.1, Z46787.1, Z94057.1, AL035070.3, AP001819.1, AJ011930.1, AP001068.1, AP001067.1, AB029041.1, AB020662.1, D84549.1, M98498.1, AI092201.1, AA155014.1, W29097.1, AW150169.1, AV127431.1, AA089195.1, AI606060.1, AI967815.1, AV359357.1, AV328696.1, AV287587.1, AV313495.1, AV272703.1, AV233789.1, AV233050.1, AA690806.1, AW708128.1, AV338709.1, AV332139.1, AV290604.1, AV323766.1, AV027087.1, AI240775.1, AI170252.1, AW679928.1, AW584240.1, AW581584.1, AW581582.1, AW369753.1, AV354655.1, AL044559.1, AL037429.1, AU059236.1, AA780678.1, D81647.1, AC024509.2, AL355978.2, AC019168.3, AC023267.2, AC024691.2, AC018403.4, AC009011.2, AC012473.5, AC012487.3, AC006724.1, AP001523.1, AC037470.2, AC040171.2, AC009636.3, AC025660.2, AC022983.2, AC023750.1, AC015865.1, AC016040.2, AC017166.1, AL354654.1, AL138479.1,

SEQ ID NO.262

NGO-St-124

55 YS173/T7 3'

AF039690.1, U79271.1, AL117525.1, AF136378.1, AL031650.21, X79703.1, AC006919.5, AC008056.6, NM_012776.1, NM_001619.2, AF193021.1, AC007538.5, S81843.1, AF121782.1, AF064857.1, AL163281.2, AL133283.9, U08438.1, Z50044.1, Z68282.1, AL121757.7, AL049544.4, AL031681.13, S48813.1, U39678.1, U39674.1, L23127.1, M34073.1, M80776.1, X61157.1, M74822.1, M87854.1, X53421.1, AI735499.1, AW028371.1, AI445418.1, AI266387.1, AI288955.1, AW193663.1, AI298467.1, AI168222.1, AI148323.1, AI140814.1, AI089322.1, AA879456.1, AA843811.1, AA829894.1, AA102109.1, AA029201.1, W72147.1, N51485.1, AI808317.1, AI033069.1, AA161465.1, AA812519.1, N64528.1, H99906.1, AA886109.1, R71679.1, AI970343.1, AA744290.1, AW021346.1, AA099913.1, AW195719.1, AI267979.1, AA083859.1, AI038590.1, N51277.1, AA883684.1, R07471.1, H98684.1, R36854.1, R39448.1, F25334.1, AA083954.1, R54092.1, H09074.1, AA346369.1, AA910762.1, AW873705.1, N21975.1, W29097.1, D59844.1, AW195087.1, H11525.1,

AA971254.1, W77907.1, AW057648.1, AL041060.1, AI659852.1, AA878973.1, AW392482.1, AI057361.1, AA715235.1, F35739.1, AW022199.1, AW427844.1, AA860455.1, AI963422.1, AA026096.1, AI481147.1, T26899.1, AW413553.1, AW04673.1, AI529534.1, AI661769.1, AA269966.1, N71178.1, AI614472.1, AI713205.1, AI575014.1, AI112396.1, AI073194.1, AA026516.1, AI651890.1, AI575171.1, AA466212.1, AV162955.1, AA690806.1, AI397450.1, AC022960.2, AP001333.1, AC044855.2, AC060801.2, AC018648.2, AC068004.1, AC013699.2, AC026224.1, AC021912.3, AC018685.5, AF202962.1, AL139349.16, AL132661.15, AL117190.2,

SEQ ID NO.263

NGO-St-125

10 YS3710/T3 5'

AF099990.1, AF068261.1, D88190.1, AC005950.1, AC001228.1, D64137.1, NM_002840.1, AF099988.1, AL137556.1, Y19224.1, Y00815.1, NM_000076.1, AC024753.1, AE003481.1, AE003458.1, NM_002653.1, AF109719.2, AC004367.1, AF009648.1, AL157480.1, Z83844.5, U48869.1, U22398.1, AB018791.1, NM_014961.1, AE003669.1, AF112221.1, AC005811.10, AF082296.1, AC004466.1, AL008583.1, AK000911.1, AB020678.1, M63356.1, AE003487.1, AF047034.2, AF071810.1, AC004797.1, U09808.1, AE003663.1, U90653.2, NM_012699.1, AC022517.1, AF071813.1, AC004876.2, AC005259.1, L81775.1, X95703.1, X98993.1, X62681.1, AF189262.1, NM_014341.1, AF176006.3, AF192559.3, NM_013024.1, AF189289.1, AF071815.1, NM_009453.1, NM_006460.1, AC007395.3, AF139177.1, U86410.1, M83196.1, U40628.1, U40627.1, X00618.1, AL031107.1, J02675.1, AB021179.1, D45205.1, D83484.1, X00254.1, X76232.1, M63348.1, U03771.1, AF255552.1, AF168787.1, AC007774.1, AC006486.1, AJ004801.1, Z77662.1, AL136295.2, U14656.1, AW070197.1, AI873022.1, AW575715.1, AW271726.1, AW172297.1, AW170107.1, AI524194.1, AI652188.1, AI623209.1, N95583.1, AA283710.1, AA573499.1, AI674687.1, AA694439.1, AI760975.1, AA731091.1, AI230984.1, AA805306.1, AA927565.1, AW369632.1, AI425458.1, AI578926.1, AI043684.1, AA851538.1, AA221745.1, AW028244.1, AI873396.1, AI492967.1, AI192683.1, AI854240.1, AI850380.1, AI575971.1, AI461919.1, AW047118.1, AA997145.1, AI008247.1, AA408914.1, AA408939.1, AA402099.1, CI1942.1, AA305260.1, AW869895.1, AJ272945.1, AI429741.1, AW595481.1, AI595277.1, AI327425.1, AA481582.1, AA061204.1, W98922.1, AV408902.1, AW696319.1, AW677099.1, AW513114.1, AW280634.1, AW280527.1, AW243892.1, AW193511.1, AI852364.1, AI803180.1, AI784610.1, AI671129.1, AI640998.1, AA998163.1, AA964571.1, AI159402.1, AW244421.1, AW624533.1, AW593458.1, AW574954.1, AW149459.1, AW092856.1, AI987240.1, AI876971.1, AI356089.1, AI225774.1, AI166942.1, AA791749.1, AA544523.1, W16147.1, W18003.1, W13961.1, N42977.1, H19168.1, AC013791.3, AC010216.4, AC008470.3, AC023467.2, AL355519.2, AC025716.1, AC008350.3, AC010714.3, AC020195.1, AC008232.3, AC006903.1, AC006727.1, AC006751.1, Z98864.1, AC008406.5, AC014744.1, AC024725.3, AC026968.2, AC021248.3, AC014187.1, AC014191.1, AL035406.22, AC021024.3, AC009570.7, AC034220.3, AC021091.2, AC009061.8, AC027682.2, AC011430.4, AC007732.2, AC026759.1, AC009911.9, AC010848.12, AC011707.7, AC021618.3, AC019638.1, AC014137.1, AC014975.1, AC010024.2, AC007831.1, AL121908.11, AC024215.7, AC068810.1, AC010648.5, AC022274.4, AC015462.5, AC022307.7, AC024047.2, AC024708.2, AC010003.5, AC009369.5, AC011244.3, AC010703.2, AL122034.8, AL137066.5, AL354940.3, AL157708.2, AC027810.3, AC027796.3, AC058789.9, AC026270.2, AC016631.5, AC011514.2, AC027800.2, AC067434.1, AC026167.2, AC027040.2, AC019234.3, AC012236.3, AC009915.4, AC024159.1, AC023852.1, AC013273.2, AC020327.1, AC020433.1, AC020525.1, AC007925.4, AC017941.1, AC018090.1, AC008228.2, AC013124.1, AC013189.1, AC013210.1, AC014106.1, AC014400.1, AC015146.1, AC007822.3, AL031258.10, AL355153.1, AL080247.3,

SEQ ID NO.264

NGO-St-126 combined

AC067976.1, AC010763.2, AC067721.3, AC063926.3, AC026210.1, AC022240.2, AC025076.3, AP001541.1, AP000614.3, AC009543.4, AC026325.3, AC026317.5, AC026311.4, AC025580.3, AC012112.2, AC022926.2, AC020012.1, AC018212.1, AL137864.6, AL356371.1, AL356260.1, AC040919.1, AC044905.2, AC036192.2, AC023648.3, AC068679.1, AC027464.2, AC021200.4, AC012512.2, AC012164.10, AC017097.2, AC013273.2, AC012352.3, AC022183.2, AC011018.2, AC018224.1, AC015182.1, AC009742.3, AF181895.1, AF128834.1, AL355143.4, AL354814.1, Z92852.20, AL021149.3, AP002000.1, AP001361.1, AP000786.1, AP000785.1, AL021347.1, AI469428.1, AW004984.1, AW675448.1, AW780423.1, AW239395.1, AW651755.1, AA535069.1, AI378367.1, AA879433.1, AA971454.1, AI394371.1, AI564549.1, AA446421.1, AW553616.1, AA928053.1, N78225.1, AI431285.1, AA870109.1, AW674657.1, AI364000.1, AA305698.1, AA760173.1, AW674987.1, AW087890.1, N59764.1, AW548602.1, AW881866.1, AA897396.1, AW673412.1, AW674408.1, AA056907.1, AI202011.1, AA213076.1, AI047089.1, AW392852.1, AI747290.1, T36030.1, AW544283.1, AI131751.1, AW340239.1, T19014.1, T96204.1, R94457.1, AA518752.1, AI115877.1, AI119061.1, AA123206.1, AI753769.1, AI787898.1, AA765346.1, AI715715.1, AA999172.1, AA221877.1, AI460161.1, T81090.1, C03806.1, N86797.1, AW079585.1, AW672700.1, AW527002.1, AU076916.1, AI741285.1, R00722.1, AI892500.1, R00723.1, AA644165.1, AI916149.1, AI482319.1, AI325806.1, T81139.1, AA438060.1, AA561307.1, AI873729.1, AA561305.1, AV040805.2, AV235074.1, AV220284.1, AI614757.1, AW275744.1, AV265274.1, AV248478.1, AV245335.1, AV263802.1, AV270362.1, AV043755.2, AV048190.1, AV370590.1, D25791.1, AV114853.1, AV111421.1, AV256037.1, AI795876.1, AV374021.1, AV261192.1, AV320489.1, AV252321.1, AV366822.1, AV299835.1, AV312541.1, AA450537.1, AC067976.1, AC010763.2, AC067721.3, AC063926.3, AC026210.1, AC022240.2, AC025076.3, AP001541.1, AP000614.3, AC009543.4, AC026325.3, AC026317.5, AC026311.4, AC025580.3, AC012112.2, AC022926.2, AC020012.1, AC018212.1, AL137864.6, AL356371.1, AL356260.1, AC040919.1, AC044905.2, AC036192.2, AC023648.3, AC068679.1, AC027464.2,

AC021200.4, AC012512.2, AC012164.10, AC017097.2, AC013273.2, AC012352.3, AC022183.2, AC011018.2, AC018224.1, AC015182.1, AC009742.3, AF181895.1, AF128834.1, AL355143.4, AL354814.1, Z92852.20, AL021149.3, AP002000.1, AP001361.1, AP000786.1, AP000785.1,

5 SEQ ID NO. 265

NGO-St-126

YS136/T3 5'

10 NM_003875.1, U10860.1, X87562.1, AL139077.2, AB033168.1, AC007956.5, AE003718.1, NM_004879.2, AC004877.1, AF010313.2, AC006052.5, AL035671.5, NC_001139.1, AC020580.9, AC002382.1, AC006064.9, AC005895.1, Z72999.1, AL022328.21, AL049781.4, AL133068.1, AL133399.1, M88277.1, X59698.1, X78987.1, D90899.1, AB037724.1, AK001986.1, AB023482.2, U03425.1, AB009050.1, AW239395.1, AW651755.1, AW672700.1, AU076916.1, AI119061.1, AW527002.1, AI787898.1, AI115877.1, AI614757.1, AA123206.1, AA450537.1, AI892500.1, AI325806.1, AW372007.1, AW367352.1, AI930281.1, AA561307.1, AA561305.1, AW732597.1, AW732373.1, AW248209.1, AV300605.1, AW163311.1, AV204617.1, AI550018.1, AW699234.1, AW653532.1, AW653462.1, AW336984.1, AW163624.1, AI929457.1, AI739490.1, AI069011.1, R58474.1, R57620.1, R46363.1, R14654.1, T38036.1, T33110.1, Z43008.1, AC010763.2, AC026210.1, AC044905.2, AC023648.3, AC019035.5, AC018958.2, AC013273.2, AC012669.2, AC018224.1, AC009742.3, AC012522.7, AC068285.2, AC021891.2, AC008692.4, AC010373.4, AC011116.3, AC018696.3, AC024931.3, AC018996.3, AC009621.4, AC022213.3, AC021265.3, AC022930.2, AL133416.3, AL137161.3, AL137855.2, AL135924.10, AL080247.3,

20 SEQ ID NO.266

NGO-St-126

YS136/T7 3'

25 NM_003875.1, U10860.1, AC006380.2, AF006203.1, AC009396.5, Z50794.1, U21627.1, AI469428.1, AW004984.1, AI564549.1, AW675448.1, AA535069.1, AI378367.1, AW780423.1, AA879433.1, AI394371.1, AA971454.1, AI431285.1, AA928053.1, AW674657.1, AI364000.1, AA305698.1, AW674987.1, AW087890.1, AW673412.1, AI202011.1, N59764.1, AW674408.1, AI741285.1, AA056907.1, AA897396.1, AW340239.1, AW553616.1, AW548602.1, AA870109.1, AW544283.1, AI131751.1, AI753769.1, AI460161.1, AA765346.1, AI715715.1, AA999172.1, AA221877.1, N78225.1, T81090.1, AW079585.1, R00723.1, AI747290.1, AI482319.1, AA446421.1, AI873729.1, AW275744.1, T96204.1, 30 AV263802.1, AV235074.1, AV248478.1, AW881866.1, D25791.1, AV245335.1, AV370590.1, AV265274.1, AV220284.1, AV040805.2, AV114853.1, AV111421.1, R94457.1, AV261192.1, AV320489.1, AV048190.1, AV043755.2, AV270362.1, AV256037.1, AV374021.1, AV312541.1, AV366822.1, AV352771.1, AV299835.1, AV261104.1, AV337229.1, AV254627.1, AV257886.1, AV252321.1, AV261234.1, AV255806.1, AV380586.1, AV281906.1, AV283090.1, AW681473.1, AV279890.1, R00722.1, AV359752.1, AA218130.1, AV351363.1, T81139.1, AW634678.1, 35 AW634655.1, AV263948.1, AW766970.1, AW460442.1, BB001634.1, AW198719.1, AW148282.1, AV228798.1, AC067976.1, AC067721.3, AC024615.2, AC009550.3, AC037444.2, AC037467.2, AC027003.2, AC010679.3,

SEQ ID NO.267

NGO-St-126

40 YS1613/T3 5'

NM_003875.1, U10860.1, U67598.1, U39471.1, U28733.1, M64282.1, AE003537.1, AB012242.1, AC008993.3, AE003781.1, AC008063.2, AC005061.2, AC004605.1, AC007090.3, AE001176.1, AF067215.1, AL161532.2, AF016678.1, Z93778.1, Z30215.1, AC002109.1, AL078621.19, AL050399.1, U42844.1, AC000120.1, Z94044.1, AL035447.3, AP002067.1, X60691.1, M93038.1, M14115.1, M16632.1, M59809.1, M59810.1, M59808.1, M14707.1, 45 AA760173.1, AI047089.1, AA518752.1, N86797.1, C03806.1, AA644165.1, T36030.1, T19014.1, AA438060.1, AI916149.1, AA213076.1, AI795876.1, AA123206.1, AA561308.1, AA561307.1, AA561305.1, AW392852.1, AW651755.1, AI325806.1, AI892500.1, AI878306.1, AI119061.1, R94029.1, AV346184.1, AW154885.1, AW031455.1, AW725845.1, AW271459.1, AW201020.1, AV376365.1, AI990909.1, AV174444.1, AI353515.1, AA909030.1, T70524.1, AC063926.3, AC067721.3, AC022240.2, AC009543.4, AC012112.2, AC022926.2, AL137864.6, AL356371.1, 50 AL356260.1, AC025076.3, AC027464.2, AC015773.4, AC012512.2, AC020668.4, AC012352.3, AC015182.1, AF181895.1, AF128834.1, AP001541.1, AP000614.3,

SEQ ID NO.268

NGO-St-126

55 YS1613/T7 3'

NM_003875.1, U10860.1, AC006380.2, AF134842.1, AC002127.1, NM_004849.1, AL022067.1, Y11588.1, AC004450.2, AC009396.5, AC006145.2, AC003953.1, Z50794.1, X97212.1, AI469428.1, AW004984.1, AW675448.1, AW780423.1, AA535069.1, AI378367.1, AA879433.1, AA971454.1, AI394371.1, AI564549.1, AA928053.1, AI431285.1, AW553616.1, AW674657.1, AI364000.1, AA870109.1, AA305698.1, AW674987.1, AW087890.1, N59764.1, AW548602.1, 60 AA897396.1, AW673412.1, AA056907.1, AW674408.1, N78225.1, AI202011.1, AW544283.1, AI131751.1, AW340239.1, AI753769.1, AI715715.1, AA765346.1, AI747290.1, AA999172.1, AA221877.1, AI460161.1, AA446421.1, T81090.1, AW079585.1, AI741285.1, AW881866.1, T96204.1, R00723.1, R94457.1, AI482319.1, AI873729.1, AV275744.1, AV265274.1, AV248478.1, R00722.1, AV245335.1, AV263802.1, AV270362.1, AV043755.2, AV048190.1, AV370590.1, D25791.1, AV114853.1, AV111421.1, AV256037.1, AV374021.1, AV261192.1,

- AV320489.1, AV252321.1, AV352771.1, AV366822.1, T81139.1, AV299835.1, AV312541.1, AW681473.1, AV254627.1, AV261104.1, AV337229.1, AV261234.1, AV257886.1, AV255806.1, AV283090.1, AV281906.1, AV279890.1, AV380586.1, AW634678.1, AW634655.1, AV359752.1, AV351363.1, AV280423.1, AA218130.1, AV263948.1, AW460442.1, AW766970.1, W88512.1, AW484561.1, AI705688.1, AA112455.1, N94345.1, AC067976.1, AC067721.3, AC025580.3, AL355980.2, AL162491.3, AC044895.1, AC021200.4, AL133509.7, AL138917.3, AP001361.1, AP000786.1, AC044809.3, AC026450.2, AC034188.2, AC025241.2, AC027415.1, AC026201.1, AC023147.3, AC024449.2, AC022004.2, AC022219.2, AC010987.4, AL136109.3, AL139230.6, AP001828.1, AP000653.1, AP000595.2,
- 5
- 10 SEQ ID NO.269
NGO-St-126
YS1722/T3 5'
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- 15
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- 35 SEQ ID NO.270
NGO-St-126
YS377/T3 5'
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- 40
- 45
- 50 SEQ ID NO.271
NGO-St-127
YS263/T3 5'
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5 SEQ ID NO.272

NGO-St-127

YS263/T7 3'

- NM_014753.1, D80009.1, AE003451.1, AC011294.3, Z85996.1, AC007244.2, AJ271079.1, M22462.1, AE003815.1, AE003364.1, AC004963.2, AF153352.1, AC007068.17, AE001389.1, Z78067.1, AP000419.1, L15320.1, AC007042.2, AC006544.19, AF135026.1, AE003557.1, AE003528.1, AC003060.1, AF228703.1, U91325.1, AC004832.3, AC004876.2, AC007368.11, AC007461.8, AC004950.2, AC005033.1, AC003065.1, AC005548.1, U21933.1, AF010237.1, AC004167.1, AC004104.1, AC002324.1, AE001032.1, AL050342.42, Z98949.1, Z77662.1, Z50015.1, AL022315.1, AL121723.36, AL157498.1, AL137325.1, U31447.1, AL023800.1, L19655.1, AP000475.3, M73822.1, AP001111.1, AP000023.1, AB028621.1, D87018.1, AB029018.1, AC006481.3, AF050157.1, AL121656.2, AL022310.1, AB016885.1, AW237092.1, AW237137.1, AI935281.1, AW467637.1, AI963620.1, AI650475.1, AI628080.1, AA927690.1, AI338027.1, AI590556.1, AA604575.1, AA203521.1, AI281023.1, AI609068.1, AI689223.1, AW058425.1, AA483799.1, AW473973.1, AA278635.1, AW083923.1, AA915891.1, AA766731.1, AI984984.1, AW803966.1, AI281118.1, AI131367.1, AI537394.1, AI278563.1, AA159506.1, AI304815.1, AI033401.1, AI049943.1, AW004875.1, AA047286.1, T87897.1, AW029023.1, AA480172.1, AI285145.1, AA252803.1, AA261816.1, AI867812.1, AA554061.1, AI753409.1, W81534.1, AI015310.1, AA099000.1, T87990.1, AI184520.1, R00576.1, AI824434.1, AL047806.1, W81533.1, T79535.1, AA047147.1, R33795.1, AA864952.1, AI149983.1, R00680.1, AI810930.1, AW263579.1, AI866914.1, T97738.1, AW796065.1, AA278634.1, AI802574.1, AI651401.1, AW004034.1, AW175987.1, AI005967.1, AA793158.1, H62063.1, AA571438.1, AI376279.1, AA623849.1, AW194865.1, AW428271.1, AW175972.1, AA616918.1, AW205363.1, AA762572.1, AA223495.1, H61156.1, AA421215.1, AA411512.1, AA405999.1, AA293345.1, AA555719.1, T97844.1, AA914529.1, AA726890.1, AA262513.1, AA058106.1, AW910545.1, AW416674.1, AW416666.1, AI406390.1, AA421216.1, AA411513.1, AA399425.1, AW523356.1, AL022344.1, AL023808.2, AC036220.3, AC023099.2, AC022264.2, AC011753.3, AC023723.2, AC014984.1, AC009785.4, AC011191.3, AC013532.2, AC025638.3, AC010033.7, AC068739.2, AC034244.3, AC008481.6, AC027517.2, AC036185.1, AC015925.3, AC015724.4, AC019168.3, AC017420.1, AC013378.3, AC007107.1, AC025011.2, AC022061.3, AC012431.6, AC015990.5, AC058333.2, AC020904.5, AC011543.3, AC011491.4, AC018880.2, AC021111.3, AC024638.2, AC022297.7, AC017059.2, AF215848.1, AL158846.3, AL139404.2, AL139110.2, AL121828.8, AL161618.5, AP001102.2, AP001005.1, AP000813.1,

SEQ ID NO.273

NGO-St-127

35 YS324/T7 3'

- NM_014753.1, D80009.1, AE003451.1, Z85996.1, AC007244.2, AJ271079.1, M22462.1, AC004963.2, AF153352.1, AC007068.17, Z78067.1, Z83844.5, AL078477.5, AP000419.1, L15320.1, AC007042.2, AC006544.19, AF135026.1, AC027657.1, AE003557.1, AF228703.1, AC004832.3, AC004876.2, AC005003.2, AC006371.2, AC008078.11, AC008010.10, AC007368.11, AF134488.1, AC004961.2, AC007461.8, AC006432.15, AC004950.2, AC002082.1, AC005033.1, AC003065.1, U21933.1, AF010237.1, AC004167.1, AC004104.1, AC002324.1, AE001032.1, Z98949.1, Z77662.1, Z50015.1, U93037.1, AL022315.1, AL121723.36, AL031767.13, AL049838.3, AL157498.1, AL137325.1, U31447.1, AL023800.1, AL031665.18, L19655.1, AB040962.1, M73822.1, AP001111.1, AP000023.1, AB028621.1, AB005049.1, AB029018.1, NM_001702.1, NM_013146.1, AL121656.2, AL022310.1, U18419.1, X54171.1, AB005297.1, AI963620.1, AW467637.1, AW237092.1, AW237137.1, AI628080.1, AI935281.1, AI650475.1, AI338027.1, AA604575.1, AA927690.1, AI609068.1, AI590556.1, AI281023.1, AW058425.1, AI689223.1, AA203521.1, AA483799.1, AW473973.1, AA278635.1, AA915891.1, AW083923.1, AA766731.1, AI984984.1, AI281118.1, AI131367.1, AI537394.1, AI278563.1, AA159506.1, AI304815.1, AI049943.1, AI033401.1, AW004875.1, AI285145.1, AA047286.1, AW803966.1, AW029023.1, T87897.1, AA480172.1, AA252803.1, AA261816.1, AI753409.1, AI867812.1, W81534.1, AA554061.1, AI015310.1, AA099000.1, AI184520.1, R00576.1, AI824434.1, T87990.1, AA047147.1, AI866914.1, AA864952.1, R33795.1, AI149983.1, AI810930.1, T79535.1, AI802574.1, AW263579.1, T97738.1, R00680.1, W81533.1, AW004034.1, AL047806.1, AW194865.1, AI376279.1, AI651401.1, H62063.1, AW205363.1, AW428271.1, H61156.1, AA421215.1, AA411512.1, AA405999.1, AA293345.1, AA223495.1, AW796065.1, AA278634.1, AA421216.1, AA411513.1, AA399425.1, AA455122.1, AA402812.1, AA402916.1, AA402630.1, AW523356.1, AW522183.1, AW469155.1, AW469154.1, AW469148.1, AI406390.1, AW910545.1, AI005967.1, AA623849.1, AA408648.1, W77672.1, AA914529.1, AA793158.1, AA571438.1, AL022344.1, AL023808.2, AC036220.3, AC023099.2, AC022264.2, AC011753.3, AC023723.2, AC014984.1, AC022146.3, AC009785.4, AC011191.3, AC013532.2, AC010033.7, AC068739.2, AC034244.3, AC008481.6, AC036185.1, AC025473.2, AC015925.3, AC015724.4, AC023857.2, AC025011.2, AC022061.3, AC012431.6, AC015990.5, AC009757.8, AC018634.2, AC058333.2, AC040949.2, AC021893.10, AC012640.4, AC011491.4, AC026040.3, AC021111.3, AC025749.2, AC009899.5, AC013391.3, AC018679.5, AC022297.7, AC023325.2, AC022908.2, AC017059.2, AC011329.5, AC014174.1, AC010826.2, AC011098.1, AL158846.3, AL139404.2, AL137004.3, AL137793.2, AL133402.10, AL121828.8, AL161618.5, AL161739.2, AL161448.3, AP001936.1, AP001102.2, AC009857.2, AC026077.3, AC022258.3, AC021240.3, AC023451.2, AC013609.2, AC014418.1, AC007118.1, AC003115.1, AC003118.1, AL138846.3,

-141-

SEQ ID NO.274

NGO-St-127

YS345/T7 3'

- 5 NM_014753.1, D80009.1, AE003451.1, AC011294.3, Z85996.1, AC007244.2, AJ271079.1, M22462.1, AE003815.1, AE003418.1, AC004963.2, AF153352.1, AC007068.17, AE001389.1, Z78067.1, AL132792.2, AP000419.1, L15320.1, AC007042.2, AC006544.19, AF135026.1, AC027657.1, AE003557.1, AE003528.1, AC003060.1, AF228703.1, U91325.1, AC004832.3, AC008078.11, AC007368.11, AF134488.1, AC007461.8, AC004950.2, AC002082.1, AC005033.1, AC003065.1, AC005548.1, U21933.1, AF010237.1, AC004167.1, AC004104.1, AC002324.1, AE001032.1, AL050342.42, Z98949.1, Z77662.1, Z50015.1, AL022315.1, AL121723.36, AL031767.13, AL157498.1, AL137325.1, U31447.1, 10 AL023800.1, L19655.1, AB040962.1, AP000475.3, M73822.1, AP001111.1, AP000023.1, AB028621.1, AB005049.1, AB029018.1, AC006481.3, AF050157.1, AL121656.2, AL022310.1, AB016885.1, AW237092.1, AW237137.1, AI935281.1, AI628080.1, AW467637.1, AI650475.1, AI963620.1, AI338027.1, AA927690.1, AA604575.1, AI281023.1, AI590556.1, AA203521.1, AI609068.1, AI689223.1, AW058425.1, AA483799.1, AW473973.1, AA766731.1, AA278635.1, AW083923.1, AA915891.1, AI984984.1, AI281118.1, AI131367.1, AI537394.1, AI278563.1, AA159506.1, 15 AI304815.1, AW803966.1, AI033401.1, AI049943.1, AW004875.1, AA047286.1, T87897.1, AW029023.1, AA480172.1, AI285145.1, AA252803.1, AA261816.1, AI867812.1, AA554061.1, AI753409.1, W81534.1, AI015310.1, AA099000.1, AI184520.1, R00576.1, T87990.1, AI824434.1, AA047147.1, R33795.1, AA864952.1, T79535.1, AI149983.1, AI810930.1, AI866914.1, AW263579.1, T97738.1, W81533.1, R00680.1, AL047806.1, AI802574.1, AI651401.1, AW004034.1, H62063.1, AI376279.1, AW194865.1, AW796065.1, AW428271.1, AA278634.1, AW205363.1, AA223495.1, H61156.1, 20 AA421215.1, AA411512.1, AA405999.1, AA293345.1, T97844.1, AW175987.1, AI005967.1, AA793158.1, AA623849.1, AA914529.1, AA571438.1, AI406390.1, AA421216.1, AA411513.1, AA399425.1, AA455122.1, AA402812.1, AA402916.1, AA402630.1, AW910545.1, AW469155.1, AW469154.1, AW469148.1, AW523356.1, AW175972.1, AW522183.1, AL022344.1, AL023808.2, AC036220.3, AC023099.2, AC022264.2, AC011753.3, AC023723.2, AC014984.1, AC009785.4, AC011191.3, AC013532.2, AC025638.3, AC010033.7, AC068739.2, AC008481.6, 25 AC027517.2, AC036185.1, AC015925.3, AC015724.4, AC019168.3, AC017420.1, AC020219.1, AC013378.3, AC007107.1, AC025011.2, AC022061.3, AC012431.6, AC015990.5, AC058333.2, AC036174.2, AC020904.5, AC011543.3, AC011491.4, AC026658.2, AC021111.3, AC022297.7, AC012664.3, AC017059.2, AF215848.1, AC011098.1, AL158846.3, AL139404.2, AL139110.2, AL121828.8, AL161618.5, AL157699.2, AP001936.1, AP001005.1, AP000813.1, AC024232.2, AC008060.3, AC026077.3, AC021240.3, AC022518.2, AC023451.2, AC013609.2, 30 AC014418.1, AC006738.1, AC003118.1, AL138846.3, AL136371.2,

SEQ ID NO.275

NGO-St-128

YS1714/T3 5'

- 35 D83327.1, D83077.1, D84296.1, D84295.1, D84294.1, NM_009441.1, AB008516.1, AJ001866.1, AL163273.2, AP001728.1, AP001429.1, AP000150.1, D83253.1, AP000009.2, AP000151.1, AF099914.1, AL132992.2, AL132977.1, AC006017.2, AC010170.3, U67510.1, AL021684.1, X60399.1, D64005.1, AB018108.1, AC008865.3, AE003786.1, AE003627.1, AE003085.1, AF198444.1, AC006367.3, AC005666.1, AC004053.1, Z82058.1, Z82278.1, Z19156.1, AL034408.2, AL049643.12, X69058.1, AB030387.1, X16640.1, AW510696.1, AW130658.1, AI955031.1, AI365371.1, 40 AW272845.1, AI655615.1, AI651380.1, N75792.1, N22573.1, R49365.1, T65109.1, AA733976.1, AL044710.1, AA968229.1, AI834826.1, AI956999.1, AI935572.1, AA226473.1, F11111.1, AI462554.1, AV373371.1, AV349801.1, AV348118.1, AA226308.1, BB006439.1, AV172670.1, AV348357.1, AA387528.1, AA822624.1, N45260.1, AV331075.1, AI580340.1, H83303.1, AA612013.1, AA054190.1, AI508671.1, AW691731.1, AW690698.1, AW637870.1, AW446918.1, AI662108.1, AI528491.1, AU033435.1, N50729.1, AC020718.3, AC009801.3, AC026848.2, AF206725.1, AC025470.3, 45 AC026616.2, AC011632.3, AL161426.3, AC068145.2, AC009685.3, AC024156.2, AC021196.3, AC011260.4, AC015861.5, AC021000.3, AC007728.1, AC021983.1, AP001378.1, AC025412.3, AC068288.2, AC008905.5, AC026474.3, AC009131.4, AC034282.2, AC067842.1, AC015971.3, AC011726.3, AC009671.3, AC024525.2, AC019359.3, AC025009.2, AC013450.4, AC009746.10, AC018485.6, AC016129.10, AC010667.9, AC023015.2, AC020798.2, AC025338.1, AC020183.1, AC012419.2, AL356317.1, AL133326.8, AL355392.2, AL356017.1, 50 AL161745.5, AL162505.3, AL133241.3, AL117187.2, AL117331.1, AL031011.20, Z98859.1,

SEQ ID NO. 276

NGO-St-128

YS1714/T7 3'

- 55 D83077.1, D84296.1, D84295.1, D84294.1, D83327.1, AL163273.2, AP001728.1, AP001429.1, AP000151.1, D83253.1, AP000009.2, NM_009441.1, AB008516.1, AC007023.3, AL022395.2, AF037454.1, NM_008395.1, AC010283.5, AC007198.6, AC020717.3, AC005310.2, AC007955.4, AF090190.1, AC005008.2, AC005034.1, AF131865.1, AF064058.1, AF032967.1, U42213.1, AC005571.1, AC005224.1, AC005304.1, AL049832.2, L28005.1, AB017653.1, AP000463.1, AB025607.1, AB023656.1, AB011163.1, AI336910.1, AI337091.1, AW665117.1, AI885338.1, AL042620.1, 60 AA722789.1, AA743347.1, AA887657.1, AI678227.1, AI18428.1, AW772752.1, AA515769.1, AW341881.1, AA554904.1, AA112857.1, AA083921.1, AW803145.1, AI568131.1, AW237011.1, AI657054.1, AI653679.1, AL040434.1, AW612699.1, AA470557.1, AA662541.1, AA470510.1, AA502576.1, AA852823.1, AW629888.1, R13859.1, AL039361.2, AA021274.1, AW352731.1, AA722688.1, AI003122.1, AW488299.1, AA669782.1, H31610.1, AW525528.1, AA997915.1, AW743421.1, AI646427.1, AI145984.1, W50656.1, AW108450.1, AA794421.1, AI019132.1, H06584.1,

- AI666638.1, AA270792.1, AA417656.1, AW296426.1, AI838089.1, AW466371.1, AA308558.1, AI839685.1, AA048256.1, AV170771.1, AV136593.1, AI846084.1, Z42452.1, AI412296.1, AV278830.1, AV319373.1, AV332268.1, AV327734.1, AV259825.1, AV157173.1, AV378262.1, AV341338.1, AW245310.1, AW822071.1, AV326279.1, AA155001.1, AI812831.1, AA543759.1, AW923586.1, AW921274.1, AW908406.1, AW760328.1, AW349130.1, AW310768.1, AW258283.1, AW202374.1, AI957871.1, AI931902.1, AI790763.1, AA940042.1, AA839623.1, AA758570.1, AA739484.1, AA739481.1, AA387131.1, AA110637.1, AC012032.1, AL139409.3, AL356276.1, AC019259.3, AC025596.1, AC021573.4, AC068169.1, AL161450.4, AC026096.2, AC021484.3, AC012528.2, AC024127.1, AC019061.3, AL139134.4, AL355876.2, AC025076.3, AC037466.3, AC046139.4, AC012506.4, AC025541.4, AC051657.2, AC010256.3, AC018539.4, AC026993.2, AC009654.3, AC025060.3, AC026080.2, AC023271.3, AC019312.3, AC026058.2, AC021552.2, AC012571.3, AC025075.2, AC011170.3, AC009699.6, AC021042.3, AC026842.1, AC021914.3, AC013779.3, AC021694.2, AC008418.1, AC023168.6, AC023000.2, AC013266.3, AC011239.2, AC007373.1, AL136124.8, AL356216.1, AL356055.1, AL137126.4, AL162375.4, AL161640.6, AL160234.1, AP001541.1, AP000945.2, AP000940.2, AP000914.2, AP000614.3,
- 15 SEQ ID NO.277
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YS223/T3 5'
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- 30 SEQ ID NO.278
NGO-St-128
YS223/T7 3'
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- 55 SEQ ID NO.279
NGO-St-128
YS394/T7 3'
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- 60

- 5 AF015413.1, U21135.1, Z81117.1, L21456.1, L21357.1, L21465.1, L21461.1, L21458.1, L21452.1, L21448.1, L21446.1, L21444.1, L21439.1, L21429.1, L21425.1, L21424.1, L21371.1, L21364.1, L21360.1, L21354.1, L21351.1, L214161.1, L21340.1, L21330.1, L21329.1, L21327.1, AF224041.1, AC007955.4, AC005008.2, AF064058.1, AF032967.1, AF014360.1, AF014357.1, AF014343.1, AF014290.1, AF014286.1, U31582.1, AC005224.1, AC005304.1, AF020713.1, AF043433.1, AL022147.3, U79857.1, AL049832.2, AL132975.1, AL132870.2, U53784.1, L28005.1, Z70723.1, D84371.1, AI336910.1, AI337091.1, AW665117.1, AI885338.1, AL042620.1, AA722789.1, AA743347.1, AA887657.1, AI318428.1, AI678227.1, AW772752.1, AA515769.1, AW341881.1, AA554904.1, AA112857.1, AA083921.1, AW803145.1, AI568131.1, AW237011.1, AI657054.1, AI653679.1, AW612699.1, AL040434.1, AA662541.1, AA470557.1, AA470510.1, AA502576.1, AA852823.1, AW629888.1, R13859.1, AA021274.1, AL039361.2, AW352731.1, AA722688.1, 10 AW488299.1, AA669782.1, H31610.1, AI003122.1, AW525528.1, AA997915.1, AW743421.1, AI646427.1, AI145984.1, W50656.1, AW108450.1, AA794421.1, AI019132.1, H06584.1, AI666638.1, AA270792.1, AW466371.1, AW296426.1, AA417656.1, AI838089.1, AA308558.1, AI839685.1, AA048256.1, AV170771.1, AV136593.1, AI846084.1, Z42452.1, AV278830.1, AI412296.1, AV319373.1, AV332268.1, AV327734.1, AV259825.1, AV157173.1, AV378262.1, AV341338.1, AW245310.1, AW822071.1, AV326279.1, AW425970.1, AA155001.1, AI812831.1, AI968847.1, 15 AI889183.1, AV142455.1, AW923586.1, AW908406.1, AW760328.1, AW349130.1, AW310768.1, AW202374.1, AI957871.1, AI931902.1, AI790763.1, AA940042.1, AA839623.1, AA739484.1, AA739481.1, AA110637.1, AC012032.11, AC012528.2, AL139409.3, AL356276.1, AL139134.4, AL355876.2, AC019259.3, AC025596.1, AC035146.2, AC025777.3, AC008784.5, AC021573.4, AC068169.1, AC023488.5, AL161450.4, AC069119.1, AC026469.3, AC021484.3, AC011853.3, AL354715.2, AC037466.3, AC024462.3, AC046167.2, AC046139.4, 20 AC026328.3, AC026307.7, AC023236.8, AC051657.2, AC026709.2, AC026426.2, AC026418.2, AC025289.2, AC018539.4, AC040967.1, AC023271.3, AC019312.3, AC026058.2, AC012571.3, AC025075.2, AC011170.3, AC026842.1, AC021178.3, AC021914.3, AC021694.2, AC008801.1, AC008418.1, AC023388.2, AC021185.2, AC023502.3, AC013266.3, AC007373.1, AC002419.1, AL136124.8, AL161640.6, AL162251.3, AL353637.1, AP001887.1, AP001362.1, AP000940.2, AP000925.2,

25
SEQ ID NO.280
NGO-St-129
YS1639/T3 5'

- 30 NM_004999.1, AB002387.1, U90236.1, Z35331.1, NM_008662.1, U49739.1, AF017303.1, AL096862.18, AF146793.2, AE003650.1, AE003436.1, AE003415.1, AL161595.2, AL078620.2, AL023494.12, AL096821.2, NC_001146.1, AC020912.4, AE003764.1, AC002524.1, AF221108.1, NM_012415.1, AF112481.1, AF118397.1, AC006236.1, AF084206.1, AL009050.9, AL032632.1, AL109759.3, AJ251914.1, X13464.1, X03975.1, Z71468.1, M14045.1, D37977.1, AW629832.1, AA129385.1, AA028987.1, AA577227.1, AW300529.1, AW316711.1, AI863551.1, AI829419.1, AI366126.1, AI310303.1, AA910369.1, AA523580.1, AA522566.1, AI698448.1, AW235712.1, AA889126.1, 35 AW741450.1, AW663829.1, AI747845.1, AW660315.1, AI093634.1, AA790620.1, AW696022.1, AW601223.1, AI413054.1, AA037700.1, AW831515.1, AJ392575.1, AI820852.1, AI820850.1, AI792698.1, AI792696.1, AI666405.1, AI252501.1, AI252429.1, AA880900.1, AA696342.1, C80997.1, C70576.1, AA542732.1, AL136093.4, AC016868.4, AC021058.7, AC036192.2, AC007365.2, AC061984.2, AC018880.2, AC021861.3, AC018545.4, AC062006.2, AC011374.4, AC011406.2, AC009544.4, AC026565.2, AC016859.2, AC017680.1, AC014098.1, AC007515.1, 40 AL096873.2, AP001924.1, AP001384.1, AP001359.1, AP001163.1, AP000674.1, AP000666.1, AC069305.1, AC024019.3, AC022898.4, AC024035.3, AC009511.12, AC027644.4, AC007780.2, AC020897.5, AC067776.1, AC058782.1, AC018508.4, AC019309.3, AC025687.2, AC020989.5, AC013547.2, AC021008.1, AC020767.1, AC018878.1, AC013527.2, AC015353.1, AC012474.1, AL355972.3, AL139002.4, AL121828.8, AL139814.5, AL355312.3, AL354743.1, AL162852.3, AP001167.1, AP000942.2,

45
SEQ ID NO.281
NGO-St-129
YS1639/T7 3'

- 50 NM_004999.1, AB002387.1, AC000117.1, AC006050.1, AE001131.1, AC005494.1, AC003068.1, AL161585.2, AL035521.1, AL163227.2, AC000374.1, Z98748.1, AP001115.1, AC005529.7, AC005617.2, AF172282.1, AC000025.2, AC004539.1, AC003080.1, AF058919.2, AC008261.3, AC004682.1, AE001579.1, AC005527.3, AC002991.1, AC003682.1, L06196.1, AF036692.1, AL161545.2, AL161472.2, Z99281.1, Z97342.2, AL022393.1, AL035661.16, AL109837.21, Z35331.1, AW772270.1, AI971254.1, AW242758.1, AW772647.1, AW168128.1, AA129322.1, AW450254.1, AI208776.1, AW613386.1, AW172995.1, AW513273.1, AW073777.1, AI921929.1, AW452837.1, 55 AW450587.1, AI911506.1, AA625890.1, AI925526.1, AI991532.1, AW473956.1, AA166906.1, AI318048.1, AW448948.1, AI304536.1, AW451044.1, AW451217.1, AA429372.1, AI061190.1, N63006.1, AW614329.1, N39073.1, AI357971.1, AW449081.1, N49974.1, H15162.1, AA493764.1, AA632762.1, AA503650.1, AW072577.1, H88721.1, H88672.1, N62772.1, R37296.1, AA365146.1, AA492569.1, W01757.1, D62451.1, AA482738.1, N52751.1, AI373764.1, AA235474.1, AI631867.1, AI740513.1, AA330423.1, AW169179.1, AW195663.1, AI537958.1, AI767492.1, AI654090.1, AA620412.1, AA861190.1, AI659277.1, AA025688.1, AI375865.1, AI928490.1, AI651240.1, AA846667.1, AA161244.1, AI36973.1, AA114997.1, AW594496.1, AW573252.1, AV305797.1, AW149932.1, AV221167.1, AW085043.1, AW048157.1, AI871868.1, AI870057.1, AI859823.1, AI689778.1, AI678876.1, AI678873.1, AI669925.1, AV024912.1, AI550341.1, AI537625.1, AI350956.1, AI278232.1, AI187925.1, AI160733.1, AA822328.1, AA742262.1, AA422443.1, AA217420.1, AL136093.4, AC068777.3, AC063951.3, AC026784.2, AC024037.2, AL021152.1, AC055882.3,

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5 SEQ ID NO.282

NGO-St-129

YS1772/T3 5'

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20 SEQ ID NO. 283

NGO-St-129

YS1772/T7 3'

NM_004999.1, AB002387.1, AL161585.2, AL035521.1, AC018833.3, AL161536.2, AL049608.1, AL078604.10, U60176.1, AC005494.1, AC000374.1, Z98748.1, AC003080.1, AC007390.3, AC004069.1, AF036692.1, Z68227.1, AW772270.1, AI971254.1, AW772647.1, AW242758.1, AA129322.1, AW168128.1, AW450254.1, AI208776.1, AW613386.1, AW513273.1, AI921929.1, AW073777.1, AW172995.1, AW452837.1, AW450587.1, AI911506.1, AA625890.1, AI925526.1, AA166906.1, AI991532.1, AW473956.1, AW448948.1, AI304536.1, AI318048.1, AW451044.1, AW451217.1, N63006.1, AA429372.1, N39073.1, N49974.1, AI061190.1, H15162.1, AW614329.1, AW449081.1, AI357971.1, AA632762.1, AA493764.1, H88672.1, AA503650.1, H88721.1, R37296.1, AA365146.1, AW072577.1, N62772.1, W01757.1, AA492569.1, D62451.1, AA482738.1, AI373764.1, AA235474.1, NS2751.1, AI631867.1, AI740513.1, AA330423.1, AW169179.1, AW195663.1, AI537958.1, AI767492.1, AI654090.1, AA620412.1, AA861190.1, AI659277.1, AA822328.1, AI790656.1, AI528811.1, AA718487.1, AA070821.1, AI013854.1, AA025688.1, AI006104.1, AA087822.1, AI153153.1, AW573252.1, AW151175.1, AW085043.1, AW073863.1, AI700842.1, AI501875.1, AI187925.1, AI160733.1, AI026889.1, AA907037.1, AA120798.1, AL136093.4, AC020732.3, AL161450.4, AC068777.3, AC063951.3, AC022918.2, AL136990.14, AC024086.3, AC037486.2, AC025666.2, AC013411.2, AL354827.1, AP001448.1, AC021173.3, AC026702.3, AC009095.5, AC015707.3, AC026526.2, AC024476.2, AC013727.3,

40 SEQ ID NO. 284

NGO-St-129

YS1781/T7 3'

NM_004999.1, AB002387.1, AL161585.2, AL035521.1, AC018833.3, AL049608.1, AL078604.10, AF077341.1, AF132734.1, AC006050.1, AE001131.1, U60176.1, AC005494.1, AC003068.1, AC000374.1, Z72521.1, Z98748.1, AP001115.1, AC005617.2, AC003080.1, AC004069.1, AF036692.1, Z68227.1, AI971254.1, AW772270.1, AW242758.1, AW772647.1, AA129322.1, AW168128.1, AW450254.1, AI208776.1, AW613386.1, AW513273.1, AI921929.1, AW073777.1, AW172995.1, AW452837.1, AW450587.1, AI911506.1, AA625890.1, AI925526.1, AA166906.1, AI991532.1, AW473956.1, AW448948.1, AI304536.1, AI318048.1, AW451044.1, AW451217.1, N63006.1, AA429372.1, N39073.1, N49974.1, AI061190.1, H15162.1, AW614329.1, AW449081.1, AI357971.1, AA632762.1, AA493764.1, H88672.1, AA503650.1, H88721.1, W01757.1, R37296.1, AA365146.1, AW072577.1, N62772.1, AA492569.1, D62451.1, AA482738.1, AI373764.1, NS2751.1, AA235474.1, AI631867.1, AI740513.1, AA330423.1, AW169179.1, AW195663.1, AI537958.1, AI767492.1, AI654090.1, AA620412.1, AA861190.1, AI659277.1, AA822328.1, AI790656.1, AI528811.1, AA718487.1, AA070821.1, AI013854.1, AA025688.1, AI375865.1, AI181759.1, AI006104.1, AA087822.1, AI153153.1, AI501875.1, AL136093.4, AC020732.3, AC022938.3, AC068777.3, AC063951.3, AC026784.2, AC018914.3, AC022918.2, AL136990.14, AL356054.2, AL354827.1, AC013401.2, AC026702.3, AC015707.3, AC024673.2, AC026526.2, AC024476.2, AC013727.3, AL109660.3,

55 SEQ ID NO. 285

NGO-St-130

YS111/T3 5'

NM_001981.1, U07707.1, Z29064.1, NM_007943.1, L21768.1, L14298.1, AC008269.3, AF229843.1, AC004527.2, AC006557.2, AL162295.1, AL163259.2, AL163205.2, AP001714.1, AP001660.1, AP001634.1, AP000180.1, AP000272.1, AP000104.1, AC005824.2, AE003551.1, AF173983.1, AC002449.1, AF091848.1, AF067807.1, U24215.1, AL133376.6, AL033521.2, X56494.1, D21071.1, AL041882.1, C17654.1, AW368006.1, AA140007.1, AI557588.1, AA349569.1, AA839181.1, AW891551.1, AU079083.1, AV105710.1, AV041867.2, AV011556.1, AV010206.1, AV441258.1, AW562154.1, AW288397.1, AW221715.1, AV383554.1, AL043683.1, AL043682.1, AI774525.1, AI486675.1,

- AA907496.1, AA728511.1, AA570698.1, AA041001.1, R65462.1, Z34628.1, AC048367.2, AL138904.2, AL354990.1, AC068561.1, AC065048.1, AC062150.1, AC058723.1, AC035761.1, AC024413.3, AC012403.5, AC016964.5, AC022169.2, AC024287.3, AC027418.2, AC016498.4, AC024433.2, AL356266.3, AL157813.3, AL354698.2, AP001004.2, AP001130.1, AC009179.15, AC009386.6, AC024905.7, AC023600.13, AC024523.2, AC025446.3, AC011537.6, AC036127.2, AC067715.1, AC066596.1, AC040168.1, AC020779.3, AC018827.4, AC009659.3, AC016890.4, AC022475.2, AC011266.3, AC022978.3, AC016853.4, AC007495.3, AC010043.4, AC018976.2, AC022048.1, AC020151.1, AL161660.6, AL133318.4, AL137779.1, AP000895.2, AP001578.1,
- 5
- SEQ ID NO.286
- 10 NGO-St-130
YS111/T7 3'
NM_001981.1, AF052132.1, Z29064.1, U07707.1, AF119858.1, AC007504.3, AF235098.1, AF191069.1, AC003092.1, AF096876.1, AL163252.2, AL115814.1, AP001707.1, AC007376.8, AL021811.1, Z69729.1, AC002113.1, AL031767.13, M22886.1, AC010143.3, AC010971.3, AF002223.1, AF063866.1, AC003665.1, AC005808.1, AL035079.14, AL163232.2, X71844.1, AP001687.1, AP000459.3, AL043535.1, AA781358.1, AI692447.1, N32153.1, AI453034.1, AI813894.1, AI115267.1, AI288222.1, N25318.1, AA534309.1, AA115291.1, AI718641.1, AI978915.1, AI208237.1, AI169456.1, AI275885.1, AW769406.1, AI693511.1, AA886343.1, AA150461.1, N49086.1, AA825660.1, AW075886.1, AA813360.1, AW614630.1, AI520942.1, AA534862.1, Z44586.1, AA164418.1, AA702296.1, AA485200.1, N66885.1, AI920898.1, AW087764.1, N78949.1, R68155.1, N25787.1, AW813048.1, R62156.1, T10010.1, AA478744.1, AI810955.1, F10989.1, AA748186.1, T28758.1, H13536.1, AA644498.1, AW769677.1, AI472645.1, AA385221.1, AI472603.1, AW188171.1, WI7317.1, H13535.1, AA585349.1, R59914.1, AA300847.1, AA251517.1, F03176.1, AW050401.1, AA485087.1, AI267611.1, AW366454.1, T25018.1, D19928.1, Z46052.1, AA251530.1, R63487.1, X85627.1, AI060900.1, AA833154.1, AI119303.1, AV361642.1, C80702.1, AV251200.1, AW053510.1, AA630896.1, W02559.1, N48143.1, N38997.1, AW804902.1, AW776207.1, AW775801.1, AW362615.1, AV368479.1, AI452571.1, AI309292.1, AA845594.1, AA505330.1, AA287832.1, AA287578.1, D48726.1, AC048367.2, AC055751.2, AC020941.3, AC017093.2, AC025170.3, AC008488.6, AC019332.3, AC026475.3, AC068066.1, AC015876.3, AC011112.3, AC018392.3, AL354712.2, AL354760.1, AC048389.3, AC068130.2, AC024164.2, AC004898.2, AC027226.2, AC058798.1, AC011152.4, AC010104.2, AL139125.3, AL133282.13, AL035554.1, AP001590.1,
- 20
- 25
- 30 SEQ ID NO.287
NGO-St-130
YS383/T3 5'
NM_001981.1, U07707.1, Z29064.1, NM_007943.1, L21768.1, NM_002396.1, Z95117.1, AP002054.1, U00021.1, M55905.1, AE003677.1, NM_007944.1, AC004862.1, AF111169.2, AC007543.4, AF131768.1, AC005758.1, AC004476.1, Z35601.1, AL133299.2, AL096802.11, U29156.1, AB027020.1, AI936583.1, AA837424.1, AW340591.1, AA832056.1, AI663323.1, AA642291.1, AL043493.1, AI151900.1, AA637559.1, AA877097.1, AA140007.1, AI584949.1, AW503469.1, AI979367.1, AW372581.1, AU051615.1, AA625121.1, AA490194.1, AA442710.1, AA229914.1, AA229604.1, T70290.1, AW765795.1, AV406101.1, AW186947.1, AI324049.1, C44114.1, R54352.1, R52338.1, F06891.1, F05583.1, T34448.1, Z43889.1, AL138904.2, AL354990.1, AC026989.2, AC026390.1, AC022373.1, AL157785.3, AL162716.4, AL355332.1, AC040919.1, AC046143.3, AC009078.4, AC021477.3, AL136170.3, AL139022.1, AP001845.1, AC037471.3, AC024404.3, AC046166.2, AC012212.4, AC067723.2, AC024891.8, AC025243.3, AC005883.9, AC068054.2, AC068389.1, AC026821.2, AC021585.3, AC023102.2, AC025339.1, AC016044.4, AC008094.4, AC021901.2, AC021342.2, AC022837.1, AC020679.2, AC014595.1, AL136121.5, AL356133.2, AL355176.1, AP001542.1, AL008872.1,
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- 45
- SEQ ID NO.288
NGO-St-130
YS383/T7 3'
NM_001981.1, AF052132.1, Z29064.1, U07707.1, AF119858.1, AC007504.3, AF235098.1, AF191069.1, AC003092.1, AF096876.1, AL163252.2, AL115814.1, AP001707.1, AC007376.8, AL021811.1, Z69729.1, AC002113.1, AL031767.13, M22886.1, AC010143.3, AC010971.3, AC002479.1, AF002223.1, AF063866.1, AC003665.1, AC005808.1, AL035079.14, AL163232.2, AL035458.35, X71844.1, AP001687.1, AP000459.3, AL043535.1, AA781358.1, AI692447.1, N32153.1, AI453034.1, AI813894.1, AI115267.1, AI288222.1, N25318.1, AA534309.1, AA115291.1, AI718641.1, AI978915.1, AI208237.1, AI169456.1, AI275885.1, AW769406.1, AI693511.1, AA886343.1, AA150461.1, N49086.1, AA825660.1, AW075886.1, AA813360.1, AW614630.1, AI520942.1, AA534862.1, Z44586.1, AA164418.1, AA702296.1, AI920898.1, AA485200.1, N66885.1, AW087764.1, N78949.1, R68155.1, N25787.1, R62156.1, T10010.1, AA478744.1, AI810955.1, F10989.1, AA748186.1, T28758.1, H13536.1, AA644498.1, AW769677.1, AI472645.1, AA385221.1, AI472603.1, R59914.1, AA585349.1, AA300847.1, AA251517.1, AA485087.1, AW050401.1, F03176.1, AI267611.1, AW188171.1, WI7317.1, H13535.1, AW813048.1, AW366454.1, T25018.1, D19928.1, AA251530.1, X85627.1, AI060900.1, AA833154.1, AI119303.1, AV361642.1, C80702.1, AV251200.1, AW053510.1, AA630896.1, W02559.1, N48143.1, N38997.1, AW776207.1, AW775801.1, AW362615.1, AV368479.1, AW154919.1, AI868315.1, AI452571.1, AI401460.1, AA845594.1, AA505330.1, AA287832.1, AA287578.1, AC048367.2, AC020941.3, AC017093.2, AC025170.3, AC008488.6, AC008948.5, AC019332.3, AC026475.3, AC015876.3, AC011112.3, AC018392.3, AL354712.2, AL354760.1, AC068130.2, AC024164.2, AC004898.2, AC027226.2, AC011152.4, AC010104.2,
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-146-

AL139125.3, AL133282.13, AP000793.1,

SEQ ID NO.289

NGO-St-131

5 YS161/T3 5'

AB002318.1, NM_011602.1, X56123.1, AF177198.1, NM_006289.1, AF078828.1, AB028950.1, AF178534.1, AC009044.3, AE003535.1, AF224669.1, U41384.1, X59601.1, Z66108.1, Z66107.1, NM_016559.1, AC020610.6, AE003745.1, AC002044.1, NM_011027.1, AC005145.1, AC005544.1, U51243.1, AL080195.1, AL021918.1, AB032593.1, AB032592.1, Z57921.1, AJ009823.1, AI751285.1, AW900719.1, AA452483.1, AA387755.1, AW336094.1, W17774.1, AA474115.1, AA718262.1, AI593159.1, AA657201.1, AA615519.1, AI331130.1, R17242.1, AW437322.1, AW654277.1, AW336729.1, AA015516.1, AA013971.1, R54389.1, AW640826.1, AW403043.1, AL042809.1, AL047970.1, AI343291.1, D31413.1, T27372.1, T06850.1, AI691500.1, AW137249.1, AI980726.1, AI387487.1, AA748793.1, AA737559.1, AC026030.2, AC068233.1, AL133410.11, AC009122.5, AC011056.3, AC024491.4, AC009696.5, AC018797.3, AC026049.2, AC024629.1, AC015146.1, AP002018.1,

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SEQ ID NO.290

NGO-St-131

YS161/T7 3'

AB002318.1, AF085910.1, AL137080.2, NM_016761.1, AC005825.3, AF221104.1, AF221103.1, AF221102.1, AF110520.1, AC003958.1, AL031276.1, AL008627.1, D49544.1, AI823644.1, AW629480.1, AI751284.1, AA290619.1, AA290618.1, AW136798.1, AW195082.1, AI566119.1, AI866810.1, AI307663.1, AI417845.1, AW242353.1, AI479172.1, AI311003.1, AI522054.1, AI952372.1, R99633.1, AI249792.1, AI366767.1, AW469603.1, AA854194.1, AA582699.1, AI380822.1, AW303332.1, R99089.1, AW902895.1, AW136171.1, AW902834.1, AI985231.1, T16297.1, AI985222.1, T17377.1, AA291006.1, T32600.1, AA291005.1, AW902806.1, AI142264.1, W22495.1, T20064.1, AW898163.1, AW251506.1, AA998450.1, AI072764.1, AI851526.1, AI787438.1, AI465290.1, AA967834.1, AA718676.1, AA039087.1, AA511363.1, AV252009.1, AV272145.1, D80367.1, D80366.1, D80352.1, D80351.1, D80339.1, D80331.1, D80330.1, D80314.1, D80261.1, D80254.1, D80253.1, D80252.1, D80251.1, D59773.1, D59717.1, AI705776.1, AV175623.1, D80293.1, D59809.1, AV249990.1, AW488444.1, AW389528.1, AW218598.1, AI507221.1, C85503.1, AA709996.1, W83532.1, AC026030.2, AC016814.4, AC022910.2,

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SEQ ID NO.291

NGO-St-131

YS101/T3 5'

AB002318.1, NM_011602.1, X56123.1, AF177198.1, NM_006289.1, AF078828.1, AB028950.1, AF065739.1, AF178534.1, AC005145.1, AC009044.3, AF224669.1, U41384.1, X59601.1, Z66108.1, Z66107.1, NM_016559.1, AC020610.6, NM_011027.1, AC005544.1, U51243.1, AL080195.1, AL021918.1, AB032593.1, AB032592.1, Z57921.1, AJ009823.1, AI751285.1, AW900719.1, AA452483.1, AA387755.1, AW336094.1, W17774.1, AA474115.1, AA718262.1, AI593159.1, AA657201.1, AA615519.1, AI331130.1, AW437322.1, R17242.1, AW654277.1, AW336729.1, R54389.1, AW640826.1, AA015516.1, AA013971.1, T06850.1, AW403043.1, AL042809.1, AL047970.1, AI343291.1, D31413.1, T27372.1, AW137249.1, AI980726.1, AA748793.1, AA737559.1, AC026030.2, AC068233.1, AC009122.5, AL133410.11, AC024491.4, AC009696.5, AC018797.3, AC026049.2, AC024629.1, AP002018.1, AC026959.3, AC025148.3, AC007653.4, AC012337.3, AC009772.4, AC021650.9, AC011827.3, AC064839.3, AC010074.6, AC013614.4, AC013733.3, AC013405.1, AC021095.1, AC020569.1, AC008076.8, AL355819.2, AL117336.18, AP001007.1,

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SEQ ID NO.292

NGO-St-131

YS101/T7 3')

AB002318.1, AF085910.1, AF011399.1, AF011398.1, AL137080.2, NM_016761.1, AC005825.3, AF221104.1, AF221103.1, AF221102.1, AF110520.1, AC003958.1, AL031276.1, AL157416.1, AL138642.1, AL008627.1, D49544.1, AI823644.1, AW629480.1, AI751284.1, AA290619.1, AA290618.1, AW136798.1, AW195082.1, AI566119.1, AI866810.1, AI307663.1, AI417845.1, AW242353.1, AI479172.1, AI311003.1, AI522054.1, AI952372.1, R99633.1, AI249792.1, AI366767.1, AW469603.1, AA854194.1, AA582699.1, AW303332.1, R99089.1, AW136171.1, AI380822.1, AW902895.1, AW902834.1, AI985231.1, T16297.1, AI985222.1, T17377.1, AA291006.1, T32600.1, AA291005.1, AW902806.1, AI142264.1, AW898163.1, W22495.1, T20064.1, AW251506.1, AA998450.1, AI072764.1, AA718676.1, AI851526.1, AI787438.1, AI465290.1, AA967834.1, AA039087.1, AA511363.1, AV252009.1, AV272145.1, AI705776.1, D80367.1, D80366.1, D80352.1, D80351.1, D80339.1, D80331.1, D80330.1, D80314.1, D80261.1, D80254.1, D80253.1, D80252.1, D80251.1, D59773.1, D59717.1, D80293.1, D59809.1, AV175623.1, AV249990.1, AA370498.1, AW488444.1, AW389528.1, AW218598.1, AI507221.1, AA960722.1, AA960721.1, C85503.1, AA709996.1, W83532.1, L38220.1, AC026030.2, AC016814.4, AC022910.2,

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SEQ ID NO.293

NGO-St-132

YS011/T3 5'

NM_000346.1, AC007461.8, S74506.1, Z46629.1, AF029696.1, AF006571.1, U12533.1, AB012236.1, AB035888.1,

AB035887.1, AF106572.1, AB006448.1, D83256.1, NM_006941.1, AF006501.4, AL031587.3, AJ001183.1, AF191325.1, AF164104.1, AF226675.1, Z99757.12, AF047389.1, AF047043.1, AF017182.1, U66141.1, U66105.1, AJ001029.1, AE002049.1, AL135162.1, AW701461.1, AW323770.1, AW232285.1, AA220077.1, T18789.1, AW924151.1, AW747248.1, AW746893.1, AW746873.1, AW746213.1, AW681012.1, AW680640.1, AW677948.1, AW677800.1, 5 AW672276.1, AW672019.1, AW665912.1, AW471059.1, AW384568.1, AW384558.1, AW384516.1, AW384461.1, AW371943.1, AW286733.2, AW406345.1, AW321606.1, AW298118.1, AW290875.1, AW289095.1, AW245072.1, AW161855.1, AW161352.1, AW103014.1, AW007471.1, AI885013.1, AL035821.1, AI682325.1, AI539787.1, AI497991.1, AI410380.1, AI351117.1, AI350368.1, AI338712.1, AI335760.1, AI286186.1, AI266340.1, AI186949.1, AI167245.1, AI144319.1, AI134312.1, AI062232.1, AA973886.1, AA906673.1, AA904015.1, AA873306.1, AA836977.1, 10 AA688139.1, AA634800.1, AA630304.1, AA592961.1, AA472666.1, AA449553.1, AA449122.1, AA433810.1, AA314988.1, AA287892.1, AA243383.1, W57682.1, T49849.1, AC040983.1, AC009041.5, AC012004.3,

SEQ ID NO.294

NGO-St-132

15 YS1637/T3 5'

NM_000346.1, Z46629.1, AF029696.1, AB012236.1, U12533.1, AC007461.8, S74505.1, AF106572.1, AF265207.1, AF061784.1, NM_006941.1, AJ001183.1, S74504.1, AB035887.1, AF226675.1, AF006501.4, AL031587.3, S74506.1, U66141.1, AJ001029.1, AF047389.1, AF047043.1, AF017182.1, AF006571.1, Z18958.1, X79250.1, AF164104.1, AB035888.1, Z99757.12, AF152356.2, AJ245601.1, AB006448.1, AF191325.1, Z18957.1, Z18959.1, D83256.1, 20 U70441.1, NM_011441.1, D49474.1, D49473.1, L29085.1, NM_005986.1, AX001335.1, Y13436.1, NM_007084.1, AF107044.1, AB033888.1, X65664.1, U31967.1, NM_011443.1, NM_009233.1, NM_009234.1, AF009414.1, AX001334.1, AX001333.1, X96997.1, X94127.1, X94126.1, AB011802.1, L29086.1, NM_003107.1, NM_009236.1, L35032.1, X70683.1, AF116571.1, NM_009238.1, NM_005686.1, AF098915.1, X70298.1, Z31560.1, AB014474.1, L07335.1, S69429.1, NM_006942.1, AC007421.12, U12532.1, D50603.1, AB006867.1, AF193760.2, L12010.1, 25 AJ004858.1, M86315.1, AB026622.1, AE003776.1, AJ251580.1, AJ001730.1, NM_011446.1, NM_009237.1, U12467.1, X94125.1, AB023419.1, AB011803.1, M86335.1, X73038.1, AF001047.1, L12022.1, L12020.1, X65660.1, L12013.1, M86313.1, AI594348.1, AA616534.1, AL120408.1, AW321606.1, AW153579.1, AW184648.1, AV116901.1, AW343046.1, AV120409.1, AW231213.1, AW227743.1, AW210917.1, AWS13608.1, AW152310.1, AI935610.1, AI821650.1, AI758881.1, AI743736.1, AI743707.1, AI739667.1, AI732705.1, AI635063.1, AI073502.1, AA260278.1, 30 AI765094.1, AI087935.1, AW048216.1, AA434433.1, AA427400.1, AA405793.1, AW434258.1, AW045442.1, AI574719.1, AI137262.1, AI136910.1, AA799800.1, AA959594.1, AI009328.1, AA411418.1, AW533591.1, AW533022.1, AW532784.1, AW526351.1, AI716553.1, AI029515.1, AI029109.1, AA956282.1, AA956131.1, AA924900.1, AA924896.1, AA875101.1, AI145897.1, AI136894.1, AI112078.1, AI102567.1, AA943207.1, AW244680.1, AI828016.1, AI817673.1, AI240186.1, AW766057.1, AW615144.1, AW532037.1, AW414006.1, AW235281.1, AW131791.1, 35 AW131705.1, AW071909.1, AW055151.1, AW044044.1, AW028031.1, AW005368.1, AI990431.1, AI971611.1, AI631443.1, AI611652.1, AI571299.1, AI566261.1, AI480221.1, AI423139.1, AI421743.1, AI421119.1, AI418146.1, AI373018.1, AI364349.1, AI356682.1, AI327463.1, AI292258.1, AI199308.1, AI151028.1, AI146406.1, AI146367.1, AI137787.1, AI097136.1, AI096977.1, AI094794.1, AI056908.1, AI052267.1, AI717565.1, AA405899.1, AC009041.5, AC012004.3, AF215846.1, AL355803.2, AL137061.2, AL136179.11, AL117346.16, AC024914.17, AC020788.4, 40 AC015652.6, AC008220.4, AC007975.6, AC008318.6, AC012822.1, AC020509.1, AC055113.1, AL137016.10, AC024915.10, AC058787.7, AC024069.15, AC007588.3, AC017264.1, AL121747.21, AC068951.1, AC011649.3, AC026244.2, AC021051.3, AC027243.2, AC040983.1, AC027700.1, AL162584.3, AC022980.3, AC016156.7, AC068986.3, AC022499.5, AC026376.7, AC011544.5, AC008569.5, AC021881.2, AC022532.2, AC022917.3, AC023096.1, AC022606.2, AC005528.25, AC010665.4, AC010575.3, AC023011.1, AC010892.3, AC019870.1, 45 AC013906.1, AC014152.1, AC014782.1, AC009485.2, AL139246.4, AL034405.13, AL159992.3,

SEQ ID NO.295

NGO-St-132

50 YS1637/T7 3'

NM_000346.1, AC007461.8, S74506.1, Z46629.1, AF029696.1, AC007070.4, U61951.2, AB023041.1, AB006448.1, AC022521.4, AC007196.4, AC005169.2, AE003780.1, AC012392.1, AF162444.1, AC006240.1, AL161548.2, AL161502.2, NC_001142.1, AC004669.2, AC004411.2, AC002329.2, AC018363.6, AC008134.3, AC007259.4, AC005508.1, AC004562.1, AF058914.1, AC002539.1, AL163814.1, AL163812.1, AL161561.2, AL049655.2, AL049171.1, AL022023.1, AL021637.2, Z35596.1, AL078637.1, AL132960.2, AL132970.2, AL132965.1, AL049538.8, 55 U39674.1, AP001313.1, Z20656.1, AP000367.1, AP000371.1, AW005563.1, AA576678.1, AI934455.1, AI382146.1, AA527295.1, AI870355.1, AI380233.1, AI681309.1, AI299871.1, AA913619.1, AW087477.1, AA912521.1, AA778589.1, AI453423.1, AW360836.1, AA331097.1, H90100.1, AA469143.1, AA420856.1, AW075227.1, AA884178.1, AA420456.1, AA657762.1, AI348085.1, AA333065.1, AW888412.1, AW142661.1, AI985948.1, AA400739.1, AA955408.1, AI008321.1, AW213674.1, AI852411.1, AI548994.1, W24710.1, AW360293.1, AW323128.1, AV021074.1, AW897800.1, 60 AI599999.1, AV281945.1, AV220920.1, AV144700.1, AV008800.1, AV233902.1, AA469215.1, AV360627.1, AV165338.1, AV220098.1, BB004489.1, AV349732.1, AV302326.1, AW228243.1, AW360802.1, AI504553.1, AV280305.1, BB003834.1, AV305178.1, CI5879.1, AV163514.1, AW381053.1, AV305177.1, AV318841.1, AW829173.1, AV361282.1, AV248007.1, R30640.1, AW900425.1, AW892801.1, AW776398.1, AW697226.1, AW690623.1, AW586197.1, AW586064.1, AW559610.1, AW267726.1, AW218488.1, AU061986.1, AI164072.1,

-148-

AI162251.1, AA825782.1, AA411689.1, H63328.1, T48235.1, AV424751.1, AC013323.5, AC007194.1, AC025309.2, AC006755.1, AC024521.3, AC013645.3, AC011065.4, AC024527.3, AC010190.7, AC024104.4, AC011491.4, AC026623.2, AC021142.4, AC034285.1, AC025724.1, AC015854.3, AC021507.2, AC008258.3, AL078597.4, AL163642.1, AL021576.1,

5

SEQ ID NO.296

NGO-St-133

YS102/T3 5'

- 10 NM_014820.1, AB018262.1, Z19158.1, AP000007.1, AF102137.1, Z80789.1, AB030817.1, L14331.1, AC006840.17, AC004606.1, AL031012.1, AP001425.1, AB025414.1, AC016752.2, AE003801.1, AE003726.1, AE003616.1, AE003485.1, AE003420.1, AF127577.2, AC015450.3, AC008040.7, AC006596.2, AC006050.1, AL035331.1, AL078611.1, AL163243.2, Z71182.1, AP001698.1, Z79997.1, AP000208.1, AP000247.1, AP000130.1, AW468485.1, W76094.1, AA449405.1, AW230655.1, AA313460.1, AI325788.1, AI892481.1, AA116789.1, AA076346.1, AA373986.1, AV145606.1, AW227769.1, AW320879.1, AI535287.1, Z19251.1, AW765531.1, AW281101.1, AA985348.1, 15 AW656932.1, AW481973.1, AW410280.1, AW356980.1, AW336895.1, AW200321.1, AW050865.1, AI834977.1, AL048825.1, AI646136.1, AI478830.1, AA345311.1, AA278482.1, AA203592.1, R10075.1, T99341.1, T81329.1, AC015462.5, AC023782.2, AC025607.3, AC018351.8, AC068119.1, AC026858.2, AC016229.3, AC012437.3, AL138879.3, AP001901.1, AC036213.3, AC010464.4, AC026644.2, AC011615.3, AC008293.1, AL354734.3, AL353707.1, AL162311.1, AL157757.1, AC012413.4, AC023891.7, AC026770.3, AC011960.3, AC027067.2, 20 AC015595.3, AC017094.5, AC007521.11, AC015996.2, AC012972.1, AL157905.3, AL354800.3,

SEQ ID NO.297

NGO-St-133

YS102/T7 3'

- 25 NM_014820.1, AB018262.1, AF010516.1, AC005406.2, Z70268.1, AC009044.3, AE003547.1, NM_006021.1, Z74035.1, X95549.1, AL022722.1, AL109925.11, AJ243368.2, Z70688.1, Y15228.1, AP000382.1, AE003736.1, AL049612.11, AI769448.1, AI581514.1, AW471382.1, AI671783.1, AW044465.1, AI795924.1, AW009918.1, AW167186.1, AI278004.1, N49863.1, AW083882.1, AI283007.1, AI833063.1, AI478170.1, AI078346.1, AA707693.1, AI770160.1, AI126207.1, AW513624.1, N59383.1, H11342.1, AI679546.1, D60203.1, AW102995.1, AA047406.1, N67748.1, AI373915.1, 30 AA937689.1, AA535637.1, AW770695.1, AA088722.1, AI278065.1, AW470297.1, AI984753.1, AI281086.1, AI088753.1, N50512.1, N78439.1, AI089934.1, N50443.1, R75994.1, AI418032.1, AW069428.1, H28047.1, AA722233.1, AA934810.1, AW194761.1, AI679985.1, N70890.1, R82859.1, AW576214.1, R82647.1, R60689.1, AI383079.1, AW603760.1, R40078.1, H92752.1, H39632.1, AW388643.1, R44445.1, AA320578.1, R92461.1, AW118280.1, D55592.1, AA857398.1, AA579529.1, R82696.1, D52213.1, AA152134.1, C14917.1, N47394.1, AA369996.1, N47395.1, AA150127.1, 35 AI863820.1, AL079976.2, AA047526.1, AW545304.1, AW213944.1, AI844034.1, AI225307.1, AA175289.1, AW741826.1, AW324264.1, AW228128.1, AI849427.1, AI265537.1, AA175781.1, AI600081.1, AI111343.1, AV331675.1, AW254554.1, AW253791.1, AI714131.1, AI029154.1, AI171980.1, AV115523.1, AV340409.1, AV227184.1, AW914053.1, AC015462.5, AC023782.2, AC044821.2, AC013713.4, AC021761.3, AC021241.3, AL355341.3, AL157875.4, AL049756.16, AC025190.4, AC016797.4, AC024935.8, AC008595.4, AC025060.3, 40 AC023784.3, AC010907.3, AC022253.2, AC017109.2, AC018889.1, AL355378.1, AL118557.1,

SEQ ID NO.298

NGO-St-133

YS1783/T3 5'

- 45 NM_014820.1, AB018262.1, Z19158.1, AP000007.1, AF102137.1, AE001690.1, Z80789.1, AB030817.1, AB025414.1, AE003713.1, AC004606.1, AL009175.1, AL139077.2, AL031012.1, AC007359.2, AC016752.2, AC003040.2, AF248484.1, AE003801.1, AE003616.1, AC007505.4, AE002280.1, AF127577.2, AF208226.1, AC007682.2, AC008175.2, AC015450.3, AC006481.3, AC012394.3, AC008040.7, AF166527.1, AC006463.3, AC006949.8, AC006578.5, AC006596.2, U00670.1, AC004293.1, AC005261.1, AC004473.1, AE001065.1, AL035536.1, Z82266.1, Z78065.1, 50 AL078611.1, AL163255.2, AL163243.2, AL163207.2, S38096.1, AL138657.1, AL132957.1, AL021069.1, Z71182.1, U07798.1, AP001710.1, AP001698.1, AP001601.1, Z79997.1, AP000208.1, AP000247.1, X71802.1, AP000130.1, M95516.1, AW468485.1, W76094.1, AA449405.1, AW230655.1, AA313460.1, AI325788.1, AI892481.1, AA076346.1, AA116789.1, AA373986.1, AV145606.1, AW227769.1, AW320879.1, AI535287.1, Z19251.1, AA155457.1, AW765531.1, AW281101.1, AI430671.1, AA985348.1, W33868.1, AW656932.1, AW481973.1, AW410280.1, AW356980.1, 55 AW336895.1, AW200321.1, AW050865.1, AL048825.1, AI478830.1, AA345311.1, AA278482.1, AA203592.1, W44281.1, R10075.1, T99341.1, T81329.1,

SEQ ID NO.299

NGO-St-134 combined;

- 60 NM_003611.1, Y16355.1, Y15164.1, AC003037.1, AC010682.2, AC006991.2, AC016707.2, AC008175.2, AC007379.2, AC009947.2, AF121351.1, AE003417.1, AC005039.1, AF117269.1, AF077408.1, U09819.1, AL161498.2, AF016655.1, AL050231.2, Z99121.1, X71360.1, AP002039.1, NC_001144.1, AC009411.2, AC010498.4, AF140536.1, AE003805.1, AE003690.1, AE003542.1, NM_002062.1, AC009514.2, AC006026.2, AC006065.3, AC005839.1, U44051.1, U85195.1, U01156.1, AC004289.1, AC005179.1, AC004475.1, U22383.1, AE000658.1, AL163244.2, AB016214.1, U51234.1,

- AL136501.2, AL035690.10, AL008732.1, AL021367.1, U62778.1, U10037.1, U01157.1, AP001699.1, AP001604.1, M24635.1, X75598.1, D16413.1, L23503.1, U01104.1, AA463600.1, Z46206.1, R93559.1, R18599.1, C03715.1, AA493510.1, AA610816.1, AI954758.1, Z24812.1, AV373707.1, AV274641.1, AV261266.1, AI482404.1, T63643.1, AW851555.1, AW782871.1, AW764717.1, AW199070.1, AW187754.1, AI867176.1, AI779970.1, AI778733.1, AI778732.1, AI777779.1, AV072748.1, AU052904.1, AI191468.1, AI061454.1, C25733.1, AA517468.1, AA491434.1, C07818.1, H30070.1, AC025449.3, AC068719.1, AC025246.5, AC017005.4, AC068601.3, AC024183.3, AC022848.3, AC069130.1, AC009235.2, AC007322.3, AC024236.3, AC008061.1, AC007965.2, AC007315.2, AC068541.3, AC053495.3, AC022486.3, AC010146.5, AL354667.1, AC058810.3, AC026605.3, AC069232.1, AC021756.11, AC024043.4, AC021311.4, AC018967.3, AC022602.1, AC020065.1, AL356234.2, AL354755.2,
- 10 SEQ ID NO.300
NGO-St-134
YS1695/T3 5'
- 15 NM_003611.1, Y16355.1, Y15164.1, AC003037.1, AC006991.2, AC016707.2, AC008175.2, AC007379.2, AC010682.2, AC009947.2, AF121351.1, AE003417.1, AC005039.1, AF077408.1, AL161498.2, AF016655.1, AL050231.2, NC_001144.1, AC010498.4, AF140536.1, AE003690.1, AE003542.1, NM_002062.1, AC009514.2, AC006026.2, AC006065.3, U44051.1, U85195.1, U01156.1, AC005179.1, U22383.1, AE000658.1, AL163244.2, AB016214.1, U51234.1, AL136501.2, AL035690.10, AL008732.1, AL021367.1, U62778.1, U10037.1, U01157.1, AP001699.1, AP001604.1, M24635.1, L23503.1, U01104.1, AA463600.1, Z46206.1, R93559.1, R18599.1, C03715.1, AA493510.1, AA610816.1, AI954758.1, AV373707.1, AV274641.1, AV261266.1, AI482404.1, T63643.1, AW782871.1, AW764717.1, AW199070.1, AW187754.1, AI779970.1, AI778733.1, AI778732.1, AI777779.1, AV072748.1, AI191468.1, AI061454.1, AA517468.1, AA491434.1, C07818.1, AC025449.3, AC068719.1, AC007322.3, AC024236.3, AC008061.1, AC007965.2, AC007315.2, AC068541.3, AC053495.3, AC022486.3, AC069130.1, AC009235.2, AC024183.3, AC022848.3, AC068601.3, AC010146.5, AL354667.1, AC058810.3, AC026605.3, AC069232.1, AC021756.11, AC018967.3, AC020065.1, AL356234.2, AL354755.2, AC044879.3, AC009545.4, AC018905.4, AC068284.2, AC023596.7, AC023105.4, AC068275.2, AC025586.1, AC022448.3, AC010423.5, AC011378.3, AC011404.4, AC019198.2, AC044779.3, AC026076.2, AC009692.3, AC025038.3, AC026529.2, AC034290.1, AC015988.3, AC022937.3, AC019039.2, AC021936.1, AC021312.1, AC020414.1, AC012565.2, AC014964.1, AC007645.3, AL139147.3, AL133402.10, AL162739.4, AL160167.5, AL353621.2, AP001998.1, AP000916.2, AP001524.1, AP001491.1, AP000723.1, AP000629.1,
- 20
- 25
- 30
- SEQ ID NO.301
NGO-St-134
YS1695/T7 3'
- 35 NM_003611.1, Y16355.1, Y15164.1, AC003037.1, AC007379.2, AC016752.2, AC008175.2, NM_007845.1, S77750.1, U12565.1, AC024823.1, AE003682.1, AE002142.1, AF165124.1, AC005220.1, AL021328.1, AE002140.1, NM_010077.1, AF143381.1, AC003042.1, AL117375.12, Z99772.1, X55674.1, D67043.1, AC005310.2, AC009327.6, AC008125.9, U21319.1, AC005371.1, AC002090.1, AJ235271.1, AB026658.1, AI916605.1, AI867405.1, AI971431.1, AI867404.1, AI376969.1, AI769120.1, AI634116.1, AI245948.1, AW167287.1, AA399610.1, AA173950.1, AA778870.1, AW118555.1, AI627406.1, AI769378.1, AI804265.1, AI309530.1, AW296642.1, D52284.1, AI277389.1, AI304731.1, N57735.1, AI280957.1, AA504821.1, AI049632.1, CI4646.1, AA780326.1, CI4712.1, AA994778.1, R41679.1, AI916018.1, T16276.1, N57749.1, AA173595.1, AA824530.1, AA621466.1, AW009492.1, D53159.1, AI917863.1, H05597.1, AW885416.1, AI908207.1, D60992.1, AI908204.1, AI561264.1, AI277708.1, W35241.1, AI620904.1, Z41831.1, AI277709.1, D53722.1, AI277707.1, AA428032.1, AA514458.1, D60582.1, D80593.1, AW118344.1, AI824750.1, AI719888.1, AI908201.1, D60909.1, R93560.1, D80428.1, AW887698.1, AW450863.1, AI333241.1, AA707111.1, AA693788.1, AW072670.1, AI022424.1, CI4580.1, AI471729.1, AA398975.1, AI719895.1, AW271458.1, W23787.1, AW416841.1, AW554784.1, AW542764.1, AI480837.1, AW785419.1, AW785418.1, AI554988.1, AA634447.1, AW485325.1, AW375050.1, AW297567.1, AA871518.1, AA869166.1, AV197217.1, R14712.1, AW563271.1, AW270811.1, AI507728.1, AA247528.1, AC025449.3, AC068541.3, AC022486.3, AC007322.3, AC007965.2, AC007315.2, AC018789.2, AC008061.1, AC022783.2, AC020972.1, AC063924.3, AC008611.4, AC026910.2, AC021619.3, AC006879.2, AC006796.1, AC068165.1, AC021471.2, AC010873.3, AC015517.2, AL137069.2, AL158045.2, AC013318.4, AC063960.2, AC034138.2, AC012686.3, AC018872.2, AL137125.2, AL136218.7, AL353607.2,
- 40
- 45
- 50
- 55
- SEQ ID NO.302
NGO-St-134
YS318/T3 5'
- 60 NM_003611.1, Y16355.1, Y15164.1, AC003037.1, AC010682.2, AC007379.2, AC006991.2, AC008175.2, AC009947.2, AE003417.1, AC005039.1, AF117269.1, U09819.1, AF016655.1, AL050231.2, Z99121.1, X71360.1, AP002039.1, NC_001144.1, AC009411.2, AF140536.1, AE003690.1, NM_002062.1, AC009514.2, AC006026.2, AC006065.3, AC005839.1, U44051.1, U85195.1, U01156.1, U22383.1, AE000658.1, AL163244.2, AB016214.1, U51234.1, AL035690.10, AL008732.1, AL021367.1, U62778.1, U10037.1, U01157.1, AP001699.1, AP001604.1, M24635.1, X75598.1, D16413.1, L23503.1, U01104.1, R93559.1, AA463600.1, C03715.1, Z46206.1, R18599.1, AA493510.1, Z24812.1, AV373707.1, AV274641.1, AV261266.1, AI482404.1, AW851555.1, AW782871.1, AW764717.1,

AW199070.1, AW187754.1, A1867176.1, A1779970.1, A1778733.1, A1778732.1, A1777779.1, AU052904.1, C25733.1, AA517468.1, AA491434.1, C07818.1, H30070.1, AC025449.3, AC068719.1, AC025246.5, AC017005.4, AC068601.3, AC024183.3, AC022848.3, AC069130.1, AC009235.2, AC068541.3, AC022486.3, AC007322.3, AC024236.3, AC008061.1, AC007315.2, AC010146.5, AL354667.1, AC058810.3, AC026605.3, AC069232.1, AC024043.4, AC021311.4, AC022602.1, AC020065.1, AL356234.2, AC044879.3, AC009545.4, AC018905.4, AC026076.2, AC026925.2, AC022937.3, AC016803.2, AC019039.2, AC012507.3, AC020414.1, AC007645.3, AC005059.1, AL139147.3, AL133402.10, AL162739.4, AP001998.1, AP000723.1,

SEQ ID NO.303

10 NGO-St-134

YS318/T7 3'

NM_003611.1, Y16355.1, Y15164.1, AC003037.1, AC007379.2, AC016752.2, AC008175.2, AC024823.1, AE003682.1, AE002142.1, AC005046.3, AF165124.1, AC005220.1, AE002140.1, AF143381.1, AC005922.1, AC003042.1, AL121674.12, AL033378.12, AL117375.12, Z99772.1, AL031285.1, D67043.1, AC005310.2, AC006029.2, AC009327.6, AC005827.3, AC005371.1, AJ235271.1, AL137189.1, AL008729.1, AB026658.1, A1867405.1, A1916605.1, A1971431.1, A1376969.1, A1867404.1, A1769120.1, A1634116.1, A1245948.1, AA173950.1, AA399610.1, AA778870.1, AW167287.1, AW118555.1, A1769378.1, A1627406.1, A1804265.1, A1309530.1, AW296642.1, A1277389.1, A1304731.1, N57735.1, D52284.1, A1280957.1, AA504821.1, A1049632.1, AA780326.1, C14646.1, AA994778.1, R41679.1, A1916018.1, C14712.1, T16276.1, N57749.1, AW009492.1, AA824530.1, AA621466.1, A1917863.1, D53159.1, AA173595.1, H05597.1, AW885416.1, D60992.1, W35241.1, A1908207.1, A1620904.1, Z41831.1, A1908204.1, AA428032.1, AA514458.1, D53722.1, D60582.1, A1561264.1, D80593.1, A1277708.1, A1277709.1, A1824750.1, A1719888.1, A1277707.1, R93560.1, D60909.1, D80428.1, AW887698.1, AW118344.1, A1908201.1, C14580.1, A1471729.1, A1719895.1, AW450863.1, AW072670.1, W23787.1, AW271458.1, A1333241.1, AA398975.1, A1022424.1, AA707111.1, AA693788.1, AW416841.1, AW554784.1, AW542764.1, A1480837.1, AW785419.1, AW785418.1, A1554988.1, AW485325.1, AV197217.1, R14712.1, AW563271.1, AW270811.1, AW119241.1, A1507728.1, AA247528.1, AC025449.3, AC068541.3, AC022486.3, AC007322.3, AC007965.2, AC007315.2, AC018789.2, AC008061.1, AC024524.3, AC063924.3, AC008611.4, AC021619.3, AC006796.1, AL136367.2, AL158205.4, AC021471.2, AC023409.1, AC010873.3, AC012501.1, AL159970.8, AP001318.1, AC012543.3, AC053523.2, AC008890.3, AC008732.4, AC034138.2, AL137125.2, AL136218.7,

SEQ ID NO.304

NGO-St-135 5'combined;

NM_014781.1, D86958.1, Z35085.1, X82318.1, NC_001865.1, AB001684.1, Z72514.1, AC002302.1, AC007486.1, AL049755.2, X79489.1, Z35853.1, AC010151.3, AC009234.3, AF083915.1, AL139074.2, AL132862.1, AC013737.4, U36927.3, AE003692.1, AC006473.2, AF056336.1, AL136363.4, AW502603.1, A1632607.1, A1889925.1, R59196.1, Z40222.1, H28996.1, Z30060.1, AW663145.1, N36767.1, T32056.1, T39659.1, T40715.1, AA063364.1, AW271526.1, AA795138.1, AW771911.1, AA998419.1, A1466480.1, AA880393.1, A1482282.1, A1841402.1, WS2752.1, A1786567.1, AV221321.1, BB006621.1, AV254733.1, AW865505.1, AV330249.1, AL044138.1, A1655038.1, AV316950.1, AV348716.1, AV274459.1, AV317688.1, AV280612.1, AV352758.1, AV349442.1, AV245740.1, AV318689.1, AV330001.1, AV328749.1, A1138828.1, AA047474.1, R17528.1, R13828.1, T38143.1, AW861328.1, AW426185.1, A1980387.1, A1959585.1, A1621380.1, Z29358.1, AW851165.1, AV440128.1, AW203956.1, AV347279.1, A1830629.1, A1488952.1, A1361260.1, A1281023.1, A1276138.1, AA828299.1, AA682840.1, AA449644.1, AA425466.1, AC018960.3, AC037464.2, AC018621.3, AC023756.2, AC024448.2, AC016201.5, AL161663.1, AC023777.3, AC006279.6, AL022285.6,

SEQ ID NO.305

NGO-St-135

YS374/T3 5'

NM_014781.1, D86958.1, Z35085.1, X82318.1, AL049755.2, D87675.1, AP001442.1, AP000141.1, AP000089.1, AC010151.3, AC009234.3, AC005771.1, AC006761.1, AE003692.1, AF172282.1, AC006478.2, AE001577.1, AC006473.2, AC006222.1, AF100669.1, AF016420.1, AL050322.10, AL022166.1, AB009049.1, A1889925.1, AW663145.1, H28996.1, Z40222.1, N36767.1, T32056.1, R59196.1, T39659.1, T40715.1, AA063364.1, AW271526.1, AA795138.1, AW771911.1, AA998419.1, A1482282.1, A1841402.1, AV221321.1, BB006621.1, AV254733.1, Z30060.1, AW865505.1, AV330249.1, A1655038.1, AV316950.1, AV348716.1, A1786567.1, AV274459.1, AV317688.1, AV280612.1, AV352758.1, AV349442.1, AV245740.1, AV318689.1, AV330001.1, AV328749.1, A1138828.1, AA047474.1, R17528.1, R13828.1, R20722.1, AW861328.1, A1980387.1, Z29358.1, AW851165.1, AW816256.1, AW572236.1, AV391062.1, AW328120.1, AV347279.1, AV220950.1, AW140056.1, A1830629.1, A1281023.1, A1276138.1, A1042194.1, AA682840.1, AA411650.1, AA194887.1, AA189098.1, H85292.1, R55580.1, AC018960.3, AL138741.3, AC022235.2, AC022198.2, AC023756.2, AL161663.1, AC023777.3, AC022224.20, AC019223.2, AL109767.2, AC022148.4, AC009138.5, AC016516.3, AC026891.1, AC016272.3, AC013530.3, AL354668.1, AL162211.3, AL049185.4,

SEQ ID NO.306

NGO-St-135

YS382/T3 5'

NM_014781.1, D86958.1, NC_001865.1, AB001684.1, AC006443.1, Z72514.1, AC004401.2, AC002302.1, AC007486.1, X79489.1, U41015.1, Z35853.1, Z35852.1, AL050403.13, AB019235.1, AC013737.4, U36927.3, AF121898.1, AE001381.1, AC004171.1, AF056336.1, AL136363.4, AL109983.1, AW502603.1, AI632607.1, Z30060.1, R59196.1, AI466480.1, AA880393.1, W52752.1, Z40222.1, H28996.1, AI786567.1, AL044138.1, T39659.1, T38143.1, AW426185.1, AI959585.1, AI621380.1, AV440128.1, AW614639.1, AJ396349.1, AW467130.1, AW251790.1, AW251721.1, AW203956.1, AV381555.1, AW139206.1, AV384482.1, AW047876.1, AI996020.1, AI849553.1, AI776841.1, AI774351.1, AU073206.1, AI712752.1, AI584023.1, AI488952.1, AI474049.1, AI373038.1, AI361260.1, AI175635.1, AI081464.1, C92808.1, AA828299.1, AA449644.1, AA425466.1, AA397984.1, AA192413.1, W80808.1, N34826.1, R27823.1, AC018960.3, AC037464.2, AC024448.2, AC012389.10, AL356295.3, AL160257.3, AC037454.2, AC064864.1, AC013328.5, AC004153.5, AC010985.3, AC006903.1, AL354763.1,

SEQ ID NO.307

NGO-St-135

15 YS382/T7 3'

NM_014781.1, Z35085.1, D86958.1, X82318.1, AE003435.1, AC007371.16, AC007489.3, AC024763.1, AE003558.1, U80446.1, AW771911.1, AW271526.1, AI138828.1, AI655038.1, AA047474.1, R13828.1, AI122747.1, AA047435.1, R23393.1, R55580.1, H10270.1, AA374617.1, W60007.1, R17528.1, C75251.1, R22753.1, F13181.1, F11154.1, AI889925.1, N36767.1, R20722.1, AA952920.1, T77023.1, AA206152.1, AI153537.1, AI841402.1, AA795138.1, AA063364.1, AA692714.1, AV316950.1, AI785170.1, AA200762.1, AV330249.1, AA998419.1, AV274459.1, AA976511.1, AA823667.1, AV221321.1, AW130616.1, BB006621.1, R16741.1, AV254733.1, AV280612.1, AV317688.1, AV349335.1, AV348716.1, AA808066.1, AW551190.1, AI627011.1, AV318248.1, AI447566.1, AI302306.1, AA974918.1, T24196.1, AC018960.3, AC051613.3, AC014392.1, AC013253.6, AC013535.4, AC016130.13, AC010113.4, AC017388.1, AC010557.2, AC006714.2, AC006746.1, AL355924.1,

SEQ ID NO.308

NGO-St-136

YS042/T3 5'

NM_002707.1, AX002424.1, Y13936.1, U81159.1, NM_008014.1, U42383.1, AX002422.1, AL049551.1, L31397.1, AF249327.1, NM_011577.1, AF105069.1, L42456.1, U41021.1, AJ009862.1, M57902.1, AB009874.1, AC006592.5, NM_011668.1, NM_010473.1, NM_008272.1, AF114039.1, AC007130.2, AF158597.1, AF132218.1, AF082835.1, AL022070.1, U18428.1, U96636.1, U82122.1, AL138558.1, U61980.1, X55318.1, X07647.1, M35603.1, AC010285.4, AC003692.1, AC010556.4, AC005908.1, AC005943.1, Z66566.1, AL136039.2, AL109967.2, Z85987.13, AP001595.1, AI650583.1, AI992326.1, AW384902.1, AW239336.1, AI879664.1, AW249422.1, AA070392.1, AW577345.1, AW659941.1, AW659925.1, AL042520.1, AW367060.1, AW361618.1, AI894150.1, AA211434.1, AW672699.1, AW161662.1, AI928871.1, AA320736.1, AW850023.1, AI878909.1, AW849906.1, AI879284.1, T06191.1, AW490146.1, AA383664.1, H32905.1, AW163699.1, D76591.1, AA115688.1, AW160907.1, AW082745.1, AI417405.1, AA834611.1, AA085449.1, AI878881.1, AI929038.1, AA074643.1, N88715.1, AW578051.1, AW382863.1, W39347.1, W34891.1, AW321752.1, AL045879.1, AA171301.1, W65536.1, AA383628.1, AI879435.1, AW062337.1, AW630504.1, AW872109.1, AA510019.1, AW871903.1, AW782552.1, AW760420.1, AI940409.1, AI323364.1, AA646479.1, AA190384.1, AC009427.2, AC025903.1, AC007497.2, AC027499.3, AC025642.2, AC022174.2, AL356108.2, AL158171.3, AP001128.1, AC026954.3, AC008006.3, AC027299.6, AL158816.4, AL117187.2, AC064846.3, AC026413.2, AC016575.6, AC026833.2, AC025898.2, AC016837.3, AC015677.4, AC021697.4, AC023379.2, AC023804.7, AC008841.1, AC024264.1, AC012531.1, AF165178.1, AL035477.5, AP001099.1,

SEQ ID NO: 309

NGO-St-136

YS042/T7

NM_002707.1, Y13936.1, AX002424.1, NM_008014.1, U42383.1, U81159.1, U83913.1, Z81114.1, Z78415.1, AL163233.2, U28789.1, AP001688.1, AP000961.2, AF213465.1, AC004519.1, AC002428.1, AC004839.1, AC007237.3, AF147259.1, U23527.1, AC004503.1, AL161507.2, AL163254.2, AL135744.2, AL049539.21, Z71782.1, AP001709.1, X87579.1, AP000204.1, AP000244.1, AP000126.1, M20814.1, AI623188.1, AI949680.1, AI769584.1, AW003495.1, AI016791.1, AW514319.1, AI674866.1, AA708807.1, AI954672.1, AI690420.1, AW771608.1, AW129519.1, AI563921.1, AA418416.1, AL044111.1, AI432554.1, AI634705.1, AI570350.1, AW087864.1, AA938139.1, AI917417.1, AI802218.1, AI432562.1, AW250025.1, AW675447.1, AI697620.1, AI686700.1, AI359192.1, AI634891.1, AI587529.1, AI290844.1, AI619769.1, AW163096.1, AI150541.1, N53494.1, AI933325.1, AA190579.1, AI687672.1, AI204201.1, AI435812.1, AI335028.1, AW079871.1, AI587523.1, AI885074.1, AA831968.1, AA292839.1, AI378193.1, AA418531.1, AA115707.1, AI983072.1, AI991100.1, AL046114.1, AA132539.1, AJ057142.1, AI962687.1, AI825350.1, AI637949.1, AI754481.1, AA460426.1, N36716.1, AW516535.1, AI445408.1, AA126965.1, N26077.1, AA613447.1, AA133683.1, AA994318.1, T30419.1, AI207138.1, AA470639.1, AW612812.1, AA151641.1, AA079391.1, AI683064.1, AI655486.1, W38314.1, AW806697.1, AW605433.1, AI018391.1, AA580007.1, AA398657.1, AW136714.1, AA465129.1, AA070393.1, AA465723.1, W38641.1, AI634337.1, C02081.1, AI675741.1, AI372924.1, AA621622.1, AI909888.1, AA587456.1, F22497.1, Z39444.1, AW361020.1, AI909859.1, AI690302.1, R53936.1, AI963691.1, AL160290.3, AC048362.2, AC027484.3, AC026473.3, AC009169.4, AC009664.4, AC022478.3, AC010735.3, AC015622.3, AL137066.5,

AL009206.1, AC037452.2, AC068637.3, AC069218.1, AC024094.8, AC006337.3, AC019043.3, AC040940.1, AC020685.3, AC011849.3, AC009549.3, AC021114.3, AC021002.3, AC016989.4, AC018717.5, AC020892.3, AC009665.4, AC016746.3, AC012529.1, AC004624.6, AC007913.1, AC007438.6, AC006086.7, AC006087.12, AC004670.1, AC005141.1, AL162264.4, AL355531.1, AL354876.1, AP001562.1,,

5

SEQ ID NO: 310

NGO-St-137

YS1671/T3

10 NM_015873.1, D88154.1, AP000497.1, J03781.1, AC007630.3, AL049867.2, AC008989.6, NM_009509.1, AF009332.1, X85787.1, Z94160.1, AL163292.2, AP001747.1, AP001625.1, M98454.1, D26083.1, AL040451.1, AW226642.1, AW344693.1, AA222407.1, AA272458.1, AA109911.1, AW049791.1, AI842717.1, AW336334.1, H31419.1, AI944648.1, AA871446.1, AJ003346.1, AC015624.2, AC055818.1, AC015627.1, AC009292.7, AC021133.3, AL109918.24, AC023547.3, AC025871.3, AC058789.9, AC064818.3, AC027567.2, AC021876.3, AC011132.4, AF235106.1, AC009837.2, AL136090.10, AL136966.6, AP001274.,

15

SEQ ID NO: 311

NGO-St-137

YS1671/T7

20 NM_015873.1, D88154.1, AP000497.1, AE003608.1, AC005750.1, AC005164.1, AC004453.1, AE002079.1, AC007870.3, L48729.2, AC006211.1, U50713.1, U52431.1, AP000003.1, AB004870.1, AI207789.1, AI828390.1, AI887514.1, AI991204.1, AW087315.1, AI004782.1, AI394648.1, AW627720.1, AI660044.1, AA088690.1, AI699257.1, AA088827.1, AI440449.1, T57294.1, AW197506.1, AA641469.1, AL040452.1, AA992660.1, W85454.1, AV270064.1, AV143508.1, AW701384.1, AW908944.1, AW701603.1, AI182951.1, AW911867.1, AW665415.1, AW629286.1, AW593227.1, AW575674.1, AW573162.1, AW573006.1, AW510703.1, AW340616.1, AW340493.1, AW274644.1, AW183086.1, 25 AW104924.1, AW082305.1, AI927494.1, AI868632.1, AI829672.1, AI827875.1, AI810093.1, AI809958.1, AI808895.1, AI805139.1, AI740990.1, AI685360.1, AI290316.1, AI276754.1, AI273268.1, AI247350.1, AI222006.1, AA919014.1, AA913475.1, AA411451.1, AC015624.2, AC015627.1, AC022034.3, AC020275.1, AC018448.8, AL139236.3, AC069272.3, AC016257.6, AC009466.7, AC024947.2, AC026456.2, AC032008.2, AC027694.2, AC023136.3, AC024720.3, AC023437.2, AC016168.3, AC020778.4, AC010833.3, AC018492.3, AC024158.1, AC021911.1, 30 AC004958.1, AL139342.4, AL133291.3, AP001031.2, AP001802.1, AP001500.1, AP000880.1,

SEQ ID NO: 312

NGO-St-138

YS171/T3

35 NM_002310.2, X61615.1, NM_013584.1, S73495.1, D26177.1, S73496.1, D17444.1, D86345.1, U97364.1, M95099.1, AC010140.3, AC006446.3, AE003824.1, AE003687.1, AE003458.1, AF077407.1, AC004829.2, AC005965.1, AC003688.1, U15422.1, AL132902.2, AL132950.1, AB005248.1, AE003742.1, AE003521.1, U89335.1, AC006193.3, AF086440.1, Z81565.1, Z47547.1, AL353871.1, AL138664.1, AL136538.1, AL049550.5, AL035423.4, U19467.1, U28735.1, AJ224683.1, Z11527.1, AB000565.1, T18495.1, AA207338.1, AI226136.1, W20740.1, AI894070.1, 40 AA023181.1, AI195387.1, AA245317.1, AW626804.1, AW529846.1, AW529284.1, AW527135.1, AJ397726.1, AW434719.1, AW355500.1, AW299470.1, AV334964.1, AV294188.1, AW083883.1, AI715801.1, AI575955.1, AA997228.1, AI415987.1, AI011427.1, AA534664.1, AA440412.1, AA193084.1, W81340.1, W81339.1, W79447.1, N42705.1, D69835.1, H59829.1, AC010457.5, AC016324.4, AC022850.3, AC023948.2, AC068662.1, AC025882.2, AC015938.3, AC024169.1, AL354889.4, AL355587.3, AL161660.6, AL162852.3, AC026954.3, AC010176.7, 45 AC010395.5, AC012610.4, AC008782.4, AC027785.2, AC021621.3, AC013642.3, AC019195.4, AC022040.2, AC025285.1, AC021883.2, AC020182.1, AC020286.1, AC013646.3, AC008232.3, AC018232.1, AC007770.4, AC007822.3, AL158053.2, AC020639.4, AC068892.1, AC010376.3, AC012316.4, AC068216.1, AC009627.3, AC026038.2, AC009833.3, AC019141.3, AC013466.2, AC011172.4, AC010003.5, AC009368.5, AC021801.1, AC019524.1, AC020018.1, AC008200.3, AC007910.1, AC006714.2, AL139190.4, AL139098.4, AL137780.2, 50 AL160263.3, AL353606.2,

SEQ ID NO:313

NGO-St-138

YS171/T7

55 NM_002310.2, U66563.1, AC018748.3, AF220294.1, AC020728.4, AC009526.4, AC004861.1, AC002457.1, U12386.1, AF064866.1, AE000722.1, AF043945.1, U23517.1, AC000103.1, AL355916.1, AL163283.2, U19289.1, U02537.1, AB017064.1, AC006991.2, AC007661.2, AE003735.1, AE003696.1, AE003562.1, AE003559.1, AC009947.2, AC004746.1, AC004081.1, AF077407.1, AF051985.1, NM_000810.2, AC004453.1, AC004993.1, AC006044.2, U42580.2, AF039907.1, AC007159.4, AC006409.2, AC005965.1, U89714.1, AC005176.1, Z83105.1, AL022289.1, U73646.1, 60 U73642.1, AL163261.2, AL121787.22, U65744.1, AL161666.2, X70645.1, X96995.1, L08485.1, AP001716.1, AP000188.1, AP000044.1, AP000298.1, AP000112.1, AI915539.1, AI439137.1, N67017.1, AI140597.1, R38064.1, R38159.1, AW766681.1, AW760222.1, AW645026.1, AW644379.1, AW643145.1, AI769415.1, AA825445.1, AA601263.1, AW633848.1, AW384967.1, AV361643.1, AI856958.1, AI807646.1, AI787356.1, AA833639.1, AA631386.1, AA322964.1, AA176759.1, D68013.1, AC010457.5, AC040167.2, AC008074.2, AC021418.3, AC026685.1,

AC018821.3, AC018829.3, AC007906.2, AC068278.2, AC026811.2, AC068398.1, AC018958.2, AC024235.2, AC040994.1, AC024454.2, AC019295.3, AC022600.1, AC004133.1, AL138931.2, AL157936.3, AL163540.3, AP001536.1, AP000609.2,

5 SEQ ID NO: 314

NGO-St-139

YS313/T3

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35 SEQ ID NO:315

NGO-St-139

YS313/T7

NM_004404.1, AC005104.1, AF038404.1, D63878.1, D28540.1, NM_010891.1, D49382.2, AL031779.5, Z98754.1, AL163229.2, AP001684.1, AP000657.1, AP000561.1, NM_015759.1, AF017369.1, AF038172.1, AE003820.1, 40 AC004615.1, AC008165.3, AC005078.1, AC006572.2, AC005184.1, AC005242.1, AL049557.19, AC000386.1, AL157991.1, AL121963.10, AL132846.1, Z68276.1, AP001306.1, M63453.1, AI753689.1, AI114531.1, AI754501.1, AI088934.1, AW152364.1, AI609395.1, AA639591.1, AI160331.1, AI951387.1, AI955165.1, AI573059.1, AW473653.1, AI956125.1, AI126301.1, N21100.1, AI089658.1, AI632807.1, AW273787.1, N35895.1, AW020474.1, AI094932.1, AW026345.1, N67318.1, AW339045.1, AW886537.1, AA234940.1, AA137035.1, AW514047.1, AI346269.1, 45 AA218642.1, N67464.1, AA516108.1, AI829564.1, AI683327.1, AI355722.1, AA516499.1, AW022200.1, AA234941.1, AA206067.1, AI564619.1, AW769271.1, AI357439.1, AW517058.1, AI635685.1, AI087118.1, AI273328.1, AI143819.1, AI051872.1, AW474968.1, AW167451.1, AI754942.1, AI708338.1, AA775507.1, AA565842.1, AI130699.1, AA809247.1, AA430153.1, T15553.1, AW023986.1, AW469297.1, AI039303.1, AI521676.1, AA971524.1, AA487437.1, AW302623.1, AI880684.1, AI143019.1, AA812690.1, AI081421.1, AA043265.1, AW771795.1, AA599961.1, AA181698.1, AA071074.1, 50 AI754299.1, AI355732.1, AI027964.1, AI338308.1, AA808182.1, AA209392.1, AW192277.1, AI858793.1, AI304415.1, AI225151.1, AI139335.1, AW337224.1, AI434203.1, AI565741.1, AI217047.1, AI190711.1, AW129449.1, N25544.1, N53355.1, AW771405.1, AI636810.1, AI096434.1, AA928349.1, AA599844.1, AI024553.1, AI830555.1, AC068782.1, AC012304.2, AC019318.2, AC013382.3, AC022958.1, AL137008.2, AC027057.3, AC024706.3, AC011210.3, AL121819.2, AC010600.3, AC008525.4, AC027182.1, AC009146.2, AL133383.6, AC058801.2, AC027523.2, 55 AC022912.3, AC025164.8, AC021662.8, AC018548.7, AC021873.7, AC012514.8, AC069223.1, AC068763.2, AC069025.1, AC069013.1, AC068070.2, AC068708.2, AC007511.2, AC011209.3, AC067953.2, AC027344.2, AC026410.2, AC010419.3, AC046162.2, AC027812.2, AC067899.1, AC026935.2, AC020684.4, AC020778.4, AC024053.2, AC022986.3, AC021111.3, AC025706.3, AC013303.3, AC011774.4, AC024503.2, AC022923.3, AC016515.3, AC013637.3, AC023560.2, AC022568.3, AC025489.1, AC008853.1, AC005472.14, AC007472.5, 60 AC022016.2, AC014851.1, AF166490.1, AC007702.1, U82207.1, AL157761.2, AL157402.2, AL356218.1, AL353136.3, AL132868.12, AL355373.1, AL354809.1, AL161933.3, AL353731.1, AL159980.3, AL136360.7, AL135818.2, AL035066.20, AL021573.1, AP001848.1, AP001487.1, AP001486.1, AP001018.1, AP000875.1, AP000789.1,

SEQ ID NO: 316

NGO-St-140

YS2312/T3

- 5 NM_004724.1, U54996.1, AJ250458.1, AE003557.1, AC003949.1, AJ012166.1, U39676.1, AL031785.1, AC006332.3, AF244289.1, AF244276.1, AF244264.1, AF244262.1, AF244261.1, AE003628.1, AC003060.1, AC004830.1, AC004887.2, AE001709.1, AC005454.1, AF081108.1, AC005293.1, Z81567.1, Z69386.1, AL133334.16, S70930.1, AL138655.1, M80829.1, AL049861.18, AL137961.1, AW107591.1, AA693260.1, AV046551.2, AV147645.1, AA692808.1, AJ396591.1, AJ395373.1, AW375854.1, AV362443.1, AW003698.1, AI887627.1, C77594.1, AA541074.1, Z92701.1, AA148712.1, AC036188.2, AC068190.1, AC036226.1, AC020808.2, AP001882.1, AP000913.2, AP000744.1, AC021176.3, AC006591.12, AC018042.1, AC008303.1, AC026900.3, AC027690.4, AC027341.2, AC010276.5, 10 AC024383.3, AC023774.3, AC025551.3, AC019145.5, AC013693.3, AC023632.1, AC022652.1, AC010885.3, AC018617.2, AL138884.3, AL138796.3, AL136086.3, AL096819.12, AC036166.3, AC027821.3, AC060778.2, AC009783.7, AC012040.9, AC068764.2, AC012526.20, AC019041.3, AC053479.2, AC036181.2, AC060829.2, AC021082.2, AC010631.4, AC026474.3, AC026464.3, AC018646.1, AC064794.1, AC019055.3, AC024067.3, AC053522.1, AC051661.1, AC026561.2, AC012130.2, AC019058.3, AC023881.2, AC021469.3, AC011562.4, 15 AC015523.3, AC011972.3, AC011277.4, AC023013.2, AC024630.1, AC020607.2, AC021317.2, AC015973.1, AC013268.1, AC009849.6, AC012796.1, AL355853.3, AL355005.2, AL356117.1, AL136118.3, AL135915.2, Z98876.1,

SEQ ID NO: 317

NGO-St-140

20 YS2312/T7

- NM_004724.1, U54996.1, AF003951.1, AC008085.1, AC004520.1, AF011889.1, AE001131.1, Z99162.1, AL031275.1, AP002068.1, AE003825.1, AE003435.1, AC007636.19, AC018833.3, NM_006389.1, AC005483.1, AC007395.3, AC011663.5, AC005966.1, AC006442.1, AF004556.1, U65785.1, AC004518.1, AF045265.1, AC004237.1, AL163002.1, Z75552.1, AL096712.20, AL022397.1, J02027.1, V01170.1, Z73477.1, AB005240.1, AB005531.1, D86408.1, 25 AW235646.1, AA599145.1, AW575031.1, AW851090.1, AW057979.1, AL290602.1, AA076428.1, AI937662.1, AI025335.1, AI680594.1, AI810264.1, AA416982.1, AA252056.1, R38913.1, AW170221.1, Z41148.1, AA251899.1, R01885.1, T90448.1, AA812446.1, AW851089.1, T82954.1, AI684285.1, C21581.1, AI230413.1, AA940442.1, AA163727.1, AI060892.1, AV428214.1, AW644211.1, AW087475.1, AW045499.1, AI976733.1, AV048357.1, U21463.1, AA574864.1, AA365430.1, AA298325.1, AA175204.1, C17935.1, W30805.1, H86313.1, H85644.1, H06905.1, R13668.1, 30 T74922.1, AC036188.2, AC068190.1, AC022429.3, AL121796.4, AC021596.1, AC026129.3, AC009518.6, AC016934.4, AC026863.3, AC068174.1, AC023845.2, AC020874.2, AL356464.2, AC044882.3, AC026004.3, AC069274.1, AC069259.1, AC061981.2, AC034288.2, AC022101.3, AC022096.3, AC016602.5, AC010398.6, AC008842.4, AC008950.3, AC008687.3, AC068557.1, AC068310.1, AC009440.2, AC009309.2, AC009471.3, AC019043.3, AC011711.2, AC048354.1, AC026667.2, AC025706.3, AC015999.3, AC026819.1, AC026206.1, AC024518.2, 35 AC016750.4, AC021121.3, AC022773.2, AC022011.2, AC018835.3, AC007578.4, AC016394.3, AC022381.1, AC010165.2, AC019815.1, AC018014.1, AC006910.2, AL121928.11, AL157364.2, AL139000.3, AL135842.5, AL355335.3, AL139347.3, AL356461.1, AL356373.1, AL139424.3, AL157386.3, AL354956.1, AL353646.1, AP001983.1, AP001182.1, AP001098.2, AP000909.1, AP000877.1, AP000854.1, AP000833.1, AP000710.1,

40 SEQ ID NO: 318

NGO-St-141

YS1653/T3

- AF220152.2, AF176646.1, AF095791.1, AB041546.1, AC009145.4, AF110520.1, U48455.1, AC007686.5, AC004000.1, AC006365.3, AC005820.1, AF135125.1, AC005519.2, AC006957.1, AL049734.11, Z84466.1, X60322.1, AA307658.1, 45 AW295050.1, AW381667.1, AW654821.1, AW762888.1, AW062585.1, AW820659.1, AI450529.1, W40612.1, AW295045.1, AF150311.1, AI019873.1, U49254.1, AW451671.1, AL044797.1, C93889.1, AA215860.1, AW870886.1, AW870865.1, AW286314.1, AI711921.1, AI695573.1, AI450513.1, AI415393.1, T46771.1, AA381620.1, AA381302.1, AA224113.1, AA036086.1, AA008214.1, AA007765.1, W41129.1, AL135793.5, AC006180.1, AC040174.2, AC027279.2, AC009451.6, AC025959.3, AC055713.2, AC048331.5, AC046170.2, AC009449.2, AC025963.2, AC016438.3, 50 AC026894.1, AC024530.3, AC011061.4, AC010844.5, AC011318.8, AC068982.2, AC069010.1, AC025987.3, AC006534.3, AC068877.1, AC068837.1, AC068519.1, AC027824.2, AC068364.1, AC012272.2, AC025697.2, AC026378.4, AC055858.1, AC027031.2, AC040998.1, AC032017.1, AC023034.2, AC025368.1, AC013786.2, AC019340.2, AC021315.1, AC015706.2, AL355366.2, AL139109.2, AL138749.7,

55 SEQ ID NO: 319

NGO-St-141

YS1653/T7

- AF220152.2, AF176646.1, AF095791.1, TS4480.1, AA197191.1, AW103791.1, AW131855.1, AW379901.1, AW856286.1, AW856267.1, AW856115.1, AW856067.1, AW815565.1, AW815555.1, AW815535.1, AW815392.1, AW815391.1, 60 AW582306.1, AW582296.1, AW582282.1, AW391319.1, AW380346.1, AW362647.1, AI525534.1, AW815543.1, AW605996.1, AW605995.1, AW605994.1, AW605992.1, AW605991.1, AW605988.1, AW582313.1, AW582268.1, AW380347.1, AW380331.1, AW380323.1, T29399.1, W25677.1, N57107.1, AW861030.1, AW861031.1, AW753790.1, AA133029.1, AW238260.1, AL135793.5, AL353777.6,

SEQ ID NO.320

NGO-St-142

YS1703/T3 5'

- 5 NM_003920.1, AF098162.1, AB015597.1, AK000721.1, NM_011589.1, AF098161.1, AF071506.1, AB019001.2, AB015598.1, AF126480.1, AB019576.1, AC007043.3, AP000354.1, AC000105.41, AC011456.2, AE003430.1, NM_006118.1, AC007655.1, AC007541.9, AC004032.7, U20824.1, U82696.1, AL132975.1, AL132954.1, U68566.1, AL035693.19, AL022330.4, AL034552.22, AJ248285.1, NC_001136.2, AC020912.4, AC016662.5, AC012679.3, NM_007682.1, NM_001717.1, AC005035.1, AC007784.7, AF135787.1, AF135397.1, AF135395.1, AC007787.1, AF091398.1, AC006380.2, AC005069.2, AC006062.4, L34162.1, L19443.1, AF022365.1, U59694.1, AL049569.13, Z85996.1, Z74369.1, Z74368.1, Z26875.1, Z46796.1, Z95210.1, X55038.1, M26440.1, M15410.1, X68757.1, M19540.1, L03427.1, X82086.1, AW839959.1, W87879.1, AW672754.1, AW379444.1, AW840009.1, AW277013.1, AA853284.1, AW326647.1, AW658376.1, AW802270.1, AW614491.1, AW407158.1, AW343382.1, AW161333.1, AW055155.1, AJ640251.1, AJ494066.1, AJ028107.1, AJ017338.1, AA987779.1, AA550998.1, AA476555.1, AA378527.1, AA373491.1, AA348092.1, AA324524.1, AA324379.1, AA321961.1, AA216551.1, AA213579.1, W82846.1, C04452.1, C03261.1, W07180.1, W04378.1, W03539.1, W02741.1, N99738.1, N40129.1, N35204.1, N28312.1, H91970.1, R91592.1, AW485342.1, AW435759.1, AW426330.1, AW163683.1, AW013483.1, AV003759.1, AI618639.1, AI416196.1, AI201312.1, AA561002.1, D81215.1, R25330.1, AC025574.6, AC024884.6, AC009289.5, AC009056.3, AC012534.2, AC007424.20, AC024096.7, AC022438.3, AC032035.2, AC023767.3, AC020703.3, AC024418.2, AC025107.1, AC010532.2, AC010113.4, AC014387.1, AL354980.1, AL080246.13, AL121812.1, AP001652.1, AP001636.1, AP000576.2, AC018995.4, AC023130.3, AC034245.2, AC027309.2, AC010503.5, AC010862.5, AC010533.3, AC009139.5, AC023572.3, AC022217.3, AC016168.3, AC025100.2, AC009577.3, AC021762.3, AC017022.3, AC023341.3, AC015473.3, AC024019.2, AC023579.2, AC016018.7, AC023321.1, AF200455.1, AC011694.2, AL121901.18, AL136114.2, AL079336.13, AL353140.3, AL139274.6, AL160258.3, AL354822.1, AL353779.2, AL158845.2, AL157699.2, AL121715.2, AL132640.1, AC000382.1, AL139247.1,
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SEQ ID NO.321

NGO-St-142

YS1703/T7 3'

- 30 NM_003920.1, AF098162.1, AK000721.1, AL022149.2, NM_003599.1, AC009294.8, AF064804.1, AF069734.1, AF073930.1, AC004508.1, AL163285.2, AL163912.1, AL080243.21, M62354.1, AW136364.1, AI333322.1, AA809127.1, AW512259.1, AW167047.1, AW675811.1, AW418601.1, AI802251.1, AI283089.1, AI885862.1, AW769136.1, AW181883.1, AI969152.1, AI825472.1, AI494276.1, AW189438.1, AI278255.1, AA115381.1, AW731809.1, AW275265.1, AI559688.1, AI283087.1, AA679712.1, AW089758.1, AI002252.1, AW058036.1, AI696514.1, AA853283.1, T16124.1, AI446312.1, AI468188.1, AI417732.1, AA115380.1, AW134955.1, AW386251.1, AW372691.1, AW372725.1, AW386250.1, AW386246.1, AW386230.1, AW384593.1, AW373076.1, AW386279.1, AW386226.1, AW372712.1, AW151342.1, AW749244.1, AW372690.1, AW384617.1, AW373100.1, AW372711.1, AW386261.1, AI913828.1, AI878884.1, AW372727.1, AW386248.1, AW386266.1, AA564588.1, AC025574.6, AC024884.6, AC012647.15, AP000938.2, AP000894.2, AC068984.3, AC025188.3, AC020927.4, AC010621.3, AC008529.3, AC022553.2, AC037440.1, AC019231.3, AC025807.2, AC011035.3, AC023917.2, AC011898.2, AC017021.2, AC022999.1, AC011134.2, AL355873.2, AL161905.4, AJ011929.1,
- 35
- 40

SEQ ID NO.322

NGO-St-143 combined

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-156-

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SEQ ID NO.323

NGO-St-143

5 YS1621/T3 5'

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SEQ ID NO.324

35 NGO-St-143

YS1621/T7 3'

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SEQ ID NO.325

55 NGO-St-144

YS273/T3 5'

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-157-

- AA179371.1, AA145014.1, W63826.1, AL139040.4, AC013751.3, AC068591.1, AC018720.3, AC015940.2, AC025843.2, AC015931.4, AC015801.3, AC009558.3, AC010959.3, AC008088.2, AC018665.2, AC018521.1, AL161638.2, AC063954.2, AC036174.2, AC068728.3, AC022420.3, AC010484.3, AC008439.3, AC032019.2, AC018644.3, AC009220.7, AC011443.4, AC031998.2, AC022285.5, AC062029.1, AC026591.2, AC022227.6, AC025707.3, AC040955.1, AC026154.3, AC025931.2, AC013345.3, AC013328.5, AC015670.4, AC015988.3, AC025590.2, AC026471.1, AC020560.2, AC020706.3, AC011165.3, AC011798.3, AC023022.1, AC012489.3, AF214634.1, AC020183.1, AC020509.1, AC009849.6, AC005124.2, AL356464.1, AL122034.8, AL353092.3, AL162255.5, AL121747.21, AL355314.1, AL354714.2, AL158217.3, AP001491.1,
- 10 SEQ ID NO.326
NGO-St-144
YS273/T7 3'
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- 50 SEQ ID NO.327
NGO-St-145
YS1411/T3 5'
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- 60

SEQ ID NO.328

NGO-St-145

YS1411/T7 3'

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15

SEQ ID NO.329

NGO-St-145

YS144/T3 5'

- 20 AL133161.1, AK001729.1, AC005343.1, Z50797.1, NC_001142.1, AE003727.1, AE003462.1, AF223391.1, AC004662.1, AC004254.1, AC006820.1, AC024205.1, NM_007046.1, NM_006521.1, AF162780.1, NM_008448.1, AF207550.1, AF196779.1, AF088916.1, AC005275.1, AF049895.1, AE000113.1, AF068862.1, AC003694.1, AF070717.1, AF069716.1, AC004642.1, L43549.1, AL163239.2, AL133332.12, AL161985.1, AL161496.2, U86090.1, AL050138.1, Z70273.1, U29523.1, Z49452.1, D87675.1, AP001694.1, X97162.1, X96717.1, X51330.1, AP001443.1, AP000140.1, AB011100.2, AP000088.1, X54945.1, D10483.1, L27153.1, AL045394.1, AL047720.2, AW815677.1, AW447609.1, AW418275.1, 25 AI426794.1, AW668623.1, AA087606.1, AI380050.1, AA914152.1, AW774428.1, AW736393.1, AW649599.1, AW586591.1, AL138309.1, AI892798.1, AI739806.1, AA711482.1, AA692780.1, AA692302.1, AA671345.1, AA655714.1, AA415524.1, AA119710.1, AA097087.1, AA087538.1, AA087381.1, H33004.1, R50279.1, AL353736.1, AC012445.3, AC011030.4, AC009564.4, AC051613.3, AL132672.7, AP000478.2,

30

SEQ ID NO.330

NGO-St-145

YS144/T7 3'

- 35 AL133161.1, AK001729.1, AF087969.1, AF177478.1, AL159179.2, AL049835.3, AC006222.1, AC007252.2, AF081241.1, AC008125.9, AF135183.1, AC004704.2, AC005937.1, AC005180.1, U71587.1, AE000904.1, AJ271161.1, U43282.1, U41530.1, AB042823.1, AP000511.1, AB023048.1, AL043584.1, AI131161.1, AL047721.1, AJ074999.1, AI369743.1, AI191659.1, AI752102.1, AI804688.1, W63623.1, H70039.1, AA412273.1, AA345937.1, AA461564.1, W39608.1, AA346011.1, AA046569.1, AL045395.1, AA412608.1, H70038.1, AW263032.1, AA534737.1, AI854609.1, AU024381.1, AI235913.1, AI464166.1, AW556867.1, AI862154.1, AW195190.1, AW532431.1, AW134839.1, AI632675.1, AI333447.1, AW070552.1, AA776248.1, AI033598.1, AI492046.1, AI560827.1, AI307523.1, AI990263.1, 40 AI090658.1, AW131196.1, AI337152.1, AA962117.1, AA216415.1, AI377836.1, AI032741.1, AI381470.1, AW182779.1, AA865536.1, AA137689.1, AA632347.1, W61524.1, AA460639.1, W88673.1, AI278969.1, H30866.1, AW336387.1, R94150.1, AA432615.1, AW499467.1, AA294458.1, AV390623.1, AI598316.1, AI401456.1, AW706903.1, AW580849.1, AW580825.1, AW257455.1, AW217194.1, AV264232.1, AI950381.1, W28723.1, N53539.1, H60201.1, H60196.1, R45124.1, R19599.1, R19570.1, AL353736.1, AC010736.4, AC023254.3, AC061993.2, AC021751.11, AC011448.2, 45 AC025792.2, AC025734.2, AC023932.2, AL139125.3, AL158046.1, AP001127.1,

SEQ ID NO.331

NGO-St-145

YS278/T3 5'

- 50 AL133161.1, AK001729.1, NM_008958.1, AB028866.1, AB010833.1, NM_014726.1, AF217796.1, AC002432.1, AC002303.1, AF077302.2, AC007298.17, AC005520.2, AF112866.1, U60822.1, AC004233.1, AL135752.2, AJ131018.1, AL096699.11, U10895.1, AK001621.1, AB018318.1, AW500657.1, AW673603.1, AW868998.1, AW869117.1, AI608224.1, AA387916.1, AW288019.2, AW654284.1, AW493485.1, AW487305.1, AW487276.1, AW461989.1, AW437659.1, AW403475.1, AW319454.1, AW239228.1, AW239051.1, AV217284.1, AV215050.1, AV205793.1, 55 AV155082.1, AV166903.1, AV152358.1, AV137501.1, AV123651.1, AV120391.1, AV117483.1, AV101080.1, AV098121.1, AV091752.1, AV084455.1, AV083583.1, AI763878.1, AV061031.1, AV060485.1, AV058197.1, AV057140.1, AV056958.1, AV055574.1, AI713124.1, AV006753.1, AI575485.1, AI527477.1, AI012556.1, AI179780.1, AI175786.1, AI119288.1, AI112286.1, AI111977.1, AI111490.1, AI072849.1, AI071746.1, AA874227.1, AA810909.1, AA797102.1, AA616728.1, AA445862.1, AA278495.1, AA182075.1, AA145911.1, AA072792.1, AA059888.1, 60 AA047908.1, AA041963.1, AA032369.1, AA003397.1, H61508.1, AL353736.1, AC012683.3, AC023955.2, AC018698.4, AC047322.1, AC049120.1, AC025999.3, AC019264.3, AC025655.2, AC010754.2, AL160235.1, AP001202.1, AC021048.8, AC024727.4, AC068810.1, AC025643.3, AC068488.1, AC019093.3, AC022842.4, AC023593.3, AC010268.3, AC019129.3, AC018673.3, AC025424.3, AC027044.2, AC021421.2, AC024731.5, AC013543.4, AC036147.1, AC024883.3, AC027777.1, AC021323.2, AC025133.2, AC020994.5, AC023658.1, AC016777.3,

AF202962.1, AC013679.1, AC005054.1, AL162714.4, AL121845.18, AL121880.15, AP001556.1, AP001368.1, AP000834.1, AP000757.1, AP000683.1,

SEQ ID NO.332

5 NGO-St-145

YS278/T7 3'

- AF087969.1, AL133161.1, AK001729.1, AF177478.1, AL159179.2, AL049835.3, U40830.1, Z97055.1, AJ238394.1, X61677.1, M90087.1, AC004981.1, AF081241.1, AF135183.1, AC004704.2, AF064857.1, AL163281.2, AJ271161.1, Z82077.1, U43282.1, U41530.1, X89886.1, AB042823.1, AL045395.1, AW263032.1, AA534737.1, AI862154.1, AW195190.1, AI333447.1, AW070552.1, AI632675.1, AI492046.1, AI033598.1, AA776248.1, AI560827.1, AI090658.1, AI990263.1, AI337152.1, AW131196.1, AI377836.1, AI381470.1, AI032741.1, AA216415.1, AW182779.1, AA046569.1, W63623.1, AA632347.1, AI278969.1, AA865536.1, AI401456.1, AI439888.1, W88673.1, AW028469.1, AA810290.1, AL047721.1, AA725456.1, AI074999.1, AI752102.1, AI191659.1, AI131161.1, AA412273.1, AI369743.1, AI699071.1, AI804688.1, AA461564.1, AW611821.1, AW083337.1, AL043584.1, AA620499.1, H70039.1, H27907.1, AI991681.1, W15240.1, AI684348.1, AI424392.1, AA229511.1, AA345937.1, AA046704.1, AA346011.1, AI608926.1, AI492935.1, AA447104.1, AI235913.1, AU024381.1, AI854609.1, AI464166.1, AW556867.1, AW532431.1, AW134839.1, AW747938.1, AA962117.1, AA557671.1, AA137689.1, W61524.1, AA972005.1, W39608.1, H30866.1, H70038.1, AW336387.1, R94150.1, AW499467.1, AA294458.1, BB000336.1, AW580849.1, AW580825.1, AW257455.1, AW217194.1, AV315168.1, AV274485.1, AV264232.1, AW152551.1, AV046353.2, AI503741.1, C99210.1, AA795526.1, C79929.1, AA607081.1, AA508474.1, AA248433.1, N53539.1, R29422.1, AL353736.1, AC010736.4, AL356241.2, AC061993.2, AC032025.2, AC027704.2, AC013712.3, AC022868.4, AC025734.2, AL139231.4, AL139125.3, AL158046.1, AC015551.9, AC062004.2, AC024895.5, AC023757.4, AC068652.1, AC044787.3, AC016567.4, AC009220.7, AC021091.2, AC009061.8, AC032021.2, AC068066.1, AC023041.2, AC009994.4, AC027480.2, AC009551.4, AC062039.1, AC027682.2, AC019243.3, AC024974.2, AC019214.2, AC012429.4, AC023264.2, AC018689.2, AC012594.3, AC011138.2, AC012050.1, AL356242.2, AL356100.1, AL157905.2, AL022597.5, AP001910.1, AP001260.1, AP001093.2, AP000743.1, Z92865.1,

SEQ ID NO.333

30 NGO-St-146

YS358/T3 5'

- AC006038.2, NM_004434.1, U97018.1, AC002094.1, NM_013589.1, AC018632.1, AC005881.3, AC007887.8, AF128394.1, AC006121.1, AL163203.2, AF004874.1, AL139078.2, AL050302.2, AL049911.2, U14611.1, AB019224.1, AB026642.1, X15122.1, Y00398.1, X02806.1, D00216.1, K02646.1, AE003844.1, AC004901.1, AF125520.1, AF017299.1, Z54281.1, Z68217.1, AL035562.14, U40426.1, AK000952.1, Z81167.1, AW851191.1, AW851190.1, AW342912.1, AW306072.1, AL041588.1, AW683786.1, AW483175.1, AW471804.1, AW471754.1, AW433049.1, AW397869.1, AW397864.1, AW397818.1, AW397808.1, AW397328.1, AW397299.1, AW397225.1, AW397183.1, AW397082.1, AW396931.1, AW396867.1, AW395710.1, AW395684.1, AW395670.1, AW318300.1, AW318207.1, AW318175.1, AW318001.1, AW317912.1, AW317798.1, AW317683.1, AI941128.1, AI941087.1, AI940932.1, AI940896.1, AI795036.1, AI748210.1, AI735897.1, AI735879.1, AI735805.1, AI735804.1, AI736030.1, AI629905.1, AU024702.1, AU024209.1, AA766572.1, AA760753.1, AA501257.1, AA501255.1, T08982.1, AC013322.5, AL133368.1, AC025644.2, AC021799.1, AC013567.2, AL138963.4, AL138693.6, AC027399.2, AC007445.2, AC016201.5, AC022035.2, AC017091.3, AF215845.1, AP001402.1, AC036149.2, AC025524.2, AC021486.3, AC019188.3, AL355301.3, AL158201.7, AL158031.4,

45 SEQ ID NO.334

NGO-St-146

YS358/T7 3'

- AC006038.2, AF131753.1, Z82268.1, Z94721.1, AC002074.1, AC006377.3, AL161532.2, AL049500.1, AF114156.1, AE003579.1, AC004111.1, AC006040.2, AC005075.2, AF125448.1, AC005149.1, AC002416.1, AF006762.1, AL117694.3, AC005826.1, AC006956.15, AC004668.1, AC015445.3, AC004862.1, AC006379.2, AL163232.2, U56964.1, AL035634.7, U40410.1, AB022157.1, AP001687.1, AP001253.1, X83624.1, AC007590.1, AF070718.1, AL161536.2, AL110482.1, J04485.1, AL080250.11, AL031677.5, AL031599.1, AL049487.1, AL049656.1, U41545.1, AW173156.1, AW419091.1, AI240374.1, AI806503.1, AW152350.1, AW276130.1, AA449115.1, AW516027.1, AI290977.1, AI803121.1, AI192373.1, AI193573.1, AA587244.1, AI288196.1, AA977076.1, AI367149.1, AA421771.1, AI910966.1, AI343706.1, AI499018.1, AA927517.1, AW445056.1, AI130998.1, AW771159.1, AW592377.1, AI097006.1, AI864290.1, AI097567.1, AI884377.1, N94895.1, AW511972.1, AI304601.1, AW079658.1, AW044403.1, AW768529.1, AW151869.1, AA193343.1, AI341554.1, AI290345.1, AA193461.1, AA861909.1, AA527518.1, N29071.1, AI277874.1, AI027217.1, AA459958.1, AA716610.1, AI051389.1, AA836942.1, AA679242.1, AA553698.1, AA082407.1, AI873933.1, R38955.1, AW272553.1, AA865858.1, AA832468.1, AA417893.1, N27375.1, D11610.1, AI867049.1, AA917795.1, AA256313.1, AA034164.1, N48340.1, H10359.1, AW119101.1, AA256438.1, N23618.1, AI240601.1, AA514495.1, AI290297.1, AI061272.1, AA443213.1, AA789034.1, H08100.1, R40145.1, D12463.1, AA482526.1, AI240093.1, AA493130.1, AA122021.1, AA994372.1, AW514004.1, AI523990.1, R84780.1, AA227683.1, H06663.1, X91713.1, AA062803.1, AA585119.1, AA890144.1, AI283724.1, AA056271.1, AI634524.1, AI644019.1, AW556280.1, AW142557.1, AW550088.1, AC013322.5, AL355365.2, AL354880.3, AP000621.1, AC027141.1, AL133458.12, Z93243.1,

Z83124.1, AC012022.5, AC068296.4, AC066601.1, AC007481.2, AC016775.4, AC015473.3, AC019993.1, AL157955.1, AC067723.2, AC025164.7, AC027301.3, AC007683.3, AC026087.3, AC015625.3, AL355542.2, AL136301.4, AP001965.1, AC016255.8, AC055821.2, AC058803.1, AC026233.2, AC024181.2, AC022087.3, AC022796.3, AC006280.6, AC018594.3, AC016255.7, AL138823.3, AL096784.2,

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SEQ ID NO.335

NGO-St-146

YS112/T3 5'

- 10 AC006038.2, NM_012155.1, AF103939.1, AL096717.1, NM_004434.1, U97018.1, AE003673.1, AE001573.1, AC001655.1, NM_008519.1, NM_006007.1, AF077673.1, AF062072.1, AF110104.1, AC006121.1, AF044030.1, AF062347.1, AF062346.1, AC003029.1, AC004226.1, U14611.1, D84515.1, AE003596.1, AC005191.1, AC007077.2, AF017299.1, Z96811.2, AL035562.14, U40455.1, AA983842.1, Z81167.1, AA681706.1, AI596558.1, AA465739.1, AA850758.1, AW593841.1, AW516768.1, AW475067.1, AW303490.1, AW188604.1, AI807190.1, AI767422.1, AI740707.1, AI739199.1, AI582285.1, AI473581.1, AI458952.1, AI376302.1, AI312515.1, AA775264.1, AA743080.1, 15 AA428244.1, AA352385.1, AA043549.1, AW637997.1, AW631275.1, AW630845.1, AW483175.1, AW361213.1, AL134742.1, AA410201.1, AA298178.1, AA298197.1, AA233347.1, AA228021.1, AA165101.1, AA035737.1, AA002175.1, W73050.1, N28928.1, D56390.1, D58486.1, H04632.1, R56367.1, R33003.1, R24775.1, F05590.1, T30904.1, Z42327.1, AW608299.1, AI903729.1, AV135789.1, AI629905.1, AU024209.1, AA648943.1, AA532311.1, T50574.1, AC013322.5, AC011480.2, AL049868.12, AL133368.1, AC022275.9, AC020282.1, AC063945.3, AC068051.2, 20 AC068642.2, AC062020.2, AC067870.1, AC024948.2, AC007445.2, AC020684.4, AC022986.3, AC021885.3, AC018864.4, AC022451.1, AF215845.1, AL160266.6, AL135924.10, AC068130.2, AC069220.1, AC046133.3, AC068545.2, AC055837.2, AC036149.2, AC026720.3, AC010477.6, AC008384.4, AC008562.3, AC064860.2, AC027581.2, AC012213.3, AC016881.4, AC006400.6, AC009609.5, AC036233.1, AC025370.2, AC025090.2, AC021463.2, AC022247.2, AC016169.3, AC016690.4, AC021877.4, AC013638.3, AC010940.3, AC015567.3, 25 AC019239.3, AC007873.4, AC008086.2, AC019047.2, AC024171.1, AC011997.3, AC013885.1, AC013401.1, AC015691.1, AC012116.1, AC000016.1, AL121952.6, AL355498.2, AL158210.6, AL158043.4, AL136992.18, AP001554.1, AP001484.1, AP001375.1, AP000834.1, AP000757.1,

30 SEQ ID NO.336

NGO-St-146

YS112/T3 3'

- AC006038.2, AF131753.1, Z82268.1, AL161532.2, AL049500.1, AF114156.1, AE003579.1, AC004111.1, AC006040.2, AC005075.2, AF125448.1, AC005149.1, AC002416.1, AF006762.1, AC005826.1, AC006956.15, AC004668.1, AC002074.1, AC015445.3, AC005344.1, AL163232.2, U56964.1, Z68296.1, AL035634.7, U40410.1, AB022157.1, 35 AP001687.1, AP001253.1, X83624.1, AC004554.1, AL110482.1, AL133279.2, AL122021.3, AC000118.1, AL031677.5, AL009047.1, AL049487.1, AW173156.1, AW276130.1, AW419091.1, AI806503.1, AW152350.1, AA449115.1, AI240374.1, AW516027.1, AI290977.1, AI193573.1, AI803121.1, AI192373.1, AA587244.1, AI288196.1, AI367149.1, AA977076.1, AI910966.1, AI499018.1, AA421771.1, AW445056.1, AI343706.1, AA927517.1, AI130998.1, N29071.1, AI097567.1, AW592377.1, AW771159.1, AW079658.1, AI864290.1, AI304601.1, AI097006.1, AW044403.1, AI305161.1, 40 AW511972.1, AI884377.1, N94895.1, AW768529.1, AW151869.1, AA193343.1, AA193461.1, AI290345.1, AI341554.1, AA527518.1, AI277874.1, AA861909.1, AI027217.1, AI051389.1, AA459958.1, AA716610.1, AA836942.1, AA082407.1, AA679242.1, R38955.1, AA865858.1, AA553698.1, AA256438.1, AI873933.1, AW272553.1, AA832468.1, AA417893.1, AI867049.1, AA482526.1, AA256313.1, AA034164.1, N27375.1, D11610.1, AA917795.1, AW119101.1, N48340.1, H10359.1, AI240601.1, AI290297.1, AA514495.1, N23618.1, AA789034.1, H08100.1, AI061272.1, AA443213.1, 45 R40145.1, D12463.1, AI240093.1, AA493130.1, AA227683.1, AA122021.1, AW514004.1, AA994372.1, AI523990.1, R84780.1, AI634524.1, H06663.1, X91713.1, AA062803.1, AA585119.1, AI283724.1, AA890144.1, AA056271.1, AI644019.1, AW556280.1, AW142557.1, AW550088.1, AC013322.5, AL355365.2, AL354880.3, AP000621.1, Z93243.1, Z83124.1, AC027141.1, AC012022.5, AC068296.4, AC007481.2, AC015473.3, AC019993.1, AC006876.1, AC067723.2, AC025164.7, AC027301.3, AC007683.3, AP001965.1, AC016255.8, AC055821.2, AC025920.8, AC024162.2, 50 AC058803.1, AC026233.2, AC018555.3, AC021381.3, AC024181.2, AC022087.3, AC022796.3, AC006280.6, AC019111.3, AC016255.7, AC012410.2, AC012105.1, AL049184.5, AL096784.2,

SEQ ID NO.337

NGO-St-146

55 YS266/T3 5'

- AC006038.2, NM_004434.1, U97018.1, AC002094.1, NM_013589.1, AC018632.1, AC005881.3, AC007887.8, AF128394.1, AL163203.2, AF004874.1, AL161498.2, AL139078.2, AL050302.2, AL049911.2, AB019224.1, AB026642.1, X15122.1, Y00398.1, X02806.1, D00216.1, K02646.1, AE003844.1, AE003524.1, AC004901.1, AF125520.1, AC006121.1, AL079352.3, Z54281.1, Z68217.1, AL035562.14, U40426.1, AW851191.1, AW851190.1, Z81167.1, 60 AW851162.1, AW504697.1, AW342912.1, AW306072.1, AL041588.1, AW683786.1, AW471804.1, AW471754.1, AW433049.1, AW397869.1, AW397864.1, AW397818.1, AW397808.1, AW397328.1, AW397299.1, AW397225.1, AW397183.1, AW397082.1, AW396931.1, AW396867.1, AW395710.1, AW395684.1, AW395670.1, AW318300.1, AW318207.1, AW318175.1, AW318001.1, AW317912.1, AW317798.1, AW317683.1, AI941128.1, AI941087.1, AI940932.1, AI940896.1, AI795036.1, AI748210.1, AI735897.1, AI735879.1, AI735805.1, AI735804.1, AI736030.1,

AU024702.1, AU024209.1, AA766572.1, AA760753.1, AA501257.1, AA501255.1, T08982.1, AC013322.5, AL133368.1, AC025644.2, AC021799.1, AC013567.2, AL138963.4, AC022275.9, AC027399.2, AC026927.2, AC023790.5, AC067752.2, AC007445.2, AC022035.2, AF215845.1, AC017592.1, AC013559.2, AP001402.1, AC069220.1, AC036149.2, AC025524.2, AC024288.2, AL355301.3, AL158201.7, AL158031.4,

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SEQ ID NO.338

NGO-St-146

YS266/T7 3'

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SEQ ID NO.339

NGO-St-147

YS012/T3 5'

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SEQ ID NO.340

NGO-St-147

YS012/T7 3'

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-162-

- AW235931.1, AV264281.1, AV262910.1, AW010145.1, AW003523.1, AI969923.1, AI932268.1, AI913209.1, AI767599.1, AI683830.1, AI674202.1, AI662375.1, AI631854.1, AI623462.1, AI611342.1, AI607109.1, AI431890.1, AA999142.1, AI420398.1, AI378212.1, AI374843.1, AU001077.1, AI229770.1, AI170057.1, AI167540.1, AI092928.1, AI086083.1, AA854387.1, AA846367.1, AA830290.1, AA829162.1, AA825305.1, AA805644.1, AA764831.1, AA620645.1, AA481088.1, AA458626.1, AA450287.1, AA291148.1, AA281054.1, AA226512.1, AA226197.1, AA168415.1, AA165253.1, R42183.1, AC027238.2, AC011626.2, AC009901.3, AC040166.2, AC009040.4, AC023922.2, AC034280.2, AC016836.3, AC009967.3, AP001767.1, AP000873.1, AC025572.7, AC021850.4, AC021433.3, AC006914.1,
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- 30 SEQ ID NO.342
NGO-St-148
YS147/T3 5'
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- SEQ ID NO.343
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SEQ ID NO: 344

NGO-St-149

10 YS184/T3 5' Sequence 797 bp

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SEQ ID NO.345

NGO-St-149

YS184/T7 3'

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SEQ ID NO.346

NGO-St-150

YS255/T3 5'

55 AL137786.2, AE001106.1, AL109657.8, AE003536.1, AL032649.1, AC000095.3, AC010283.5, AC007370.7, U02206.1, U39718.1, AC005319.1, AL163237.2, U59177.1, U59176.1, AL031729.16, Z70754.1, Z98885.1, L41917.1, L41886.1, X05181.1, X04572.1, AP001692.1, AP000147.1, AP000233.1, Z99105.1, Z99104.1, D14465.1, AB006424.1, D81907.1, AA186486.1, AI752319.1, AW515316.1, AI633878.1, AA724174.1, N98699.1, AW088411.1, AI818209.1, AA360504.1, AW207435.1, R77568.1, D78858.1, AW083012.1, AI927938.1, AI669659.1, AA902264.1, AW105148.1, H83314.1, 60 AA300827.1, AW410334.1, AA431514.1, AI420205.1, AI752320.1, AI283114.1, D78824.1, AI743602.1, AI417561.1, W00707.1, N66098.1, N90043.1, AA573278.1, AA043792.1, C00128.1, AW796219.1, AI819645.1, AA329088.1, AW796258.1, AA043666.1, AI434568.1, AA973972.1, AI631297.1, AI638738.1, AI440413.1, AI048750.1, AI702887.1, AA431188.1, AA653570.1, AA348799.1, AI749472.1, AA210446.1, AW275782.1, AW275777.1, AA105091.1, AA137746.1, AA704575.1, AA561636.1, AA096434.1, AI753861.1, AJ396210.1, AJ394687.1, AI962149.1, AA809488.1,

-164-

AI440138.1, AL135399.1, AI058992.1, D62361.1, AW089455.1, AW322669.1, AA114807.1, AI925346.1, AA120374.1, AA153007.1, AW342822.1, AI982313.1, AA174177.1, AI981814.1, AU017382.1, AA561870.1, AW363585.1, AI576378.1, AW734057.1, AW333950.1, AW332559.1, AW257529.1, W31991.1, AC027672.3, AC013243.4, AL133461.2, AC023317.2, AL161659.10, AC010031.5, AC013267.2, AC017582.1, AL008876.1, AC016927.5, AC024903.5, AC068921.2, AC009463.6, AC008368.18, AC010448.4, AC009162.5, AC010727.3, AC021484.3, AC017044.2, AC022372.3, AC010901.3, AC019010.1, AC009624.2, AL353145.2, AL161451.4, AL138878.3, AL133543.2, AL031744.7,

SEQ ID NO.347

10 NGO-St-150

YS255/T7 3'

AE003626.1, AC005890.1, AL034556.3, AL008971.1, AC008873.4, AE003736.1, AE003708.1, AC005242.1, AF034902.1, AL163225.2, AL132796.2, AL031905.7, AL035530.11, AJ131836.1, AL035532.1, AC008865.3, AC007047.6, AE003545.1, AE002786.1, AC004547.1, AC005251.1, AC012680.3, AC005489.1, AF121782.1, AC006421.1, AE001428.1, AE001413.1, AF078780.1, AF064857.1, AL163281.2, AL133299.2, Z99773.1, AL096770.14, U39847.1, Z99281.1, Z68215.1, Z97055.1, Z97209.1, U32078.1, U50071.1, Z31356.1, U21731.1, AJ235270.1, AB015469.1, Y11842.1, X94355.1, AW771521.1, AA126445.1, AW514659.1, AW182807.1, AW771502.1, AA938728.1, AI090291.1, AI493810.1, AW675411.1, AA427532.1, AA349431.1, N62707.1, AW512566.1, AA058340.1, AA345941.1, AA588743.1, AW189042.1, AA187281.1, AW089555.1, AI678159.1, AI366801.1, AA829470.1, C02522.1, AI332895.1, T40865.1, AA970774.1, D79887.1, AA456027.1, AW149169.1, AI220712.1, AA310489.1, T40872.1, AI932606.1, AI587187.1, AA054496.1, D61745.1, AA126569.1, AA455387.1, AA292619.1, AA767314.1, T39804.1, T39783.1, AA766576.1, AA292620.1, AW315966.1, AW312359.1, AI551720.1, AA445754.1, AI157081.1, AA879725.1, AW347573.1, AI527455.1, H64492.1, AI341051.1, AI082974.1, AW863369.1, AW637708.1, AW618562.1, AW618323.1, AW610946.1, AW533222.1, AW528171.1, AW514564.1, AW399714.1, AW399655.1, AW349594.1, AW293159.1, AW276976.1, AI843747.1, AI663436.1, AI392688.1, AI288400.1, AA805183.1, AA561027.1, AA537476.1, AA455793.1, AA447110.1, AA434507.1, AA282194.1, AA101103.1, R81554.1, AC013243.4, AL133461.2, AC027672.3, AC018864.4, AF215845.1, AC069162.1, AL355312.3, AC020324.1, AC007291.23, AL356254.1, AC011970.1, AC009613.2, AL163537.4, AL157957.1, AC068957.1, AC067779.1, AC011562.4, AC019950.1, AL121928.10, AL157396.3,

30 SEQ ID NO.348

NGO-St-151

YS1652/T3 5'

AC003682.1, X15544.1, X16618.1, AK000267.1, M29411.1, NM_007673.1, AF104031.1, Z81009.1, S74520.1, U00454.1, AC011749.2, AE003587.1, NM_005231.1, NM_006030.1, AC004793.2, U34879.1, AF040709.1, U37521.1, AF054997.1, AF042793.1, AF042792.1, AJ251368.1, AJ251367.1, Z84492.2, AJ251914.1, AL121757.7, Z92845.1, L31886.1, AB040919.1, Z35691.1, M98343.1, AB011130.1, AA160768.1, AA454976.1, AA524918.1, AA160767.1, AW177242.1, AA524934.1, AW603587.1, AI909371.1, AW754009.1, AW604563.1, AW843725.1, AA236418.1, AA327082.1, T64077.1, AI981337.1, AI795303.1, AI639685.1, W78194.1, AW761561.1, AW326881.1, AW326538.1, AI327188.1, AI323297.1, AI273360.1, AI272717.1, AA876719.1, AA016882.1, W63915.1, N39838.1, AW699234.1, AW677045.1, AW658137.1, AW578415.1, AW392015.1, AW370009.1, AL134942.1, AW034847.1, AI527711.1, AA543942.1, AA378725.1, AA315097.1, W14378.1, W07354.1, U18015.1, T49796.1, AC068266.1, AC011089.4, AC006330.3, AC061995.1, AC024115.7, AC021247.4, AC027349.1, AC022585.1, AC011166.2, AL133331.12, AL158834.4, AL353680.3, AL158065.3, AP001374.1, AP001339.1, AC010299.4, AC009143.4, AC009123.5, AC009041.5, AC017067.3, AC010131.2, AC025353.2, AC046157.1, AC023825.3, AC026070.2, AC035886.1, AC035885.1, AC028189.1, AC019231.3, AC022608.2, AC016716.2, AC011035.3, AC017033.2, AC024117.1, AC012004.3, AC021764.1, AC015049.1, AC008228.2, AL356241.2, AL355483.2, AL356116.1, AL356007.1, AP001554.1,

SEQ ID NO.349

NGO-St-152

50 YS1704/T3 5'

AB033096.1, AF031242.1, M84990.1, L06863.1, U82671.2, AC003991.1, AF134576.1, AF070552.1, AC004040.1, U82696.1, AC001231.1, AL135745.2, AL121774.3, AC001477.1, AL133220.1, Z69655.1, Z33874.1, AW847517.1, AW762077.1, AW437401.1, AW463000.1, AI005887.1, AA133529.1, AI959464.1, AI650192.1, AA578951.1, R15953.1, M75813.1, AC026573.3, AL353588.2, AL353672.2, AC010195.7, AC009520.7, AC010274.3, AC010464.4, AC046150.2, AC025353.2, AC010864.2, AL139090.3, AL022344.1, AC011966.3, AC024727.4, AC009362.5, AC009180.7, AC011967.3, AC009621.4, AC007846.2, AC023959.2, AC023850.2, AC007608.2, AC007728.1, AC021596.1, AL136171.6, AL162741.3, AL162731.2, AL161933.3, AL139405.2, AP001591.1,

SEQ ID NO.350

60 NGO-St-152

YS1704/T7 3'

AB033096.1, AC004812.1, AL133249.1, AC000052.16, AC004019.20, U62317.2, AL163285.2, AC002091.1, AL050307.13, AC000134.14, AC007051.3, AL031289.1, AC005412.5, AC006273.1, Z98884.11, AL034350.2, AL033392.5, AC005755.1, AF001549.1, AL160237.2, AL110502.1, AF053356.1, AC010328.4, AC008518.3,

- AC007917.15, AC007066.4, AL117352.12, U75285.1, Z83823.1, AC000159.6, AC020663.1, AC005288.1, AC004821.2, AC005324.1, AL121601.13, AL035411.27, AP000555.1, AC006344.2, AC006480.3, AC005856.1, AC005215.1, AC004057.1, AC008079.23, AC016025.12, AC008101.15, AC006138.1, AL023882.2, AL031224.1, Z95152.1, AF064862.1, AC004087.1, AC005231.2, AL096700.14, AC009516.19, AC005747.1, Z97630.11, AC005500.2, AC004982.1, AF037338.1, AC005785.1, AL133353.6, AL121964.16, AL096712.20, AP000188.1, AP000044.1, AP000112.1, AC007312.1, AC007097.4, AC005486.2, AC005013.1, AC008168.3, AC010170.3, AC005037.2, AP000193.1, AC007956.5, AC007055.3, AC006207.5, AC004210.1, AL049780.2, AC008925.3, AC006046.1, AP000191.1, AP000115.1, AC007655.1, AC005089.2, AC005740.1, AL033525.10, AC005018.2, AL022727.1, AP001412.1, AP000152.1, AC006582.13, AC000081.2, AC003006.1, AC007057.3, AP000692.1, AC007565.1, AP001331.1, AC011465.4, AC007766.1, W79504.1, AF150152.1, AL246796.1, AW303196.1, AW274349.1, AA441788.1, N54902.1, AL284640.1, AW872676.1, AW473467.1, AW301350.1, AA557686.1, AL135724.1, AL1684097.1, AL041706.1, AW473163.1, AW168342.1, AW022379.1, AL633168.1, AL334435.1, T41242.1, AW338508.1, AL471481.1, AA381147.1, AL079645.1, AL732186.1, F36273.1, AL635818.1, AL569086.1, AL281881.1, AL160117.1, AL079910.1, AA598586.1, AA502155.1, AA491814.1, AA147750.1, AW057877.1, AL73916.1, AL537955.1, AA649642.1, AA487277.1, AW301809.1, AL439210.1, AA604607.1, AA179944.1, AW873290.1, AL499181.1, AL446464.1, AL432270.1, AL064864.1, AL061313.1, AA713891.1, AA482681.1, AL042856.3, AW088049.1, AA580808.1, AL561255.1, AA207129.1, AA171473.1, AA223206.1, AL085719.1, AA448858.1, AW615709.1, AW576503.1, AL138396.1, AL921061.1, AL754336.1, AL358812.1, AL079389.1, AL076766.1, AA634196.1, AA071393.1, C06339.1, AW081941.1, AW304805.1, AW152057.1, AW020992.1, AL920876.1, AL654247.1, AL571562.1, AL567712.1, AL358813.1, AL351698.1, AL289447.1, AL087133.1, AA533060.1, AL125107.1, AA765170.1, AA634272.1, AA633582.1, AA598425.1, AA551409.1, AA485930.1, AA151690.1, AA115165.1, AA082854.1, AA053128.1, W49595.1, N64547.1, AA443390.1, AL353672.2, AC026573.3, AL353588.2, AC009444.2, AC004795.2, AL137222.3, AC026413.2, AC017099.3, AC024088.3, AC008610.4, AC011442.3, AC011938.3, AC021455.3, AC018821.3, AC025287.2, AC020954.5, AC024438.2, AC013371.4, AC051660.3, AC019280.3, AL353729.2, AC017057.5, AC025341.2, AL136300.9, AL158830.5, AC023156.3, AC010607.4, AC034121.2, AC010130.4, AL117259.2, AC010395.5, AC009191.4, AC026397.2, AC013805.4, AC024990.2, AC023583.2, AC022460.2, AL161731.4, AL136311.3, AP001528.1, AC007780.2, AC026587.2, AC017083.4, AC023359.6, AC067749.2, AC026964.2, AC018989.3, AC011845.3, AC026294.1, AC022911.2, AC055890.2, AC024934.8, AC055791.2, AC025683.2, AL139109.2, AL138901.2, AC017100.3, AC009268.2, AC018862.3, AC024005.2, AC011092.1, AC025559.2, AC011443.4, AC007491.3, AC025145.2, AC027497.2, AL121971.2, AP001076.1, Y12335.1, AC026546.2, AC034181.1, AC022286.4, AC021024.2, AC021933.1, AC010455.3, AC024990.2, AC019206.3, AC021671.1, AL354986.1, AC022169.2, AC022966.2, AL355348.3, AF228728.1, AC025354.2, AC015726.3, AP001098.2, AC026050.3, AC025963.2, AC012128.3, AL160393.6, AC063960.2, AC022261.3, AC019291.4, AL356292.1, AC040922.2, AC012411.3, AC027546.1, AL353749.1, AC055767.1, AC011638.3,
- 35
SEQ ID NO.351
NGO-St-153
YS1754/T3 5'
AC004498.1, AC007956.5, AE003532.1, AF050157.1, Z37979.1, AC003028.2, AE003794.1, AE003615.1, AC006530.4, AC007977.11, AC006120.1, AE000679.1, AL133073.1, Z69662.1, U11039.1, Z99113.1, Z99112.1, AL005288.1, AL750442.1, R44564.1, F01704.1, AW614231.1, AW058657.1, AL808100.1, AL743405.1, AL726212.1, AL692280.1, AL675621.1, AL343951.1, AL342528.1, AA400627.1, AA400382.1, H00353.1, R56558.1, AW530608.1, AW530607.1, AL941583.1, AV185720.1, AL229512.1, C42486.1, C42424.1, AA470046.1, AA446177.1, AA398518.1, AA393260.1, AA090525.1, D75049.1, AL138764.3, AL355355.1, AC008528.5, AC011350.4, AC008591.4, AC011325.8, AC013337.5, AC024018.1, AL118511.22, AC024400.2, AC025205.2, AC022816.9, AC022059.2, AC019274.3, AC013814.3, AC023206.2, AC012359.3, AF215849.1, AC019852.1, AP001564.1, AC068133.2, AC026029.3, AC023332.3, AC064814.3, AC009452.9, AC068727.1, AC010398.6, AC009440.2, AC013570.3, AC011116.3, AC019264.3, AC018606.3, AC025827.2, AC011278.4, AC020571.2, AC010858.3, AC022955.3, AC022937.3, AC007838.10, AC024032.2, AC012287.2, AC020967.1, AC019998.1, AC012229.2, AC018325.1, AC008345.2, AL158837.4,
- 50
AL160235.1,
- 55
SEQ ID NO.352
NGO-St-153
YS1754/T7 3'
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AL035684.25, AL031054.1, AL031984.13, AC005895.1, M99412.1, AC004147.1, AL031674.1, U95743.1, AC006965.3, AL023804.1, AL031256.1, Z83732.1, AA583783.1, AA352852.1, AI750443.1, T97047.1, AI206381.1, AW779140.1, AW392720.1, AW392037.1, AW375505.1, AW375664.1, AI917309.1, AI245002.1, AA972389.1, AA348114.1, H83083.1, AI677865.1, AW081092.1, R68753.1, R36634.1, R36114.1, T39347.1, AL134762.1, AI950057.1, AI948415.1, AI913632.1, AL043389.1, AI760277.1, AI636038.1, AI422711.1, AI174489.1, AI097075.1, R92107.1, R36101.1, AW205700.1, AI857496.1, AI241546.1, AI052617.1, AA862242.1, AA682503.1, AA283058.1, AA010393.1, W87478.1, R98769.1, AW769350.1, AW631324.1, AW606680.1, AW380595.1, AW358828.1, AW170684.1, AI968735.1, AI916948.1, AI823617.1, AI798803.1, AI793154.1, AI692607.1, AI654898.1, AI208889.1, AI076838.1, AA770067.1, AA631910.1, AA613927.1, AA548931.1, AA426207.1, AA180428.1, AA128302.1, H54911.1, H16066.1, H14830.1, R46689.1, R09295.1, R09229.1, T91813.1, F12420.1, T74282.1, T66898.1, AW406178.1, AW113986.1, AI741532.1, AI674059.1, AA883361.1, AA754905.1, AA635120.1, W22245.1, N53160.1, H79438.1, H78261.1, Z41544.1, AL138764.3, AC017088.3, AC025558.3, AC016313.5, AL139785.1, AC018943.4, AC011652.4, AC022188.3, AC011247.3, AL109615.18, AL355388.2, AL139019.2, AL158169.1, AC068877.1, AC011388.4, AC008472.4, AC009823.3, AC016823.4, AC020766.3, AC007602.3, AC025589.6, AC025226.2, AC016399.5, AC009031.2, AC010755.1, AC007499.1, AL136368.5, AL133478.2, AL138779.3, AP001337.1, AC022844.3, AC068570.1, AC023403.2, AC022494.3, AC012666.2, AC010866.1, AL354873.3, AC009128.5, AC027486.2, AC046169.1, AC012222.3, AC018499.2, AL162293.7, AL136131.7, AP000868.1, AP000481.2, AC069233.1, AC069079.1, AC016530.3, AC015977.3, AL121889.7, AL138766.2, AC036218.2, AC007569.8, AC022362.5, AC064817.3, AC008714.2, AC008485.3, AC008484.3, AC008977.3, AC027064.2, AC011687.3, AC027580.1, AC011846.5, AC027143.1, AC024910.2, AC027081.1, AC026403.1, AC022684.2, AC022379.1, AC007607.2, AC022818.1, AC022259.1, AL121987.2, AL355875.2, AL161745.5, AL136086.2, AL162387.3, AL157942.2, Z97197.3, AP001838.1, AP000777.1, AC067823.2, AC068710.1, AC008623.3, AC023390.2, AC023825.3, AC021990.3, AC023487.3, AL355300.2, AL161795.2, AC007339.3, AC023091.2, AC022724.1, AL355865.1, AP000848.1, AC026906.2, AC025868.2, AC036238.1

25

SEQ ID NO.: 353

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50

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ZH068/T3

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10

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ZH068/T7

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35

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ZH091/T3

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55

SEQ ID NO: 357

ZH091/T7

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ZH1357/T3

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ZH156/T3

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SEQ ID NO: 361

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ZH062/T3

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SEQ ID NO: 363

ZH062/T7

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ZH085/T3

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- 20 SEQ ID NO: 365
ZH085/T7
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- 40 SEQ ID NO: 366
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-171-

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SEQ ID NO: 368

ZH1406/T3

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SEQ ID NO: 369

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SEQ ID NO: 371

20 ZH1255/T3

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SEQ ID NO: 372

35 ZH1314/T3

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55 ZH1314/T7

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-173-

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- 10 SEQ ID NO: 374
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- 20 SEQ ID NO: 375
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- 30 SEQ ID NO: 376
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ZH131/T3

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20 SEQ ID NO: 378

ZH131/T7

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ZH1371/T3

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SEQ ID NO: 380

ZH205/T3

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SEQ ID NO: 381

10 Ubiquitin-Specific protease (UBP)

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SEQ ID NO: 382

25 ZH053/T3

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SEQ ID NO: 383

45 ZH053/T7

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SEQ ID NO: 384

ZH1313/T3

- 5 NM_003368.1, AF117386.1, AL117575.1, AB014458.1, AE003523.1, AF069441.1, AL161500.2, AL032655.1, AL133421.1, Z85995.1, Z94721.1, AC006708.1, AE002611.1, AC008148.2, L29074.1, AC006060.1, AL133238.2, AL133372.2, AL121985.13, AL050322.10, AI478913.1, AW340312.1, AW340211.1, AW771501.1, AA832380.1, AA749334.1, AA743294.1, AI911716.1, AI656969.1, AA723943.1, AA099033.1, T09031.1, AA921156.1, AI050545.1, AA684326.1, AW663812.1, AA445060.1, AA016112.1, AW749359.1, AA010709.1, AW601534.1, AI764163.1, T34154.1, AA389075.1, AA110253.1, N50647.1, AW123867.1, AW121935.1, AI006640.1, AI006507.1, AI815490.1, AV074783.1, 10 C96400.1, AW605305.1, AW605290.1, AW485355.1, AV334525.1, AV316977.1, AV271577.1, AV271011.1, AI925190.1, AI880405.1, AV089080.1, AU053253.1, AI601868.1, AI577543.1, AI568768.1, AI416338.1, AI354858.1, AI132532.1, AA797782.1, AA789662.1, AA418927.1, AA242816.1, AA007209.1, N75527.1, N26669.1, H44548.1, T50640.1, AC025396.2, AL355389.1, AC011171.3, AP001167.1, AP000942.2, AC027757.2, AC025742.4, AC010054.4, AC009375.5, AC014849.1, AC022172.4, AC026984.1, AC006839.13, AL136322.2, AC026084.2, AC010594.4, 15 AC008504.4, AC027800.2, AC027392.2, AC021514.3, AC025821.2, AC009578.3, AC021258.3, AC018491.7, AC012545.1, AL136442.10, AL139406.2

SEQ ID NO: 385

ZH1313/T7

- 20 NM_016520.1, AF218421.1, AF151054.1, AL137549.1, AL008726.1, AL163249.2, AC010620.4, AC008044.4, AC002377.1, AC004921.1, AC004383.1, AL163212.2, AL096801.18, Z96074.4, Z84483.1, AP001667.1, AP000962.2, AC006055.1, AL163262.2, Z98036.1, AP001717.1, AP000191.1, AP000047.1, AP000115.1, AC006511.5, AC005089.2, AC005145.1, AL022316.2, AC006344.2, AF001550.1, AL078463.11, AP000348.1, AC004024.1, AC004076.1, AL135998.2, AL133448.3, AJ003147.1, AC004000.1, AC004491.1, AC007308.13, AC006251.3, AL023553.5, 25 AP000509.1, AC010491.3, AC005086.2, AF139813.1, AC004228.2, AC005755.1, AL163953.2, U50871.1, AL121580.8, AL033521.2, AC005231.2, AC004913.2, AC007360.2, AC007435.12, AF035396.1, AL121751.12, Z82215.1, AP000049.1, AP000311.1, AC006464.3, AC006349.3, AC004850.2, AC006317.3, AC004997.2, AC007229.1, AC006958.1, AC005562.1, AC005220.1, AL109627.18, AJ251973.1, AL008582.11, AL021453.1, Z92542.2, AL031311.1, AC018769.2, AC004999.1, AC009405.3, AC002554.1, AC002558.1, AL161670.2, AL031296.1, AC008969.5, U96629.1, AL157915.2, 30 AC004150.8, AC005808.1, AL021393.1, Z82206.1, AP000555.1, AL132986.2, Z97630.11, AL096776.12, AP000212.1, AP000134.1, AC004531.1, D83253.1, AP000009.2, AL031767.13, AI141544.1, AI651600.1, AI376077.1, AA503812.1, AA516476.1, AI458346.1, AI052479.1, AI146331.1, AI695736.1, AI812016.1, AI863150.1, AI214622.1, AI002868.1, AA639060.1, AI057130.1, AI913816.1, AI686336.1, AI685712.1, AI686315.1, AA503513.1, AA311466.1, AI765330.1, AI917006.1, AA934021.1, AW589928.1, AI763234.1, AW023167.1, AA761722.1, W80591.1, AA470915.1, AW088965.1, 35 AA579082.1, AA522864.1, AA156183.1, AA155817.1, W69639.1, N99245.1, AI459879.1, AW608403.1, AW162762.1, F00937.1, AW392038.1, AA132445.1, AW795901.1, D44871.1, W78986.1, AI242236.1, AI520984.1, AW388476.1, H89643.1, AW078646.1, AW072963.1, AI444575.1, AI344906.1, AI318548.1, AA505108.1, R87193.1, AW504667.1, AI917132.1, AI523356.1, AA947352.1, AA489939.1, AI699746.1, AA015948.1, W60000.1, W03800.1, AW247866.1, AI003391.1, AA663579.1, AL138226.1, AL044701.1, AW779609.1, AW131394.1, AW105463.1, AI918350.1, 40 AI754257.1, F35684.1, AI631299.1, AI277617.1, AA664963.1, AA633804.1, AA595370.1, AA576672.1, T99365.1, T52366.1, T40388.1, AW419288.1, AI702018.1, AA573351.1, AA526529.1, N72195.1, T71936.1, AI791664.1, AI654336.1, AA348890.1, AI809776.1, AA287363.1, AA569648.1, AA230203.1, AA419403.1, AC027008.2, AL158207.3, AC016109.3, AL138963.4, AC011638.3, AC021211.2, AC021055.6, AC012014.4, AC021026.3, AC018356.7, AC011448.2, AC020561.2, AC023268.2, AP000761.1, AL109932.2, AC044812.2, AC011501.5, AC011495.3, 45 AC021420.3, AC019162.3, AC024944.2, AC026192.1, AC010130.4, AL353653.5, AL133230.19, AC022145.4, AC017008.4, AL136135.2, AC023271.3, AC004085.1, AL354935.3, AC010247.6, AC021971.3, AC009008.2, AL139398.2, AL139109.1, AC068707.2, AC035146.2, AC027342.2, AC008784.5, AC020931.3, AC025163.7, AC008551.3, AC025370.2, AC021469.3, AC009996.3, AC023201.2, AL161787.4, AC008053.2, AC009863.2, AC013421.5, AC009027.4, AC007256.2, AC055774.1, AC007912.4, AC024583.3, AC027474.2, AC024051.3, 50 AC022021.2, AC016124.2, AL138810.6, AL136097.10, AL133446.3, AC024582.3, AC025162.7, AC011498.4, AC011480.2, AC024045.3, AC015945.3, AL161736.5, AL356140.1, AL355978.1, AL110504.2, AP000597.1, AC020558.3, AC021187.4, AC008032.12, AC019131.3, AL158156.3, AL136233.3, AL031711.23, AC027178.3, AC010264.4, AC067910.1, AC027250.2, AC062024.1, AC016385.3, AC005995.2, AL159993.3, AL160171.2, AP001084.2, AC022766.2, AC011511.4, AC011486.5, AC009127.5, AL121914.20, AL161778.2, AP001075.2, 55 AC007616.2, AC068603.1

SEQ ID NO: 386

ZH1373/T3

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-177-

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SEQ ID NO: 387

Novel DNA Binding Protein/SON

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SEQ ID NO: 388

ZH122/T3

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- 45 SEQ ID NO: 389

ZH122/T7

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-178-

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SEQ ID NO: 390

ZH1387/T3

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SEQ ID NO: 391

ZH1387/T7

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SEQ ID NO: 392

Carboxyterminus HSP70 (CHIP)

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SEQ ID NO: 393

ZH037/T3

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ZH037/T7

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ZH054/T3

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ZH054/T7

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SEQ ID NO: 397

ZH115/T3

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SEQ ID NO: 398

ZH115/T7

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SEQ ID NO: 399

ZH1254/T3

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-181-

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ZH148/T7

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ZH119/T3

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-185-

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ZH119/T7

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Zinc finger DNA binding Protein 89 kDa

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SEQ ID NO: 421

ZH016/T3

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SEQ ID NO:422

ZH016/T7

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ZH032/T3

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ZH032/T7

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ZH036/T3

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SEQ ID NO:427

5 ZH0610/T7

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ZH067/T3

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35 SEQ ID NO:429

ZH067/T7

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SEQ ID NO: 430

ZH1110/T3

- 10 NM_015642.1, AL050276.1, AF194030.1, AF185576.1, AC008843.5, NM_001166.1, U37547.1, L49431.1, AC011738.4, NM_006585.1, AC006972.2, AC006384.2, AC004828.2, AC007052.4, AF077215.1, AC005144.1, AL163249.2, AL163243.2, AL109752.13, AL031283.26, AJ251713.1, AJ251712.1, AL035415.22, Z68332.1, AL035073.4, AL110503.1, D42052.1, AP001698.1, AP001601.1, D13627.1, AA578163.1, AA069836.1, AW237166.1, H85064.1, AW502748.1, AW611145.1, AW106649.1, AI828036.1, AI221632.1, AA464297.1, AI151799.1, AW729812.1, AW372984.1, AW372983.1, AW235267.1, AI032501.1, AA702174.1, AA354613.1, AA281621.1, AA034048.1, W80497.1, W17275.1, T73134.1, AW731100.1, AW730874.1, AW730644.1, AW730370.1, AW728863.1, AW728739.1, AW728717.1, AW727809.1, AW673083.1, AW618417.1, AW247278.1, AW213355.1, AI648841.1, AA984168.1, AA385412.1, AA347604.1, H88667.1, AC069063.1, AC026560.4, AC027493.2, AC055739.2, AC020896.4, AC063979.1, AC025358.3, AC036131.2, AC041009.1, AC034154.1, AC027790.1, AC012056.3, AC024606.2, AC021712.3, AC022736.2, AL161444.2, AP001959.1, AC046138.4, AC022293.9, AC032022.2, AC068656.1, AC025763.2, AC022894.2, AC025897.2, AC019309.3, AC021754.3, AC011330.5, AC011171.3, AC016135.1, AL136990.14, AP001830.1, AP001167.1, AP000942.2, AC061973.2, AC064862.2, AC040957.2, AC025767.3, AC020930.4, AC008839.4, AC036127.2, AC037456.4, AC022218.4, AC019176.3, AC034167.2, AC026542.2, AC015992.3, AC021506.3, AC021005.2, AC025891.2, AC011853.3, AC011848.5, AC012571.3, AC025009.2, AC009899.5, AC020565.4, AC011642.5, AC025346.1, AC021141.2, AC015950.2, AC017056.3, AC021047.2, AC019648.1, AC007432.7, AC009437.1, AF129075.1, AL356137.2, AL356322.1, AL162716.4, AL109751.18, AL160265.4, AL137144.4, AL355386.1, AL354778.1, AL137074.4, AL157365.3, AP002083.1, AP002013.1, AP001841.1, AP001569.1, AP001365.1, AP001356.1,
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30 SEQ ID NO: 431

ZH1110/T7

- 35 NM_015642.1, AL050276.1, AF194030.1, AF185576.1, AC008372.6, AC005874.3, AC007766.1, AF134471.1, D88148.1, AE003835.1, AC007225.2, AC005214.1, AL133258.16, AL163225.2, AL034559.3, AP001680.1, AP001138.2, AA834935.1, AW293260.1, AI798849.1, AI240155.1, AA083812.1, N26227.1, AI809178.1, AA930334.1, AA828063.1, AA943003.1, AW108541.1, AI551088.1, AI626969.1, N71750.1, AI445139.1, N99462.1, AV028027.1, AI809910.1, AA613636.1, AV137484.1, AV329304.1, AV330564.1, AV329353.1, AI610886.1, TI2777.1, AW115543.1, R93225.1, H02904.1, AW772943.1, AW601219.1, AW483664.1, AW250685.1, AW249227.1, C77465.1, AC068938.1, AC068072.7, AC025676.2, AC021032.3, AC068659.1, AC036186.2, AC010287.5, AC009164.3, AC009130.5, AC009093.5, AC008758.3, AC027250.2, AC024721.4, AC007615.3, AC021792.2, AC025394.2, AC012111.3, AC009270.2, AC015958.3, AC017038.5, AC023980.2, AC010583.3, AC022023.2, AC018792.2, AC011279.1, AL157833.5, AL136172.14, AL355594.3, AL135903.2, AL033383.25, AL158014.4, AL160280.2, AL157827.3, AL137848.1, AL138831.2, AL157883.2, AL136309.3, AL133461.2, AP001780.1, AP000853.1, AP000580.2, AC012520.8, AC046140.4, AC026763.5, AC048337.4, AC067852.1, AC027810.2, AC021443.5, AC022715.2, AC021369.3, AC025311.2, AC019313.3, AC024619.2, AC010687.2, AC020372.1, AC012281.1, AC007896.1, AP000874.1, AP000562.2,
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ZH118/T3

- 50 NM_001278.1, AF080157.1, AF009225.1, AF012890.1, U22512.1, NM_007700.1, U12473.1, AC012147.7, AE003769.1, AF227841.1, AC009888.1, AL132641.2, AL049775.2, AL132986.2, AF127936.2, AC010685.3, AC006730.1, AE003493.1, AC009464.7, AC007377.3, AF130351.1, AC007785.1, AL355094.2, AL163257.2, AL163207.2, AL132853.1, AL121808.2, AL135745.2, AL121774.3, AL031768.9, AL096710.8, AL078473.2, U29521.1, U29450.1, AP001712.1, AP000213.1, AP000031.1, AP000255.1, AP000135.1, AW611010.1, AW822592.1, AA512576.1, AW159773.1, AW159133.1, AA721189.1, AV400040.1, AI553167.1, AU004118.1, AA518188.1, AA109551.1, R03450.1, AW769650.1, AW497368.1, AW496881.1, AW485684.1, AW344422.1, AT001962.1, AI241905.1, AI200843.1, AI037034.1, AA704752.1, AA660505.1, AC018783.3, AL138921.6, AC026883.2, AL158168.5, AC018351.8, AC015797.2, AC027704.2, AC027438.2, AC024130.3, AC012204.3, AL050344.25, AL355517.2, AP001963.1, AP001816.1, AC041002.1, AC011259.3, AC021846.3, AC012202.2, AC002489.1, AL133313.1, AC016962.8, AC061978.2, AC026270.2, AC068854.1, AC068368.1, AC024134.2, AC025661.2, AC010941.3, AC013497.4, AC021403.4, AC011755.3, AC022238.1, AC010129.2, AC013189.1, AC004071.1, AL353645.2, AL139216.4, AL136362.2, AL356094.1, AL353764.1, AL139020.1,
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ZH118/T7

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ZH1214/T3

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ZH1214/T7

40 X92474.1, D43948.1, AJ251130.1, AF061744.1, AF001863.1, AF102850.1, U48696.1, AF045432.1, AJ243486.1, Y16849.1, AJ243656.1, U39066.1, U37573.1, Y16299.1, X99058.1, X99060.1, X99051.1, X99057.1, X99056.1, X99052.1, Z97178.1, Y16851.1, AF033096.1, U48697.1, AF011573.1, X99055.1, AJ270223.1, X99054.1, X99053.1, AF128444.1, Y17148.1, Y07542.1, AF224771.1, AF184239.1, U23715.1, AL161559.2, AL031326.1, AC000095.3, AC002522.2, AC004461.3, L77570.1, AL031430.1, AL109939.13, AC000121.1, AF146603.1, AE003700.1, AC000092.1, AC004099.1, AC004231.1, U82964.1, AL031277.1, U30368.1, X73502.1, X73501.1, AW374979.1, R14180.1, 45 AW407477.1, AW176568.1, AW239387.1, W27586.1, AA805103.1, AA767900.1, Z20910.1, AA094395.1, AA568734.1, AA299590.1, Z19789.1, AJ396976.1, AW409741.1, AI857031.1, AI857046.1, AI816693.1, AI816668.1, AI816651.1, AI815345.1, AI816702.1, AI816701.1, AI816700.1, AI816699.1, AI816697.1, AI816696.1, AI816695.1, AI816694.1, AI816692.1, AI816690.1, AI816689.1, AI816688.1, AI816667.1, AI816664.1, AI816663.1, AI816662.1, AI816661.1, AI816660.1, AI816659.1, AI816658.1, AI816657.1, AI816656.1, AI816655.1, AI816654.1, AI816653.1, AI816652.1, 50 AI816650.1, AI816649.1, AI816648.1, AI816647.1, AI816646.1, AI816645.1, AI816644.1, AI816643.1, AI816641.1, AI816640.1, AI816639.1, AI816638.1, AI815377.1, AI815376.1, AI815375.1, AI815374.1, AI815373.1, AI815371.1, AI815370.1, AI815369.1, AI815368.1, AI815367.1, AI815366.1, AI815365.1, AI815363.1, AI815362.1, AI815361.1, AI815360.1, AI815347.1, AI815344.1, AI815343.1, AI657485.1, AA933356.1, AA933350.1, AA933216.1, AA933125.1, AA933095.1, AA933094.1, AA660699.1, N83963.1, AI815364.1, AI816698.1, AI816642.1, AI446849.1, AI353568.1, 55 AA933275.1, AA933111.1, AA933353.1, AA933184.1, AW455598.1, AI617314.1, AI354018.1, AI353756.1, AC012054.1, AC018448.8, AC041023.2, AC068800.3, AC009452.9, AC026031.3, AC024663.3, AC068617.1, AC026659.3, AC027191.2, AC027065.2, AC025309.2, AC026522.1, AC024628.2, AC010187.6, AC023800.3, AC017028.5, AC068493.3, AC037481.2, AC023859.2, AC022133.3, AC010218.4, AC008680.3, AC008665.3, AC011500.5, AC027735.2, AC009786.2, AC026990.2, AC025484.2, AC022357.3, AC022705.3, AC011226.3, AC011795.4, 60 AC017007.5, AC020586.2, AC015529.3, AC021694.2, AC013786.2, AC016820.2, AC022281.1, AC014336.1, AC016381.1, AL137003.2, AL159970.7, AL138890.3, AL139004.3, AL355839.1, AL355497.1, AL161447.4, AL138795.1, AP001947.1, AP000812.1, AP000665.1,

SEQ ID NO:436

ZH1217/T7

- 5 M14660.1, AC006437.4, AC006560.8, AF091596.1, AC000348.2, AC016951.9, AC010252.3, AC008854.3, AC007878.2, AC007178.5, AE003561.1, AC006024.1, AC007463.3, AC002330.1, AF131858.1, AC004352.1, AC001645.1, AL161541.2, AF000198.1, AL138649.1, Z70756.1, AL132965.1, AL049745.9, Z97338.2, U00063.1, AK001541.1, AK001417.1, AP000386.1, AP000373.1, AB016873.1, AB012244.1, AC005155.1, AC007200.1, AC006952.6, AC005610.1, AL096712.20, Y17293.1, AP000884.1, AA131041.1, AI458848.1, AI740602.1, AI140291.1, AI620542.1, AI338018.1, N63988.1, AI373569.1, AI446658.1, N51262.1, AA975115.1, AA134105.1, AA810945.1, AA854597.1, AW337373.1, AA056431.1, AI301531.1, AI261334.1, AA866128.1, AW272913.1, AI469715.1, AI080333.1, AA976884.1, AI770049.1, AA516150.1, AA484050.1, AA130252.1, AA765174.1, AI924290.1, AA811287.1, AV383770.1, 10 AW232841.1, AW190734.1, AW725886.1, AA847944.1, AA188141.1, R84767.1, AW623261.1, AW443728.1, AW316855.1, AW241933.1, AW034720.1, AI985531.1, AI978628.1, AI956080.1, AI897778.1, AL043557.1, AL043510.1, AI698209.1, AI679174.1, AI611067.1, AI572570.1, AI570861.1, AI552591.1, AI527468.1, AA875645.1, AI367193.1, AI263737.1, AI247560.1, AI168145.1, AI120817.1, AI040092.1, AA780998.1, AA725576.1, AA723350.1, AA652386.1, AA493515.1, AA486562.1, AA316491.1, AA040803.1, W23971.1, W05624.1, N58119.1, N38766.1, H85097.1, H39883.1, 15 AL353751.3, AC021882.3, AL136526.15, AC068012.1, AC018910.4, AL021148.1, AC021057.4, AC051628.10, AC008613.4, AC009196.11, AC010816.3, AC010949.2, AC008677.4, AC062038.1, AC068395.1, AC027463.2, AC012221.3, AC027078.2, AL162501.2, AP001531.1, AP000920.1,

SEQ ID NO:437

- 20 ZH1217/T3
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SEQ ID NO: 438

- 45 ZH1222/T3
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SEQ ID NO: 439

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- 5 Z99129.1, NM_004506.2, M65217.1, NM_008297.1, AF045627.1, X61754.1, AF172640.1, AL163912.1, Z68160.1, L41499.1, U40424.1, D17366.1, AC011809.2, AC008126.9, AC000104.1, AL133216.10, Z92844.1, AC002329.2, AE003811.1, AE003525.1, AE003517.1, AE003486.1, AE002786.1, AC018748.3, AF102707.1, Z83318.1, AI923911.1, AI990935.1, AI203377.1, AI056677.1, AW269952.1, AI989487.1, AI472020.1, AI524322.1, AI700694.1, AI561266.1, AI979106.1, AW008963.1, AW468756.1, AW183922.1, AI688920.1, AA905319.1, AI690727.1, AA707596.1, AI499774.1, AA551748.1, AA551757.1, AI536850.1, AA969316.1, AI480249.1, AA253434.1, AA832045.1, AI270358.1, AI810705.1, AI433107.1, AA651949.1, AA969392.1, N39221.1, AA868883.1, AI142644.1, AL035757.1, AA136344.1, AI453040.1, AA860985.1, AA913304.1, AA913486.1, AW468554.1, R39144.1, AA815117.1, AI473089.1, H24055.1, AI539466.1, AA971072.1, T53314.1, H72024.1, R46149.1, D53854.1, D52415.1, AW028964.1, H72025.1, AA250730.1, D52616.1, D52419.1, H14792.1, F04785.1, T29491.1, N46665.1, C20787.1, T53313.1, AW142847.1, AI740594.1, AI230246.1, AI167251.1, AA944812.1, AI661205.1, AA268498.1, AV259149.1, AA832774.1, AI962803.1, AI556468.1, AA818911.1, AI170959.1, AI010919.1, AI102092.1, AL121954.4, AL109916.3, AC027000.2, AC068022.1, AC027082.2, AC024345.2, AL049180.3, AC011602.6, AC027648.6, AC025854.2, AC027355.1, AC022387.2, AC022480.4, AC025302.2, AC009754.3, AC009816.5, AC024260.1, AC011683.3, AC010660.4, AL121954.4, AL109916.3, AC027000.2, AC068022.1, AC027082.2, AC024345.2, AL049180.3, AC011602.6, AC027648.6, AC025854.2, AC027355.1, AC022387.2, AC022480.4, AC025302.2, AC009754.3, AC009816.5, AC024260.1, AC011683.3, AC010660.4

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- 25 AB006198.1, Y14314.1, AB014722.1, AB014721.1, AF129931.1, AF147725.1, AC007915.3, AF028338.1, L20095.1, L20680.1, NM_015933.1, AC011462.4, AE003765.1, AC000029.17, AF161448.1, AF077202.1, U39402.1, AC004196.1, U67478.1, AL163816.1, Z97832.11, AL049853.1, AL112418.1, AL021930.1, L09190.1, AK001152.1, AB023212.1, M15100.1, AB017022.1, W27222.1, AW402760.1, AL047890.1, AI594593.1, AW820827.1, AA607769.1, AI120962.1, AI509410.1, AI908693.1, AW393484.1, AW652595.1, AI964608.1, AA979854.1, AA979772.1, AI661459.1, AI642054.1, AJ228935.1, AA751847.1, AW758324.1, AI827037.1, AV417239.1, AW674436.1, AW615491.1, AW245981.1, AW074946.1, AW006944.1, AI924762.1, AI880663.1, AI880658.1, AI709253.1, AI708293.1, AI708235.1, F33596.1, F30411.1, F28809.1, F28190.1, F27897.1, AI666115.1, AI570650.1, AI459983.1, AI418553.1, AI370584.1, AI364309.1, AI339191.1, AI333234.1, AI290693.1, AI090805.1, AA910393.1, AA563619.1, AA364686.1, AA321138.1, AA280277.1, AA279851.1, AA229404.1, AA151350.1, AA149268.1, AA134303.1, AA082333.1, AA046848.1, AA026455.1, W95678.1, W76586.1, W51757.1, W04465.1, N84053.1, N80509.1, N78206.1, N76058.1, R07233.1, T91349.1, T80989.1, AP001201.4, AP000592.2, AP001191.1, AP000586.2, AC008683.4, AC018996.3, AC046141.3, AC068951.1, AC022120.4, AC008405.3, AC008658.2, AC011069.6, AC013189.1, AC055744.2, AC068667.3, AC027309.2, AC027307.3, AC022091.3, AC010377.4, AC008453.4, AC008450.3, AC064317.1, AC064056.1, AC052499.1, AC044355.1, AC045178.1, AC041917.1, AC040463.1, AC034640.1, AC028038.1, AC021328.3, AC021286.3, AC007903.2, AC026184.1, AC019127.4, AC018734.2, AC011233.2, AC023950.2, AC010899.3, AC015903.1, AC014411.1, AC018045.1, AC006579.3, AL136136.2, AL136119.3, AL109955.13, AL135939.9, AL133282.13, AL133284.12, AL032818.2

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ZHI235/T3

- 45 AJ236885.1, L04282.1, AF039019.1, U30381.1, NM_011749.1, X98096.1, AJ001165.1, U80078.1, AL133244.1, AL121656.2, AC008125.9, AL049648.6, AC007444.1, AE003754.1, AC005552.1, AJ006687.1, AL038916.1, AI158501.1, AA967471.1, AW261045.1, AW425025.1, AI093969.1, AW667700.1, AW619431.1, AW619430.1, AW359900.1, AA911993.1, D86150.1, AC019289.3, AC032043.1, AC026618.1, AC020598.3, AC019180.4, AC009770.4, AC023077.3, AC040911.1, AC034145.1, AC023199.2, AC027362.1, AC026243.2, AL139189.4, AL354939.3, AL354985.2, AC069141.1, AC020609.4, AC016965.6, AC019074.3, AC026116.7, AC026441.2, AC024588.2, AC022113.4, AC016648.4, AC010308.4, AC022554.2, AC023560.2, AC021219.2, AC020787.2, AC007825.5, AC012075.3, AC016484.1, AC016965.5, AC019694.1, AC010120.4, AC012550.1, AL353575.3, AP001972.1

55 SEQ ID NO: 442

ZHI235/T7

- 60 AF039019.1, AJ236885.1, U30381.1, NM_011749.1, U80078.1, X98096.1, AJ001165.1, U96633.1, L04282.1, AE003673.1, AF214658.1, AE001574.1, AC005379.1, AC002512.1, AC005817.7, AC004005.2, AC003063.7, AF181967.1, U90222.1, AF113957.1, AC004189.1, U97191.1, Z81052.1, AJ245414.1, AJ012638.1, AJ012636.1, AP000517.1, AB023055.1, AB023054.1, AI263859.1, AA563588.1, AI056295.1, AA287619.1, AI743361.1, AW779476.1, AI384073.1, AI382374.1, AW051393.1, AA613057.1, AA943882.1, AI848462.1, AI323627.1, AW272463.1, AW772534.1, H12745.1, AW823563.1, AA110786.1, AI467973.1, AI283469.1, AI077636.1, AI003273.1, AA622568.1, AA552124.1, AA192099.1, AW732203.1, AI955302.1, AI955293.1, AI696880.1, AI283452.1, H70711.1, AA764105.1, AI393951.1, H12746.1, AI864852.1, AW214414.1, AI589987.1, AA631115.1, C06563.1, AI202723.1, AI030160.1,

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SEQ ID NO: 443

10 ZH1239/T3

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SEQ ID NO: 444

ZH1239/T7

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SEQ ID NO: 445

ZH1246/T3

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SEQ ID NO: 446

15 ZH1246/T7
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-197-

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5 SEQ ID NO:449

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SEQ ID NO: 451

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SEQ ID NO: 453

45 ZH1275/T3
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- 5 NM_005271.1, X07769.1, X07674.1, M20867.1, M37154.1, X66312.1, J03248.1, AC006144.1, X66310.1, U08997.1, X67491.1, X66314.1, AF086070.1, NM_012570.1, NM_008133.1, X14223.1, X14044.1, X57024.1, AL021396.5, AC004944.1, AE003805.1, AC011198.2, AE001699.1, AC004335.1, X92729.1, AW008481.1, AW161914.1, AL121462.1, AI796326.1, AI767015.1, AI719871.1, AI688677.1, AI685203.1, AI683603.1, AI609634.1, AW152299.1, AW778779.1, AI936502.1, AI924085.1, AI870436.1, AI220414.1, AI017359.1, AI860803.1, AI818481.1, AI373143.1, AI476186.1, 10 AI432139.1, AI434555.1, AI052741.1, AW779007.1, AI453009.1, AA705949.1, AA612700.1, AA576729.1, AI346963.1, AA719691.1, AW440634.1, AW299819.1, AI953347.1, AI669386.1, AW316988.1, AA579763.1, AI479598.1, AI041934.1, AI865818.1, AA931220.1, AA639014.1, AW469758.1, AW105271.1, AI039164.1, AI628503.1, AI547078.1, AI580269.1, AW131820.1, AI955767.1, AI768285.1, N55432.1, AW662165.1, AI949911.1, AA968749.1, AI948510.1, H23769.1, AA205716.1, AA622009.1, AI766220.1, AI628736.1, AA961548.1, W32185.1, N58794.1, AA603980.1, 15 AI200249.1, AI433759.1, AI799717.1, AA227280.1, AW206141.1, AA507097.1, AI871324.1, AI220678.1, D19635.1, AA506817.1, AI023057.1, AI167726.1, AA984899.1, H22628.1, AL119832.1, AI590208.1, AA995612.1, T29318.1, H52944.1, AI220953.1, N62651.1, AI104010.1, AA932126.1, AW614089.1, AA352492.1, AI942453.1, H57922.1, AA541774.1, AI424426.1, R54424.1, W69491.1, AA934829.1, AW779733.1, AI932689.1, AI582068.1, AL136982.1, AL161935.5, AP001776.1, AL163534.3, AC021193.3, AC023150.2, AC007117.1, AL137063.5, AL160158.2, 20 AC025731.7, AC040988.2, AC063968.1, AC010902.3, AC022833.2, AC025924.2, AC021450.3, AC011791.3, AC016365.4, AC016802.5, AC021761.3, AC023482.2, AC016991.2, AC020959.1, AC020024.1, AC018408.1, AL160162.4, AL136088.2, AL133269.8, AL355140.2, AL354743.1

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25 ZH1278/T3

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50 SEQ ID NO:456

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- NM_003011.1, M93651.1, D45198.1, AC005666.1, X75091.1, Z95126.1, AC008865.3, U51924.1, AL121985.13, AC007649.12, AC004106.1, Y16709.1, Y16700.1, Y16698.1, AL049776.3, AC016940.7, AC016939.8, S68987.1, S68589.1, U66083.1, U69568.1, AC002385.1, AC004816.1, AC002126.1, AC000055.1, AC007277.2, AL163491.1, 55 Z86062.1, AB022692.1, AW868532.1, AW780330.1, AW591220.1, AW513750.1, AW293933.1, AW245056.1, AW244076.1, AW168969.1, AW090022.1, AW083629.1, AW044189.1, AW007774.1, AI968676.1, AI950006.1, AI936602.1, AI924906.1, AL037448.1, AI753576.1, AI654239.1, AI580115.1, AI564211.1, AI524784.1, AI355458.1, AI325543.1, AI311829.1, AI309210.1, AI276264.1, AI272933.1, AI253373.1, AI208354.1, AI161319.1, AI160942.1, AI143855.1, AI123422.1, AI056850.1, AI032559.1, AI024969.1, AA989168.1, AA989103.1, AA953828.1, AA781061.1, 60 AA721786.1, AA716380.1, AA716371.1, AA694154.1, AA669764.1, AA644321.1, AA641186.1, AA634951.1, AA634910.1, AA634838.1, AA630300.1, AA583450.1, AA577550.1, AA479216.1, AA450173.1, AA450108.1, AA371437.1, AA314939.1, AA309906.1, AA309718.1, AA223348.1, AA206857.1, AA179301.1, AA160127.1, AA062923.1, W26593.1, N67146.1, N41803.1, N32850.1, D29035.1, AA369866.1, AA074909.1, AW732805.1, AL037182.3, AA917780.1, AA669856.1, AA478675.1, AA848156.1, AA363086.1, AA206002.1, AA063530.1,

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- 10 SEQ ID NO:457
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- 40 SEQ ID NO: 459
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ZH1285/T7

- 5 AF040964.1, Z49250.1, Z83850.1, AE001145.1, AF191070.1, AC009248.6, AF016450.2, U49830.1, NM_014386.1, AF182034.1, AC024869.1, AC020647.9, AF118125.1, AC007232.5, AF130342.1, AL035464.20, AL080238.9, AL034427.1, AP000561.1, AI808442.1, AA664012.1, AI628516.1, AA630380.1, AW043655.1, R69790.1, AW513701.1, H56500.1, R69789.1, H56688.1, Z21088.1, AA652148.1, AW610692.1, AW553895.1, AI451124.1, C80481.1, AI462312.1, C85371.1, AI591821.1, AI604189.1, AA177891.1, AI449315.1, AW554802.1, U83055.1, AV314215.1, H61855.1, AV207115.1, AV295151.1, AV368467.1, AV214236.1, AV295152.1, AV257539.1, AV295169.1, AV367514.1, D29398.1, AA183653.1, AW681938.1, AW046876.1, AV145607.1, AA210324.1, AA174896.1, AA332492.1, 10 AW414996.1, AW339249.1, AW335085.1, AW158276.1, AV385524.1, AL037685.2, AV183523.1, AV178057.1, AI807819.1, AI696097.1, AI626600.1, AI544578.1, AI477034.1, AA980276.1, AA928231.1, C65891.1, C61074.1, C53590.1, AA279783.1, C10643.1, AL158068.4, AC026977.2, AC019140.3, AC040892.1, AL133373.1, AC010302.3, AC009795.3, AC013807.3, AC027533.1, AC012056.3, AC006906.2, AL133326.8, Z82209.1, AP001257.1, AP001181.1, AP000726.2, AC036220.2, AC025435.3, AC010314.4, AC009436.2, AC034172.2, AC025660.2, AC012528.2, 15 AC009957.5, AL353739.2

SEQ ID NO: 461

ZH1286/T3

- 20 AL117590.1, AC007245.3, AC003683.1, AL355072.2, AE003652.1, AC005120.1, AC006214.1, AL161550.2, AL021687.1, AC007063.5, AC004535.1, AC013453.1, AC004752.1, AL049777.5, AL096862.18, AF000265.1, AL132764.1, Z70205.1, AP000139.1, AP000226.1, AP000087.1, D85389.1, AC005970.2, AC021640.5, AC006287.1, AE001368.1, AC004629.1, AL163232.2, AL049860.8, AL031177.1, AL031733.3, AL031600.4, Z82195.1, AL031653.5, AP001687.1, AA175375.1, AI740728.1, AA332493.1, AI074062.1, AI580915.1, AI087846.1, AI810796.1, AW874606.1, AI016838.1, AA470819.1, W85623.1, W85600.1, AI449083.1, AI549242.1, AI845400.1, AV015395.1, AV375672.1, 25 AV327111.1, AV354227.1, AI383006.1, AV300969.1, AV253424.1, AI604667.1, AA771574.1, AV376539.1, AW332467.1, AW642408.1, AW636829.1, AW635398.1, AW634742.1, AW634652.1, AI467036.1, AA285835.1, AL135649.1, AV377755.1, AI915385.1, AV064014.1, AV062554.1, AA808321.1, AA525659.1, AA458724.1, AA232022.1, AA118229.1, R12836.1, T37449.1, AC034212.3, AC022121.3, AC008522.4, AC008531.2, AC011129.3, AC025069.3, AC021824.2, AC023528.3, AC020916.4, AC023808.3, AC004689.5, AL354852.3, AC036175.2, 30 AC019106.2, AC019274.3, AC015595.3, AC006280.6, AC022947.2, AC023567.2, AC022977.1, AL137780.2, AL135926.4, AC048385.2, AC016650.4, AC032009.2, AC005077.2, AC027637.2, AC015497.3, AC021515.3, AC025385.2, AC019328.4, AC021562.3, AL354805.2, AL139284.3, AL355811.2, AL031749.7

SEQ ID NO: 462

ZH1286/T7

- 35 AC007190.4, AC005698.1, AL163244.2, AP001699.1, AP001604.1, X89454.1, X95537.1, X99111.1, AF241733.1, AE003837.1, NM_010743.1, AC004240.1, AC005483.1, AC005017.1, AC010675.4, AC012561.2, AC005430.1, AF022978.1, AC005209.1, AF027390.1, AC002368.1, AL121841.5, AL133239.2, AL031856.1, Z81519.1, X65721.1, X60184.1, D26185.1, L16865.1, AB015478.1, M24843.1, Z99124.1, N78373.1, AA046865.1, AI074753.1, W23958.1, 40 W58729.1, AI570623.1, AA662071.1, AI283307.1, N24666.1, AI042238.1, AI871705.1, AI308931.1, N29591.1, N35457.1, AA121714.1, N35732.1, AA662105.1, AI077613.1, C02199.1, N94508.1, AW193423.1, AW137463.1, AW087689.1, AI932544.1, AI023068.1, AI016553.1, AA668903.1, AA603930.1, AA569968.1, W81286.1, W45153.1, AI077894.1, AW316941.1, AA046618.1, AI468297.1, AI468375.1, AI952677.1, AA534051.1, AV339939.1, AI136305.1, AA801116.1, AA801115.1, AW488840.1, AV326475.1, AV307940.1, W80228.1, AI407687.1, AW392276.1, 45 AV313326.1, AV338001.1, AV327247.1, AV220383.1, Z98519.1, AV327255.1, AV235696.1, W45104.1, AV353938.1, AV221367.1, AA472496.1, AV174463.1, AV344161.1, AV340653.1, AV229817.1, AI615511.1, AV343186.1, AV341443.1, AA561896.1, AA240049.1, AI099985.1, W43492.1, AV008073.1, AC034212.3, AC022121.3, AC008522.4, AC008531.2, AC009423.2, AL157399.2, AC018905.3, AC025281.2, AC009024.5, AC010086.3, AC034141.2, AC024681.2, AC024087.3, AC018732.5, AC022568.3, AC023249.1, AC022030.1, AC021343.1, AC009454.1, 50 AP001120.1, AC015547.5, AC063918.4, AC022275.9, AC010275.4, AC009579.3, AC027256.2, AC016073.2, AC024714.4, AC009504.3, AC018970.4, AC008709.2, AC019358.3, AC018541.3, AC013744.3, AC022913.3, AC022695.3, AC015956.3, AC020706.3, AC021955.2, AC022694.2, AC019068.3, AC020392.1, AC005415.6, AC007139.1, AL157413.7, AL138710.3, AL355887.1, AL356032.1, AL133474.8, AL121890.19, AL021152.1, AL157696.2, AP001655.1, AP001654.1, AP001381.1, AP000902.2

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SEQ ID NO: 463

ZH1288/T3

- 60 X68060.1, M27504.1, X86455.1, X86456.1, NM_009409.1, D38046.1, AB007446.1, AF087149.1, Z15115.1, AB007445.2, AB009387.1, Z19552.1, Z46372.1, L04607.1, Y16594.1, Y16595.1, NM_011623.1, D12513.1, NM_001067.1, J04088.1, AF071740.1, AJ011745.1, AJ011746.1, AF013277.1, AF087148.1, Z49069.1, M13814.1, Z94277.1, Y14559.1, AJ238786.1, Z71364.1, X89016.1, L21015.1, D82024.1, NC_001224.1, AC004622.1, AL135749.2, AJ011856.1, V00700.1, L36900.1, K00384.1, J01462.1, K01981.1, M35613.1, NM_014920.1, AF106577.2, AC005413.1, AL136296.2, Z81521.1, Z81117.1, Z30974.1, AB023153.1, X79345.1, AC008166.2, AF016677.1, AC007685.2, AF125956.1, AC004210.1, U67558.1, AL035078.32, AL134583.1, AW502948.1, D56256.1, AI649350.1, AL041840.1, AI648781.1,

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10 ZH1288/T7

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30 SEQ ID NO: 465

ZH1308/T3

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45 SEQ ID NO: 466

ZH1308/T7

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5

SEQ ID NO: 467

ZHI310/T3

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20

SEQ ID NO: 468

ZHI310/T7

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35

SEQ ID NO: 469

ZHI3310/T3

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55

60 SEQ ID NO: 470

ZHI3301/T7

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ZHI342/T7

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SEQ ID NO: 477

ZH1349/T7

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SEQ ID NO: 478

ZH135/T3

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SEQ ID NO: 479

ZH135/T7

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-207-

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SEQ ID NO: 480

ZHI377/T3

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SEQ ID NO: 481

ZHI377/T7

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SEQ ID NO: 482

ZHI381/T3

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SEQ ID NO: 483

ZH1381/T7

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SEQ ID NO: 484

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SEQ ID NO: 485

ZH1291/T3

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ZH1291/T7

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-211-

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SEQ ID NO: 490

50 ZH057/T3
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-212-

SEQ ID NO: 491

ZH057/T7

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ZH1276/T3

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45 SEQ ID NO: 493

ZH176/T3

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SEQ ID NO: 494

ZH176/T7

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SEQ ID NO:495

ZH183/T3

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SEQ ID NO:496

40 Liprins, Tyrosine Phosphatase-Interacting Protein

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SEQ ID NO:497

ZH1213/T3

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SEQ ID NO: 498

ZH1213/T7

- 5 AK000348.1, NC_001807.2, J01415.1, X93334.1, V00710.1, V00662.1, X62996.1, D38112.1, D50525.1, AB004064.1, NC_001643.1, D38113.1, X93335.1, NC_001644.1, D38116.1, X99189.1, NC_001645.1, D38114.1, X93347.1, NC_002083.1, X97707.1, NC_001646.1, D38115.1, NC_002082.1, X99256.1, AF058292.1, AF176066.1, AF004338.1, Z54552.1, Z54553.1, Z60381.1, U63507.1, U63506.1, U63505.1, U63486.1, NC_001992.1, Y18001.1, Z62861.1, Z62860.1, U63488.1, U63487.1, Z62093.1, Z57443.1, M86498.1, NC_001567.1, J01394.1, U39004.1, V00654.1, AB033608.1, Z65548.1, NC_001700.1, U20753.1, S75063.1, M86495.1, NC_001601.1, NC_001321.1, X72204.1, 10 X61145.1, M86501.1, NC_001941.1, AF010406.1, M86499.1, M35875.1, NC_001779.1, X97336.1, AJ010814.1, M55539.1, AJ010816.1, AJ010815.1, NC_001808.1, M35877.1, Y07726.1, AF203744.1, M86497.1, AF203774.1, AF203727.1, U97337.2, NC_001913.1, AF203741.1, AJ001588.1, M55541.1, NC_002391.1, AF203743.1, Y19192.1, AF203742.1, AF069538.1, M86493.1, U97336.2, AF069537.1, AB032843.1, AB032842.1, AF179288.1, M55540.1, U97339.2, U97343.1, AF179290.1, AF203726.1, AJ010812.1, AF069533.1, AJ245896.1, AW603665.1, AJ061586.1, 15 AL047741.1, AJ133246.1, AW601774.1, AI061658.1, AJ110678.1, AW849003.1, AW848377.1, AW848797.1, AW868260.1, AW848724.1, AW848653.1, AW848366.1, AI499067.1, AW848373.1, AW848226.1, AW848180.1, AW607912.1, AW837520.1, AW835394.1, AW848445.1, AW848175.1, AW867448.1, AW848368.1, AJ114451.1, AW848376.1, AW835382.1, AW161643.1, AW837509.1, AW578366.1, AA219735.1, AW867405.1, AW578361.1, AL037474.2, AW842623.1, AW157026.1, AJ983822.1, AA196173.1, AA099002.1, AA469432.1, AW867402.1, 20 AW578374.1, AA088843.1, AI525751.1, AW848920.1, AW607758.1, AW058235.1, AW837514.1, AI057519.1, AA814643.1, AA220989.1, AI961435.1, AI525710.1, AA100034.1, AW601494.1, AW842070.1, AI955201.1, AI889478.1, AW168799.1, AW864632.1, AI133661.1, AA574454.1, AA083209.1, AA776938.1, AW835463.1, AI921008.1, AI192705.1, Z98526.1, AA179899.1, AI683759.1, AW578372.1, AI983554.1, AI983243.1, AI683947.1, AI525757.1, AA467764.1, AW801146.1, AA225870.1, AW577755.1, AI557286.1, AA223928.1, AW604355.1, AI954959.1, 25 AW602132.1, AW074139.1, AI687413.1, AW839594.1, AI922568.1, AA668465.1, AW607161.1, AI961417.1, AI858348.1, AI814152.1, AI444594.1, AW848995.1, AA468311.1, AI829389.1, AA747096.1, AA469385.1, AC068619.1, AC021914.3, AL158819.2, AL135939.9, AC015935.4, AC022317.4, AC067925.1, AC021473.3, AL161450.4, AC025380.2, AC012365.3, AC018441.3, AC027019.2, AC021451.2, AC021835.3, AC024498.2, AC025283.1, AL356135.2, AL353646.1, AC023928.3, AF182108.1, AL139000.2, AC025337.1, AC024248.3, AC011954.5, 30 AC011025.4, AP001947.1, AL121927.18, AC007400.2, AC025936.2, AC058808.1, AC051663.4, AC025731.7, AL354955.1, AC024033.2, AC027175.2, AC010270.4, AC068621.1, AC009796.3, AC027008.2, AL158207.3, AC011821.4, AC013297.4, AC016052.2, AC026968.2, AL353147.3, AC018463.4, AC027413.2, AC026993.2, AC024953.3, AC019304.3, AC026519.1, AC022206.2, AL109955.13, AP001026.1, AP000919.2, AC019074.3, AC053543.3, AC026743.3, AC010496.4, AC027496.2, AC005140.6, AF202964.1, AC005139.3, AL158067.5, AL355432.1

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HI292/T3

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ZH140/T3

-216-

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ZH023/T3

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ZH023/T7

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SEQ ID NO: 506

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ZH042/T7

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SEQ ID NO: 508

ZH1347/T3

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-218-

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ZH12110/T7

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ZH13410/T3

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ZH141/T3

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-220-

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ZH072/T7

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5

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30

SEQ ID NO: 523

ZH034/T7

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55

SEQ ID NO: 524

ZH1312/T3

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ZH1312/T7

- 20 NM_003201.1, M62810.1, AL034386.2, AC009079.4, AC004695.1, AL022239.1, U91323.1, AL163304.2, AL031012.1, AP001759.1, AC008873.4, AC022073.13, AC007970.3, AL121586.28, NM_014362.1, AC009310.3, AE002743.1, AC007917.15, U66669.1, AF013711.1, AF020932.1, U73638.1, Z94044.1, M58484.1, AC006012.2, AC004991.1, AC007568.1, AC007123.1, U14101.1, AL161532.2, AL078606.1, Z93018.1, AL035522.1, AB037120.1, AB037119.1, AB013915.1, AB022126.1, AC011362.2, NC_000895.1, AC009784.2, AC007041.3, AL163216.2, AL163205.2, 25 AL139076.2, Z70311.1, AL031674.1, Z99495.1, Z99708.1, U67917.1, AB000109.1, AP001671.1, AP001660.1, AP001347.1, AI694296.1, AI862124.1, AI394089.1, AI521377.1, AI424979.1, AW663732.1, AW339172.1, AI942242.1, AI800325.1, AI473739.1, AI375299.1, AI357116.1, AI093643.1, AI092542.1, AA814953.1, AA742275.1, AA449118.1, AA316997.1, W93827.1, AA989453.1, AW085117.1, AI810160.1, AI860878.1, AA380917.1, H18451.1, AA779848.1, AA503492.1, AI928504.1, AI480401.1, AA995790.1, AW119042.1, AI261738.1, AI382337.1, AI347250.1, AI769813.1, 30 AA808771.1, AA766240.1, T15871.1, D56945.1, AA705964.1, AI696377.1, AA150777.1, AA554544.1, AW235470.1, AA649140.1, F01619.1, AI478145.1, AW269796.1, AW666007.1, AW085017.1, AI581299.1, AI375548.1, AI374841.1, W93826.1, AA082140.1, D56745.1, T28290.1, AI026148.1, AI761167.1, AI669271.1, AA936191.1, AA828857.1, AI472592.1, AA642393.1, AA669592.1, AA102838.1, AI029587.1, AI411675.1, AI103586.1, AW614668.1, AW614266.1, AW612554.1, AW572783.1, AW270957.1, AW243362.1, AI984813.1, AI823757.1, AI784606.1, AI695241.1, AI691032.1, 35 AI470941.1, AI375081.1, AI287805.1, AI217260.1, AI051344.1, AA888026.1, AA815394.1, AA628961.1, AA190577.1, AV368179.1, AC023170.3, AC011786.5, AC022065.2, AP002006.1, AP001981.1, AL355293.2, AC011389.5, AC009427.2, AC025903.1, AC016800.2, AC011844.3, AC009070.5, AC009305.1, AC022331.5, AF206725.1, AC008972.5, AC008515.5, AC025778.2, AC025277.2, AC027598.1, AC013607.3, AC020960.1, AL354877.2, AP000471.1, AC037443.2, AC067839.1, AL096793.14, AC044902.2, AC067749.2, AC008728.4, AC005079.2, 40 AC010087.3, AC034169.2, AC021523.3, AC004937.1, AI352977.1, AL161665.1, AC018360.8, AC055841.2, AC018700.3, AC031976.3, AC023718.2, AC018860.2, AJ239319.3, AC046198.2, AC036199.2, AC019206.3, AC023137.2, AC040890.1, AC025708.3, AC024411.2, AC019007.3, AC004688.6, AC011566.3, AC023942.2, AC004709.3, AL160261.4, AL161796.3, AL353617.1, AL136298.1

- 45 SEQ ID NO: 526

ZH1386/T3

- NM_014890.1, U53445.1, AC004020.1, AE003832.1, AC012039.10, Z82203.1, X52075.1, M61827.1, AC011456.2, AE003629.1, AC004595.1, AF104477.1, AC005547.1, U60149.1, AF003530.1, AC000403.1, AL079304.2, AL096867.15, Z82268.1, AL049692.13, AJ011002.1, M32612.1, AF166025.1, AF130358.2, AC008166.2, AC004021.1, AC015985.8, 50 AC007560.3, AC004125.1, AC005046.3, U41274.1, AF130342.1, L14323.2, AF112922.1, U85714.1, U85713.1, U85712.1, AF098991.1, M57500.1, U53325.1, AC003070.1, AL163206.2, AL078459.8, AL035458.35, AL021807.1, AL022717.1, Z82899.1, AL096769.7, U64852.1, X15742.1, M26915.1, M20636.1, AB020865.1, M13798.1, M96739.1, AW867011.1, AI642381.1, AW779584.1, AW779590.1, AW779587.1, AA611335.1, C05084.1, AI606223.1, AW779641.1, AV292155.1, AA611336.1, AI549138.1, AI554667.1, AI553756.1, AI402221.1, AI202123.1, AI084203.1, AI614167.1, 55 C55082.1, AA497874.1, AA196522.1, AW871954.1, AW208053.2, AW459498.1, AW439057.1, AV369587.1, AV339384.1, AV259982.1, AV245839.1, AW076711.1, AI733300.1, AI733105.1, AA910905.1, AA623952.1, AA537555.1, AA387953.1, AA386853.1, AA274292.1, H09936.1, AC022883.3, AC024938.7, AC069222.1, AC010324.4, AC009086.4, AC023831.3, AC025231.2, AC007330.5, AC015178.1, AC010696.2, AL161632.4, AL158145.4, AL132989.1, AL157819.2, AC048376.2, AC058820.2, AC022263.4, AC004906.2, AC053533.1, AC027233.2, 60 AC012056.3, AC026536.1, AC023613.1, AC014353.1, U82207.1, AL353632.4, AL136380.2, AL162389.3, AL118524.25, AC055879.2, AF267167.1, AC009794.3, AC013808.3, AC021114.3, AC024353.2, AC017103.3, AL355352.3, AL137016.10, Z82191.1, AP001026.1

SEQ ID NO: 527

ZH1386/T7

- NM_014890.1, U53445.1, L16887.1, AC009294.8, AB005241.1, AE003474.1, AE003418.1, AC004885.2, AC010175.4, AC004061.1, AL031583.2, AF096863.1, AF132287.1, AC022492.5, AE003811.1, AC007843.6, U91323.1, AC007630.3, AF099917.1, AL158088.6, AL034399.6, U49947.1, X95276.1, AJ007556.1, AI435598.1, AI810391.1, AI435391.1, AW303392.1, AI921737.1, AI401231.1, AA576134.1, AI635663.1, AA424880.1, AI016121.1, AW058260.1, AW026643.1, AI817224.1, AI139164.1, AI086061.1, D57964.1, AI185109.1, AA430212.1, AW295168.1, AA973230.1, AA609225.1, AW058427.1, AA857729.1, AI394490.1, AI783720.1, AI378381.1, AI334138.1, AI701330.1, AW083745.1, AI335721.1, AI378578.1, AI431237.1, AI804232.1, W69790.1, AI803115.1, AW118656.1, AA033582.1, AA258605.1, AI013647.1, AW413495.1, AA463851.1, AI371463.1, AA033581.1, AA925088.1, AA795013.1, AA256689.1, AI381752.1, F27521.1, R78245.1, AA568101.1, AA030472.1, D58330.1, D57334.1, AA710489.1, AA241058.1, D57996.1, AA217400.1, AA445957.1, C16405.1, C16415.1, AI473313.1, AW363711.1, AW346548.1, Z21882.1, AA891483.1, F37351.1, AA986888.1, AA432784.1, AA266373.1, AA204051.1, AW582813.1, AI464359.1, AW214616.1, AV234619.1, AV248227.1, T84055.1, AW437163.1, AA170494.1, AW363682.1, AV229961.1, AA255796.1, AA463341.1, AV343730.1, AA515391.1, AA546804.1, AA930120.1, AI181464.1, AA172829.1, AI258437.1, AJ280472.1, AW373694.1, AV203822.1, AA570905.1, D66306.1, AC069222.1, AC022883.3, AC024938.7, AC023911.4, AC012512.2, AC026770.3, AC020685.3, AC025666.2, AC026813.1, AC010014.5, AC014946.1, AC020107.1, AC010015.3, AL354827.1, AC018361.7, AC018473.10, AC044869.2, AC068725.1, AC010628.3, AC068595.1, AC026452.4, AC012321.4, AC009032.5, AC068055.1, AC027301.3, AC021537.3, AC023549.2, AC009635.4, AC012580.3, AC016130.13, AC018432.4, AC024007.2, AC024006.2, AC008342.11, AC018361.6, AC017903.1, AC009598.2, AC008004.4, AC009741.4, AL355315.2, AL356272.1, AL161632.4, AL354710.2, AL354669.1, AL161434.3, AL160274.2, AL158143.1, AL158063.1, AP000904.2, AP001829.1, AP000706.1

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ZH1394/T3

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SEQ ID NO: 529

ZH1394/T7

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60 SEQ ID NO: 530

ZH1401/T3

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- 60 SEQ ID NO: 533
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- 45 SEQ ID NO: 535
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-227-

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SEQ ID NO: 536

ZH167/T7

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SEQ ID NO: 537

ZH181/T3

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ZH181/T7

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ZH182/T3

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ZH182/T7

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ZH189/T3

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35

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60

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-232-

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ZH024/T3

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SEQ ID NO: 550

ZH024/T7

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SEQ ID NO: 551

ZH046/T3

- 40 AL163203.2, AL050302.2, AL049911.2, AP000026.1, AP000025.1, NM_014915.1, AK001137.1, AB028997.1, AC007617.10, AE003447.1, AJ223186.1, AE003494.1, AC004739.1, AC006355.3, AC006045.2, U48386.1, AF044083.1, Z70270.1, AL163224.2, Z74696.1, U41993.1, D82813.1, AP001679.1, AP001506.1, AP000961.2, AC005522.2, AC007379.2, AC006478.2, AC004996.1, AC007099.3, AC005100.2, AC005879.3, AC005331.1, AC005177.1, AC004045.1, Y18930.1, AL133465.30, AL132766.13, AL109985.2, AL022395.2, Z82193.1, AI951118.1, AW000914.1, AI922499.1, AI871874.1, AA991162.1, AU006171.1, AA661357.1, C60377.1, AA471702.1, AA095151.1, AW519678.1, 45 AV282871.1, AI902224.1, AV045752.2, AI311562.1, AI075925.1, AA828186.1, AA701829.1, AC067744.2, AL162272.4, AC007351.16, AC009401.2, AC027141.1, AC024370.2, AC014239.1, AC062032.2, AC036209.2, AC060754.3, AC007131.3, AC061987.1, AC027699.1, AC021187.4, AC013707.2, AC012410.2, AC012542.4, AC012248.2, AC013152.1, AL022284.1, AC062015.2, AC046187.2, AC022418.3, AC008885.3, AC027696.2, AC060232.3, AC004932.2, AC024466.3, AC019259.3, AC016916.4, AC023988.2, AC016444.2, AC005139.3, AL161730.3

50

SEQ ID NO: 552

ZH046/T7

- 55 AL050302.2, AL163203.2, AL049911.2, NM_014915.1, AB028997.1, AF090187.1, AL009051.1, AB011137.2, AL138654.1, AP000365.1, AP000548.1, AC011661.5, AP001302.1, AC004936.2, AC006157.2, Z99291.1, AL031599.1, U40160.1, AC008526.5, AF156143.1, AC009402.3, AC004142.1, AC009513.2, AC006475.3, AC005760.1, AC005358.1, AL161595.2, Z11874.1, X70810.1, AL022605.3, U58744.1, X68658.1, X17051.1, AJ002397.1, AW373574.1, AW170035.1, AW59177.1, AL046701.1, AI957948.1, C87958.1, AW628933.1, AW469178.1, AW338178.1, AW331138.1, AW320227.1, AW171900.1, AW087179.1, AW052899.1, AW042526.1, AI972424.1, AI950371.1, AI920706.1, AI784583.1, AU072482.1, AI684965.1, AI460172.1, AI148480.1, AI093327.1, AI025802.1, AA970354.1, 60 AA708873.1, AA151117.1, AA150449.1, AA149652.1, AA136980.1, AA101607.1, AA071350.1, W73028.1, W35448.1, H97559.1, H96023.1, AL157387.2, AL162272.4, AC022596.4, AC015940.2, AC008088.2, AL354819.2, AL157695.2, AL138965.3, AC023067.3, AC016739.2, AC025384.2, AL161912.3, AC011983.3, AL137219.1, AL049185.4, AC040973.2, AC068690.1, AC026427.2, AC020901.5, AC010248.4, AC016684.1, AC026271.3, AC025076.3, AC051644.2, AC008390.6, AC011434.2, AC026081.2, AC008426.2, AC026395.2, AC016215.4, AC019042.3,

-233-

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ZH015/T3

- 5 AL163203.2, AL050302.2, AL049911.2, AP000026.1, AP000025.1, NM_014915.1, AK001137.1, AB028997.1, AC007617.10, AE003447.1, AC007639.5, AJ223186.1, AC010340.7, AE003494.1, AC004739.1, AC004886.1, AC006355.3, AC006045.2, U48386.1, AF044083.1, Z70270.1, AL163233.2, AL163224.2, Z74696.1, U41993.1, D82813.1, AP001679.1, AP001688.1, AP001506.1, AP000961.2, AC005522.2, AC007379.2, AC006478.2, AC004996.1, AC007099.3, AC005100.2, AC005879.3, AF116775.1, AC005331.1, AC005177.1, AC004045.1, AL021879.3, Y18930.1, AL133465.30, AL132766.13, AL109985.2, AL078644.10, AL022395.2, Z82193.1, AI951118.1, AW000914.1, AI922499.1, AI871874.1, AA991162.1, AA661357.1, C60377.1, AA471702.1, AA095151.1, AW519678.1, AV282871.1, AW133941.1, AW010698.1, AI902224.1, AV045752.2, AI311562.1, AI075925.1, AA828186.1, AA701829.1, AC067744.2, AL162272.4, AC007351.16, AC009105.6, AC009054.4, AC009401.2, AC027141.1, AC024370.2, AC014239.1, AC027783.2, AC062032.2, AC036209.2, AC060754.3, AC007131.3, AC061987.1, AC027699.1, AC021187.4, AC023567.2, AC013707.2, AC012410.2, AC012542.4, AC012248.2, AC013152.1, AL022284.1, AC062015.2, AC022418.3, AC008885.3, AC027696.2, AC060232.3, AC004932.2, AC019259.3, AC016916.4, AC023988.2, AC023399.2, AC016444.2, AC005139.3, AL161730.3

SEQ ID NO: 554

20 ZH015/T7

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35 SEQ ID NO: 555

ZH082/T3

- AL050302.2, AL163203.2, AL049911.2, NM_014915.1, AB028997.1, AB011137.2, AL009051.1, AL138654.1, AP000365.1, AP000548.1, AF132960.1, NM_015954.1, AC022073.13, AE003737.1, AC004936.2, AC006157.2, Z99291.1, U40160.1, AC008526.5, AC008912.4, AC009513.2, AE001733.1, AC006475.3, AC005760.1, AC005358.1, AC004646.1, AL161595.2, AL022605.3, U58744.1, AW373574.1, AW170035.1, AA759177.1, AL046701.1, AA663940.1, AW591494.1, AW298804.1, AW236267.1, AW044611.1, AW027676.1, AI970722.1, AI957948.1, AI829478.1, AI804380.1, AI741971.1, AI719929.1, AI707567.1, AI699017.1, AI611772.1, AI474518.1, AI422776.1, AI417636.1, AI383290.1, AI375177.1, AI370228.1, AI364071.1, AI362738.1, AI355919.1, AI355185.1, AI339716.1, AI281540.1, AI280241.1, AI274583.1, AI167768.1, AI096951.1, AI085092.1, AA974155.1, AA887695.1, AA866156.1, AA854736.1, C87958.1, AA831564.1, AA723565.1, AA714063.1, AA649041.1, AA642218.1, AA576795.1, AA525504.1, AA468847.1, AA449351.1, AA243685.1, AA173664.1, AA171684.1, C00125.1, N74602.1, R94195.1, R89587.1, AW469178.1, AW338178.1, AW331138.1, AW320227.1, AW171900.1, AW087179.1, AW052899.1, AW042526.1, AI972424.1, AI950371.1, AI928717.1, AI920706.1, AI784583.1, AU072482.1, AI684965.1, AI460172.1, AI148480.1, AI093327.1, AI025802.1, AA970354.1, AA947120.1, AA708873.1, AA504469.1, AA151117.1, AA150449.1, AA149652.1, AA136980.1, AA101607.1, AA071350.1, W73028.1, H97559.1, H96023.1, AL157387.2, AL162272.4, AC022596.4, AC015940.2, AC008088.2, AL354819.2, AL157695.2, AL138965.3, AC021219.2, AL353575.3, AL353136.3, AC023067.3, AC025384.2, AL161912.3, AC026271.3, AL137219.1, AC068690.1, AC026427.2, AC020901.5, AC027253.1, AC022080.5, AC019255.2, AC017801.1, AC016684.1, AC022124.3, AC012604.3, AC027625.2, AC034168.2, AC016215.4, AC021755.4, AC009586.3, AC011286.4, AC009881.3, AL135903.2, AP001284.1

55 SEQ ID NO: 556

ZH082/T7

- AC004527.2, AL163204.2, AP001466.1, AL078614.2, AL355072.2, AL023877.1, AC007501.2, AC003682.1, AC006032.2, AC004650.1, Z93384.1, Z72505.1, AL161580.2, AL021811.1, AC001228.1, U51281.1, AC024844.1, AF007544.1, AC004659.1, Z68217.1, AL163237.2, U41019.1, AP001692.1, AE003837.1, AC004605.1, Z78416.1, AL132943.2, AL132777.2, T95599.1, AU070040.1, AA140870.1, T62163.1, AA648760.1, AW674307.1, AW664490.1, AW334871.1, AW332410.1, AW331901.1, AV383655.1, AI829650.1, AI743111.1, AI697058.1, AI570895.1, AI570177.1, AI498194.1, AI453419.1, AI368890.1, AI264827.1, AI220282.1, AI219432.1, AA878714.1, AA777557.1, AA772182.1,

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SEQ ID NO: 557

ZHI336/T3

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SEQ ID NO: 558

ZHI363/T3

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-235-

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SEQ ID NO: 559

ZH137/T3

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SEQ ID NO: 560

ZH1610/T3

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SEQ ID NO: 561

ZH171/T3

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SEQ ID NO: 562

ZH193/T3

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SEQ ID NO: 563

ZH193/T7

AL050302.2, AL163203.2, AL049911.2, NM_014915.1, AB028997.1, AB011137.2, AF090187.1, AL009051.1, AL138654.1, AP000365.1, AP000548.1, AC011661.5, AF035938.1, AP001302.1, AC004936.2, AC006157.2, U40160.1, AC009402.3, AC004142.1, AC009513.2, X17051.1, AW373574.1, AW170035.1, AL046701.1, AA759177.1, AI957948.1, C87958.1, T38511.1, AW628933.1, AW469178.1, AW338178.1, AW331138.1, AW320227.1, AW171900.1, AW087179.1, AW052899.1, AW042526.1, AI972424.1, AI950371.1, AI920706.1, AI784583.1, AU072482.1, AI684965.1, AI486778.1, AI460172.1, AI148480.1, AI093327.1, AI025802.1, AA970354.1, AA708873.1, AA151117.1, AA150449.1, AA149652.1, AI136980.1, AA101607.1, AA071350.1, W73028.1, W35448.1, H97559.1, H96023.1, AL157387.1, AL162272.3, AC015940.2, AC022596.3, AC008088.2, AC040973.2, AC023067.3, AC016739.2, AC026271.2, AC025384.2, AL161912.3, AL137219.1, AL049185.4, AC068690.1, AC011211.3, AC015737.4, AC019255.2, AC013414.2, AL158074.5, AL157695.2, AL138965.3, AC008390.6, AC023337.3, AC034160.3, AC026081.2, AC025355.2, AC016215.4, AC019042.3, AC021755.4, AC011286.4, AL356312.1

SEQ ID NO: 564

Group ZH139

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SEQ ID NO: 565

ZH139/T3

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-237-

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5

SEQ ID NO: 566

ZH1402/T3

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20

SEQ ID NO: 567

ZH1402/T7

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35

SEQ ID NO: 568

ZH154/T3

AP000025.1, AP000026.1, AL163203.2, AL050302.2, AL049911.2, NM_014915.1, AK001137.1, AB028997.1, AC007617.10, AE003447.1, AJ223186.1, AC004739.1, AC006355.3, AC006045.2, U48386.1, AF044083.1, AL163224.2, Z70270.1, Z74696.1, U41993.1, D82813.1, AP001679.1, AP001506.1, AP000961.2, AC005522.2, AC007379.2, AE003459.1, AC006478.2, AC007099.3, AC005879.3, AC005650.1, AC005331.1, AC004045.1, AL163291.2, AL132766.13, AL096867.15, AL078644.10, Z22180.1, AL021406.1, AL022395.2, Z82193.1, Y18930.1, AJ238787.1, AJ238786.1, AP001746.1, AP001623.1, AI951118.1, AW000914.1, AI922499.1, AI871874.1, AA991162.1, W08579.1, AW030402.1, AA661357.1, C60377.1, AA471702.1, AA095151.1, AW611472.1, AW519678.1, AW449940.1, AW394816.1, AV282871.1, AI902224.1, AV121102.1, AV064061.1, AV051246.1, AV045752.2, AI311562.1, AU045123.1, AI137187.1, AU021965.1, AU021770.1, AI075925.1, C87414.1, C85160.1, AA828186.1, AA701829.1, AA667026.1, AA015732.1, AC067744.2, AL162272.3, AC007351.16, AC027141.1, AC024370.2, AC022175.1, AC014239.1, AC035145.2, AC068481.1, AC061987.1, AC027699.1, AC012410.2, AC012248.2, AC013152.1, AP001455.1, AC046187.2, AC026428.2, AC022418.3, AC010622.3, AC008885.3, AC027696.2, AC004932.2, AC023988.2, AC016444.2, AC011128.2, AF186999.1, AC005139.3

50

SEQ ID NO: 569

ZH154/T7

AL163203.2, AL050302.2, AL049911.2, AP000542.1, AL163202.2, AP001464.1, NM_014915.1, AB028997.1, AB011137.2, AF077534.1, AL009051.1, U32775.1, AL161957.1, AL110120.11, AL078614.2, U19872.1, AP001465.1, AK000712.1, AC008154.6, AC005670.1, AL133475.14, AL021633.2, AL096861.9, Z84482.1, AL080283.1, AW373574.1, AI951118.1, AW297642.1, AA579752.1, AI989660.1, AI825717.1, AI084496.1, AA331953.1, AW614036.1, AI236531.1, AI180434.1, AI180260.1, AI176501.1, AA892166.1, AI058351.1, AI044283.1, AA464382.1, AW656081.1, AW656019.1, AW564696.1, AI984814.1, AV127940.1, AI770175.1, AI446107.1, AA736439.1, AA219203.1, R62950.1, AW578955.1, AW541472.1, AW540560.1, AW363481.1, AV350817.1, AV346364.1, AV322534.1, AI955034.1, AI790539.1, AV131385.1, AI647944.1, AI631727.1, AI583901.1, AI368143.1, AI324262.1, AI193904.1, AI168669.1, AI133530.1, AI086364.1, AI065683.1, AI008640.1, AA910838.1, AA738088.1, AA623276.1, AA554531.1, AA533501.1, AA518668.1, AA423412.1, AA250678.1, AA222830.1, AA046147.1, AA046322.1, W54181.1, N72190.1, Z33598.1, AL157387.1,

60

-238-

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ZH185/T3

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20

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35

SEQ ID NO: 572

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55 SEQ ID NO: 573

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SEQ ID NO: 576

ZH112/T3

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SEQ ID NO: 577

Z112/T7

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SEQ ID NO: 578

ZH1219/T3

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-241-

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SEQ ID NO: 579

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SEQ ID NO: 580

ZH1224/T3

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40 SEQ ID NO: 581
ZH1224/T7

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SEQ ID NO: 582

ZH1356/T3

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SEQ ID NO: 583

ZH1356/T7

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40 SEQ ID NO: 584

ZH1375/T3

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55 SEQ ID NO: 585

ZH1375/T7

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SEQ ID NO: 586

ZH1393/T3

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SEQ ID NO: 587

ZH1393/T7

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ZH172/T3

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ZH172/T7

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SEQ ID NO: 590

ZH184/T3

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15

SEQ ID NO: 591

ZH184/T7

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SEQ ID NO: 592

ZH204/T3

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-245-

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- 20 SEQ ID NO: 593
ZH204/T7
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- 35

Table 2: Relation between nucleotide sequences and polypeptide sequences

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3	679	201	821	399	1118
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5	763, 764, 765	203	823, 824	401	1120
6	782	204	825, 826	402	--
7	783	205	827, 828, 829	403	1121
8	767	206	830, 831	404	1122
9	604	207	832	405	1123
10	--	208	833	406	1124
11	606	209	834, 835	407	--
12	624	210	836, 837	408	--
13	599	211	838	409	1125
14	776, 777, 778, 779	212	839, 840, 841	410	--

-246-

15	780, 781	213	842, 843	411	1126
16	802	214	844, 845, 846	412	1127
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18	607	216	849	414	--
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22	598	220	--	418	1134
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25		223	861, 862, 863	421	1139
26	601	224	864	422	--
27	--	225	865	423	1140
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29	603	227	869, 870	425	1143
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47	620	245	896	443	1160
48	621	246	897	444	1161
49	--	247	898	445	1162
50	622	248	899	446	--
51	623	249	900, 901	447	1163
52	625	250	902	448	--
53	--	251	903	449	1164
54	626	252	904	450	1165
55	627, 628	253	905	451	1166

-247-

56	629	254	906	452	--
57	--	255	907, 908, 909	453	1167
58	630	256	910, 911	454	--
59	--	257	912, 913, 914	455	1168
60	631	258	915	456	--
61	632	259	916	457	1169
62	--	260	917, 918, 918	458	1170
63	633	261	920, 921	459	1171
64	634	262	922, 923	460	1172
65	635	263	924, 925, 926	461	1173, 1174, 1175
66	--	264	927, 928, 929	462	1176, 1177
67	636	265	930, 931	463	1178
68	--	266	932	464	1179
69	637	267	933, 934	465	1180
70	--	268	935	466	1181, 1182, 1183
71	--	269	936	467	1184
72	--	270	937, 938	468	1185
73	--	271	939	469	1186
74	--	272	940	470	1187
75	--	273	941, 942	471	1188
76	--	274	943, 944	472	--
77	638	275	945	473	1189
78	--	276	946, 947, 948	474	1190
79	--	277	949	475	--
80	--	278	950, 951, 952	476	1191, 1192
81	639	279	953, 954	477	1193
82	--	280	955, 956	478	1194
83	640	281	--	479	1195
84	641	282	957	480	1196
85	--	283	958	481	1197
86	642	284	959	482	1198
87	--	285	960, 961	483	1199
88	643	286	--	484	1200, 1201
89	--	287	962, 963, 964	485	1202
90	644	288	965	486	1203
91	--	289	966	487	1204
92	645	290	967, 968, 969, 970	488	1205
93	646	291	971, 972, 973, 974	489	1206
94	647	292	975, 976	490	1207
95	648	293	977, 978, 979,	491	1208

			980		
96	649, 650	294	981, 982, 983	492	1209
97	651, 652	295	984, 985	493	1210
98	653	296	986, 987	494	--
99	654	297	988, 989	495	1211
100	655	298	990	496	1212
101	656	299	991	497	1213
102	657	300	992	498	--
103	658	301	993	499	1214
104	659, 660	302	994	500	--
105	661	303	995	501	1215
106	662, 663	304	996	502	1216
107	664	305	997	503	1217
108	666	306	998	504	1218
109	667	307	999	505	1219
110	--	308	1000, 1001	506	1220
111	668, 669, 670	309	1002, 1003	507	1221
112	671, 672, 673, 674, 675	310	1004, 1005	508	1222
113	676	311	1006, 1007, 1008	509	--
114	677	312	1009, 1010	510	1223
115	680	313	1011, 1012, 1013	511	1224
116	681	314	1014, 1015	512	1225
117	682, 683	315	1016, 1017	513	1226
118	684	316	1018, 1019	514	1227
119	685	317	1020	515	1228
120	686	318	1021	516	1229, 1230
121	687, 688	319	1022	517	1231
122	689, 690, 691	320	1023	518	--
123	692	321	1024, 1025, 1026	519	1232
124	693, 694	322	1027, 1028, 1029, 1030	520	1233
125	695	323	1031, 1032, 1033	521	1234
126	696	324	1034, 1035, 1036	522	1235
127	697	325	1037, 1038	523	--
128	698	326	1039, 1040	524	1236
129	699	327	1041, 1042, 1043, 1044	525	--
130	700, 701, 702	328	1045, 1046	526	1237
131	703, 704	329	1047	527	--
132	705	330	1048, 1049	528	1238
133	706, 707	331	1050	529	1239

134	708	332	1051, 1052	530	1240, 1241
135	709, 710	333	1053	531	1242, 1243, 1244
136	711	334	1054, 1055	532	1245
137	712	335	1056	533	1246, 1247
138	713	336	1057, 1058	534	--
139	714	337	1059	535	1248
140	715	338	1060, 1061	536	1249, 1250, 1251
141	716	339	1062	537	1252, 1253, 1254
142	717	340	1063	538	--
143	718	341	1064, 1065	539	1255
144	719	342	1066	540	1256
145	720	343	1067, 1068	541	1257
146	721	344	1069	542	1258
147	722	345	1070, 1071	543	1259, 1260
148	723, 724	346	1072	544	1261
149	725, 726	347	1073, 1074	545	1262
150	727	348	1075, 1076	546	1263
151	728, 729	349	1077, 1078, 1079	547	1264
152	730, 731	350	1080	548	1265, 1266
153	732, 733	351	1081	549	1267
154	734, 735, 736	352	1082, 1083	550	--
155	737	353	1084	551	1268
156	738	354	1085	552	1269, 1270
157	739, 740	355	--	553	1271, 1272
158	741	356	1086	554	1273, 1274
159	742, 743, 744	357	--	555	1275
160	745	358	1087	556	1276
161	746	359	1088	557	1277
162	747, 748	360	1089	558	1278
163	749	361	1090	559	1279
164	750	362	1091	560	1280
165	751, 752	363	--	561	1281
166	753	364	1092	562	1282, 1283
167	754, 755, 756	365	--	563	1284, 1285
168	757, 758, 759, 760	366	1093	564	1286, 1287
169	766	367	1094	565	1288, 1289, 1290
170	768	368	1095	566	1291, 1292
171	769	369	1096	567	1293, 1294
172	770	370	1097	568	1295
173	771	371	--	569	1296, 1297, 1298
174	772	372	--	570	1299

-250-

175	773, 774, 775	373	1098	571	1300
176	784	374	1099	572	1301
177	785	375	--	573	1302, 1303
178	786, 787, 788	376	1100	574	1304
179	--	377	1101	575	--
180	789	378	1102	576	1305, 1306
181	790	379	1103	577	1307
182	791	380	1104	578	1308
183	792, 793	381	1105	579	1309
184	794	382	1106	580	1310
185	795, 796	383	1107	581	1311, 1312, 1313
186	797, 798, 799, 800	384	1108	582	1314, 1315, 1316
187	801	385	--	583	1317, 1318
188	804, 805	386	1109	584	1319
189	806	387	1110	585	1320, 1321
190	807	388	1111	586	1322
191	808, 809	389	--	587	1323, 1324
192	810	390	1112	588	1325
193	811	391	--	589	1326
194	812	392	1113	590	1327
195	813	393	1114	591	1328, 1329
196	814	394	1115	592	1330, 1331
197	815	395	--	593	1332
198	816, 817	396	1116		

Example 2: Preparation of recombinant cancer associated antigens

To facilitate screening of patients' sera for antibodies reactive with cancer associated antigens, for example by ELISA, recombinant proteins are prepared according to standard procedures. Where gaps exist in the gene sequences represented by the clones disclosed herein, or where flanking sequences are desired, such nucleic acid sequences can be isolated according to standard procedures. For example, where 5' and 3' clones of a gene sequence are known, PCR primers can be designed for amplification of the nucleotide sequence between the clones. Flanking sequences can be isolated using procedures such as RACE PCR. Such sequences also can be isolated by standard hybridization cloning protocols.

In one method of preparing recombinant cancer associated antigens, the clones encoding cancer associated antigens are subcloned into a baculovirus expression vector, and the recombinant expression vectors are introduced into appropriate insect cells.

-251-

Baculovirus/insect cloning systems are preferred because post-translational modifications are carried out in the insect cells. Another preferred eukaryotic system is the *Drosophila* Expression System from Invitrogen. Clones which express high amounts of the recombinant protein are selected and used to produce the recombinant proteins. The recombinant proteins are tested for antibody recognition using serum from the patient which was used to isolate the particular clone, or in the case of cancer associated antigens recognized by allogeneic sera, by the sera from any of the patients used to isolate the clones or sera which recognize the clones' gene products.

Alternatively, the cancer associated antigen clones are inserted into a prokaryotic expression vector for production of recombinant proteins in bacteria. Other systems, including yeast expression systems and mammalian cell culture systems also can be used.

Example 3: Preparation of antibodies to cancer associated antigens

The recombinant cancer associated antigens produced as in Example 2 above are used to generate polyclonal antisera and monoclonal antibodies according to standard procedures. The antisera and antibodies so produced are tested for correct recognition of the cancer associated antigens by using the antisera/antibodies in assays of cell extracts of patients known to express the particular cancer associated antigen (e.g. an ELISA assay). These antibodies can be used for experimental purposes (e.g. localization of the cancer associated antigens, immunoprecipitations, Western blots, etc.) as well as diagnostic purposes (e.g., testing extracts of tissue biopsies, testing for the presence of cancer associated antigens).

Example 4: Expression of breast, gastric and prostate cancer associated antigens in cancers of similar and different origin.

The expression of one or more of the breast, gastric and/or prostate cancer associated antigens is tested in a range of tumor samples to determine which, if any, other malignancies should be diagnosed and/or treated by the methods described herein. Tumor cell lines and tumor samples are tested for cancer associated antigen expression, preferably by RT-PCR according to standard procedures. Northern blots also are used to test the expression of the cancer associated antigens. Antibody based assays, such as ELISA and western blot, also can be used to determine protein expression. A preferred method of testing expression of cancer associated antigens (in other cancers and in additional same type cancer patients) is allogeneic

-252-

serotyping using a modified SEREX protocol (as described above).

In all of the foregoing, extracts from the tumors of patients who provided sera for the initial isolation of the cancer associated antigens are used as positive controls. The cells containing recombinant expression vectors described in the Examples above also can be used
5 as positive controls.

The results generated from the foregoing experiments provide panels of multiple cancer associated nucleic acids and/or polypeptides for use in diagnostic (e.g. determining the existence of cancer, determining the prognosis of a patient undergoing therapy, etc.) and therapeutic methods (e.g., vaccine composition, etc.).
10

Example 5: HLA typing of patients positive for cancer associated antigen

To determine which HLA molecules present peptides derived from the cancer associated antigens, cells of the patients which express the breast and/or gastric cancer associated antigens are HLA typed. Peripheral blood lymphocytes are taken from the patient
15 and typed for HLA class I or class II, as well as for the particular subtype of class I or class II. Tumor biopsy samples also can be used for typing. HLA typing can be carried out by any of the standard methods in the art of clinical immunology, such as by recognition by specific monoclonal antibodies, or by HLA allele-specific PCR (e.g. as described in WO97/31126).

20 Example 6: Characterization of cancer associated antigen peptides presented by MHC class I and class II molecules.

Antigens which provoke an antibody response in a subject may also provoke a cell-mediated immune response. Cells process proteins into peptides for presentation on MHC class I or class II molecules on the cell surface for immune surveillance. Peptides presented
25 by certain MHC/HLA molecules generally conform to motifs. These motifs are known in some cases, and can be used to screen the breast and/or gastric cancer associated antigens for the presence of potential class I and/or class II peptides. Summaries of class I and class II motifs have been published (e.g., Rammensee et al., *Immunogenetics* 41:178-228, 1995). Based on the results of experiments such as those described above, the HLA types which
30 present the individual breast cancer associated antigens are known. Motifs of peptides presented by these HLA molecules thus are preferentially searched.

One also can search for class I and class II motifs using computer algorithms. For

-253-

example, computer programs for predicting potential CTL epitopes based on known class I motifs has been described (see, e.g., Parker et al., *J. Immunol.* 152:163, 1994; D'Amaro et al., *Human Immunol.* 43:13-18, 1995; Drijfhout et al., *Human Immunol.* 43:1-12, 1995). HLA binding predictions can conveniently be made using an algorithm available via the Internet on the National Institutes of Health World Wide Web site at URL <http://bimas.dcrt.nih.gov>. Methods for determining HLA class II peptides and making substitutions thereto are also known (see, e.g. International applications PCT/US96/03182 and PCT/US98/01373). Computer software for selecting HLA class II binding peptides is also available (TEPITOPE; Sturniolo et al., *Nature Biotechnol.* 17:555-561, 1999; Manici et al., *J. Exp. Med.* 189:871-876, 1999). Peptides which are thus selected can be for inducing specific CD4⁺ lymphocytes and identification of peptides. Additional methods of selecting and testing peptides for HLA class II binding are well known in the art.

Example 7: Identification of the portion of a cancer associated polypeptide encoding an antigen

To determine if the cancer associated antigens isolated as described above can provoke a cytolytic T lymphocyte response, the following method is performed. CTL clones are generated by stimulating the peripheral blood lymphocytes (PBLs) of a patient with autologous normal cells transfected with one of the clones encoding a cancer associated antigen polypeptide or with irradiated PBLs loaded with synthetic peptides corresponding to the putative protein and matching the consensus for the appropriate HLA class I molecule (as described above) to localize an antigenic peptide within the cancer associated antigen clone (see, e.g., Knuth et al., *Proc. Natl. Acad. Sci. USA* 81:3511-3515, 1984; van der Bruggen et al., *Eur. J. Immunol.* 24:3038-3043, 1994). These CTL clones are screened for specificity against COS cells transfected with the cancer associated antigen clone and autologous HLA alleles as described by Brichard et al. (*Eur. J. Immunol.* 26:224-230, 1996). CTL recognition of a cancer associated antigen is determined by measuring release of TNF from the cytolytic T lymphocyte or by ⁵¹Cr release assay (Herin et al., *Int. J. Cancer* 39:390-396, 1987). If a CTL clone specifically recognizes a transfected COS cell, then shorter fragments of the cancer associated antigen clone transfected in that COS cell are tested to identify the region of the gene that encodes the peptide. Fragments of the cancer associated antigen clone are prepared by exonuclease III digestion or other standard molecular biology methods. Synthetic peptides

-254-

are prepared to confirm the exact sequence of the antigen.

Optionally, shorter fragments of cancer associated antigen cDNAs are generated by PCR. Shorter fragments are used to provoke TNF release or ^{51}Cr release as above.

5 Synthetic peptides corresponding to portions of the shortest fragment of the cancer associated antigen clone which provokes TNF release are prepared. Progressively shorter peptides are synthesized to determine the optimal cancer associated antigen tumor rejection antigen peptides for a given HLA molecule.

A similar method is performed to determine if the cancer associated antigen contains one or more HLA class II peptides recognized by T cells. One can search the sequence of the cancer associated antigen polypeptides for HLA class II motifs as described above. In contrast
10 to class I peptides, class II peptides are presented by a limited number of cell types. Thus for these experiments, dendritic cells or B cell clones which express HLA class II molecules preferably are used.

15 **Example 8: Recognition of cancer antigens by cancer patient sera**

Several of the cancer antigen identified herein were tested for reactivity with sera from normal and breast cancer patients according to standard procedures (e.g., the SEREX procedure outlined above).

20 **Table 3: Serology of antigens**

SEQ ID NO	Gene/Clone	Breast Cancer Patient Sera	Normal Sera
1	Br-38/HSP105 (MK)	6/31	0/30
2,3	Br-39/HSP105 (MK)	3/31	0/30
4,5	RGS-GAIP interacting protein GIPC (MK)	3/31	0/30
6,7	NS1-binding protein/KIAA0850 (MK)	3/31	0/30
8	Opa-interacting protein OIP2 (MK)	3/31	0/30
9,10	Kinesin family protein 3B (KIF3B) (MT)	2/31	0/30
11	Endothelial-monocyte activating protein (EMAP2) (MT)	2/31	0/30
12	Unknown TOM1 protein (MT311)	2/31	0/30
13	Outer mitochondrial membrane protein 34kDa (MT)	1/31	0/30

-255-

14,15	IPL (MK)	1/31	0/30
16,17	Mus ACF7 neural isoform (MK)	1/31	0/30
18	Cyclin D3 (MT)	1/31	0/30

The data show that proteins encoded by SEQ ID NO:1-12 were recognized by multiple breast cancer patients' sera, but not by control individuals' sera. Proteins encoded by SEQ ID NO:13-18 were recognized by only a single breast cancer patient's sera, but not by control
5 individuals' sera. The

EQUIVALENTS

Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention
10 described herein. Such equivalents are intended to be encompassed by the following claims.

All references disclosed herein are incorporated by reference in their entirety.

We claim:

-256-

Claims

1. A method of diagnosing a disorder characterized by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule, comprising:
contacting a biological sample isolated from a subject with an agent that specifically
5 binds to the nucleic acid molecule, an expression product thereof, or a fragment of an expression product thereof complexed with an HLA molecule, wherein the nucleic acid molecule is a NA Group 1 nucleic acid molecule, and
determining the interaction between the agent and the nucleic acid molecule or the expression product as a determination of the disorder.
10
2. The method of claim 1, wherein the agent is selected from the group consisting of
 - (a) a nucleic acid molecule comprising NA group 1 nucleic acid molecules or a fragment thereof,
 - (b) a nucleic acid molecule comprising NA group 3 nucleic acid molecules or a
15 fragment thereof,
 - (c) a nucleic acid molecule comprising NA group 5 nucleic acid molecules or a fragment thereof,
 - (d) an antibody that binds to an expression product of NA group 1 nucleic acids,
 - (e) an antibody that binds to an expression product of NA group 3 nucleic acids,
 - 20 (f) an antibody that binds to an expression product of NA group 5 nucleic acids,
 - (g) an agent that binds to a complex of an HLA molecule and a fragment of an expression product of a NA group 1 nucleic acid,
 - (h) an agent that binds to a complex of an HLA molecule and a fragment of an expression product of a NA group 3 nucleic acid, and
 - 25 (i) an agent that binds to a complex of an HLA molecule and a fragment of an expression product of a NA group 5 nucleic acid.
3. The method of claim 1, wherein the disorder is characterized by expression of a plurality of human cancer associated antigen precursors and wherein the agent is a plurality of
30 agents, each of which is specific for a different human cancer associated antigen precursor, and wherein said plurality of agents is at least 2, at least 3, at least 4, at least 4, at least 6, at least 7, or at least 8, at least 9 or at least 10 such agents.

-257-

4. The method of claims 1-3, wherein the agent is specific for a human cancer associated antigen precursor that is a breast cancer associated antigen precursor.
5. A method for determining regression, progression or onset of a condition characterized by expression of abnormal levels of a protein encoded by a nucleic acid molecule that is a NA Group 1 molecule, comprising
- monitoring a sample, from a patient who has or is suspected of having the condition, for a parameter selected from the group consisting of
- (i) the protein,
 - (ii) a peptide derived from the protein,
 - (iii) an antibody which selectively binds the protein or peptide, and
 - (iv) cytolytic T cells specific for a complex of the peptide derived from the protein and an MHC molecule,
- as a determination of regression, progression or onset of said condition.
6. The method of claim 5, wherein the sample is a body fluid, a body effusion or a tissue.
7. The method of claim 5, wherein the step of monitoring comprises contacting the sample with a detectable agent selected from the group consisting of
- (a) an antibody which selectively binds the protein of (i), or the peptide of (ii),
 - (b) a protein or peptide which binds the antibody of (iii), and
 - (c) a cell which presents the complex of the peptide and MHC molecule of (iv).
8. The method of claim 7, wherein the antibody, the protein, the peptide or the cell is labeled with a radioactive label or an enzyme.
9. The method of claim 5, comprising assaying the sample for the peptide.
10. The method of claim 5, wherein the nucleic acid molecule is a NA Group 3 molecule.
11. The method of claim 5, wherein the nucleic acid molecule is a NA Group 5 molecule.

12. The method of claim 5, wherein the protein is a plurality of proteins, the parameter is a plurality of parameters, each of the plurality of parameters being specific for a different one of the plurality of proteins, at least one of which is a cancer associated protein encoded by a NA Group 1 molecule.
13. A pharmaceutical preparation for a human subject comprising
an agent which when administered to the subject enriches selectively the presence of complexes of an HLA molecule and a human cancer associated antigen, and
a pharmaceutically acceptable carrier, wherein the human cancer associated antigen is a fragment of a human cancer associated antigen precursor encoded by a nucleic acid molecule comprises a NA Group 1 molecule.
14. The pharmaceutical preparation of claim 13, wherein the agent comprises a plurality of agents, each of which enriches selectively in the subject complexes of an HLA molecule and a different human cancer associated antigen, wherein at least one of the human cancer associated antigens is encoded by a NA Group 1 molecule.
15. The pharmaceutical preparation of claim 14, wherein the plurality is at least two, at least three, at least four or at least 5 different such agents.
16. The pharmaceutical preparation of claim 13, wherein the nucleic acid molecule is a NA Group 3 nucleic acid molecule.
17. The pharmaceutical preparation of claim 13, wherein the agent is selected from the group consisting of
(1) an isolated polypeptide comprising the human cancer associated antigen, or a functional variant thereof,
(2) an isolated nucleic acid operably linked to a promoter for expressing the isolated polypeptide, or functional variant thereof,
(3) a host cell expressing the isolated polypeptide, or functional variant thereof, and
(4) isolated complexes of the polypeptide, or functional variants thereof, and an HLA

-259-

molecule.

18. The pharmaceutical preparation of claims 13-17, further comprising an adjuvant.
- 5 19. The pharmaceutical preparation of claim 13, wherein the agent is a cell expressing an isolated polypeptide comprising the human cancer associated antigen or a functional variant thereof, and wherein the cell is nonproliferative.
- 10 20. The pharmaceutical preparation of claim 13, wherein the agent is a cell expressing an isolated polypeptide comprising the human cancer associated antigen or a functional variant thereof, and wherein the cell expresses an HLA molecule that binds the polypeptide.
- 15 21. The pharmaceutical preparation of claim 13, wherein the agent is at least two, at least three, at least four or at least five different polypeptides, each coding for a different human cancer associated antigen or functional variant thereof, wherein at least one of the human cancer associated antigens is encoded by a NA Group 1 molecule.
- 20 22. The pharmaceutical preparation of claim 13, wherein the agent is a PP Group 2 polypeptide.
23. The pharmaceutical preparation of claim 13, wherein the agent is a PP Group 3 polypeptide or a PP Group 4 polypeptide.
- 25 24. The pharmaceutical preparation of claim 20, wherein the cell expresses one or both of the polypeptide and HLA molecule recombinantly.
25. The pharmaceutical preparation of claim 20, wherein the cell is nonproliferative.
- 30 26. A composition comprising an isolated agent that binds selectively a PP Group 1 polypeptide.
27. The composition of matter of claim 26, wherein the agent binds selectively a PP Group

-260-

2 polypeptide.

28. The composition of matter of claim 26, wherein the agent binds selectively a PP Group
3 polypeptide.

5

29. The composition of matter of claim 26, wherein the agent binds selectively a PP Group
4 polypeptide.

10

30. The composition of matter of claim 26, wherein the agent binds selectively a PP Group
5 polypeptide.

31. The composition of claims 26-30, wherein the agent is a plurality of different agents
that bind selectively at least two, at least three, at least four, or at least five different such
polypeptides.

15

32. The composition of claims 26-30, wherein the agent is an antibody.

33. The composition of claim 31, wherein the agent is an antibody.

20 34. A composition of matter comprising
a conjugate of the agent of claims 26-30 and a therapeutic or diagnostic agent.

35. A composition of matter comprising
a conjugate of the agent of claim 31 and a therapeutic or diagnostic agent.

25

36. The composition of matter of claim 34, wherein the conjugate is of the agent and a
therapeutic or diagnostic that is a toxin.

37. A pharmaceutical composition comprising an isolated nucleic acid molecule selected
30 from the group consisting of NA Group 1 molecules and NA Group 2 molecules, and a
pharmaceutically acceptable carrier.

-261-

38. The pharmaceutical composition of claim 37, wherein the isolated nucleic acid molecule comprises a NA Group 3 or NA Group 4 molecule.

39. The pharmaceutical composition of claim 37, wherein the isolated nucleic acid molecule comprises at least two isolated nucleic acid molecules coding for two different polypeptides, each polypeptide comprising a different human cancer associated antigen.

40. The pharmaceutical composition of claims 37-39 further comprising an expression vector with a promoter operably linked to the isolated nucleic acid molecule.

41. The pharmaceutical composition of claims 37-39 further comprising a host cell recombinantly expressing the isolated nucleic acid molecule.

42. A pharmaceutical composition comprising an isolated polypeptide comprising a PP Group 1 or a PP Group 2 polypeptide, and a pharmaceutically acceptable carrier.

43. The pharmaceutical composition of claim 42, wherein the isolated polypeptide comprises a PP Group 3 or a PP Group 4 polypeptide.

44. The pharmaceutical composition of claim 42, wherein the isolated polypeptide comprises at least two different polypeptides, each comprising a different human cancer associated antigen.

45. The pharmaceutical composition of claim 42, wherein the isolated polypeptides are breast cancer polypeptides or HLA binding fragments thereof.

46. The pharmaceutical composition of claim 42, wherein the isolated polypeptides are gastric cancer polypeptides or HLA binding fragments thereof.

47. The pharmaceutical composition of claims 42-46, further comprising an adjuvant.

-262-

48. An isolated nucleic acid molecule comprising a NA Group 3 molecule.
49. An isolated nucleic acid molecule comprising a NA Group 4 molecule.
- 5 50. An isolated nucleic acid molecule selected from the group consisting of
- (a) a fragment of a nucleic acid molecule having a nucleotide sequence selected from the group consisting of nucleotide sequences set forth as SEQ ID NOs:1-593, of sufficient length to represent a sequence unique within the human genome, and identifying a nucleic acid encoding a human cancer associated antigen precursor,
- 10 (b) complements of (a),
- provided that the fragment includes a sequence of contiguous nucleotides which is not identical to any sequence selected from the sequence group consisting of
- (1) sequences having the GenBank accession numbers of Table 1, and other publicly available sequences,
- 15 (2) complements of (1), and
- (3) fragments of (1) and (2).
51. The isolated nucleic acid molecule of claim 50, wherein the sequence of contiguous nucleotides is selected from the group consisting of:
- 20 (1) at least two contiguous nucleotides nonidentical to the sequence group,
- (2) at least three contiguous nucleotides nonidentical to the sequence group,
- (3) at least four contiguous nucleotides nonidentical to the sequence group,
- (4) at least five contiguous nucleotides nonidentical to the sequence group,
- (5) at least six contiguous nucleotides nonidentical to the sequence group,
- 25 (6) at least seven contiguous nucleotides nonidentical to the sequence group.
52. The isolated nucleic acid molecule of claim 50, wherein the fragment has a size selected from the group consisting of at least: 8 nucleotides, 10 nucleotides, 12 nucleotides, 14 nucleotides, 16 nucleotides, 18 nucleotides, 20, nucleotides, 22 nucleotides, 24
- 30 nucleotides, 26 nucleotides, 28 nucleotides, 30 nucleotides, 50 nucleotides, 75 nucleotides, 100 nucleotides, and 200 nucleotides.

-263-

53. The isolated nucleic acid molecule of claim 50, wherein the molecule encodes a polypeptide which, or a fragment of which, binds a human HLA receptor or a human antibody.

5 54. An expression vector comprising an isolated nucleic acid molecule of any of claims 48-53 operably linked to a promoter.

55. An expression vector comprising a nucleic acid operably linked to a promoter, wherein the nucleic acid is a NA Group 2 molecule.

10

56. An expression vector comprising a NA Group 1 or Group 2 molecule and a nucleic acid encoding an HLA molecule.

57. A host cell transformed or transfected with an expression vector of claim 54.

15

58. A host cell transformed or transfected with an expression vector of claims 55 or 56.

59. A host cell transformed or transfected with an expression vector of claim 54 and further comprising a nucleic acid encoding HLA.

20

60. A host cell transformed or transfected with an expression vector of claim 55 and further comprising a nucleic acid encoding HLA.

25

61. An isolated polypeptide encoded by the isolated nucleic acid molecule of claim 48 or claim 49.

62. A fragment of the polypeptide of claim 61 which is immunogenic.

63. The fragment of claim 62, wherein the fragment, or a portion of the fragment, binds HLA or a human antibody.

30

64. An isolated fragment of a human cancer associated antigen precursor which, or portion

-264-

of which, binds HLA or a human antibody, wherein the precursor is encoded by a nucleic acid molecule that is a NA Group 1 molecule.

65. The fragment of claim 64, wherein the fragment is part of a complex with HLA.

5

66. The fragment of claim 65, wherein the fragment is between 8 and 12 amino acids in length.

67. An isolated polypeptide comprising a fragment of the polypeptide of claim 61 of sufficient length to represent a sequence unique within the human genome and identifying a polypeptide that is a human cancer associated antigen precursor.

10

68. A kit for detecting the presence of the expression of a human cancer associated antigen precursor comprising

15

a pair of isolated nucleic acid molecules each of which consists essentially of a molecule selected from the group consisting of (a) a 12-32 nucleotide contiguous segment of the nucleotide sequence of any of the NA Group 1 molecules and (b) complements of (a), wherein the contiguous segments are nonoverlapping.

20

69. The kit of claim 68, wherein the pair of isolated nucleic acid molecules is constructed and arranged to selectively amplify an isolated nucleic acid molecule that is a NA Group 3 molecule.

70. A method for treating a subject with a disorder characterized by expression of a human cancer associated antigen precursor, comprising

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administering to the subject an amount of an agent, which enriches selectively in the subject the presence of complexes of an HLA molecule and a human cancer associated antigen, effective to ameliorate the disorder, wherein the human cancer associated antigen is a fragment of a human cancer associated antigen precursor encoded by a nucleic acid molecule selected from the group consisting of

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- (a) a nucleic acid molecule comprising NA group 1 nucleic acid molecules,
- (b) a nucleic acid molecule comprising NA group 3 nucleic acid molecules,

-265-

(c) a nucleic acid molecule comprising NA group 5 nucleic acid molecules.

71. The method of claim 70, wherein the disorder is characterized by expression of a plurality of human cancer associated antigen precursors and wherein the agent is a plurality of agents, each of which enriches selectively in the subject the presence of complexes of an HLA molecule and a different human cancer associated antigen, wherein at least one of the human cancer associated antigens is encoded by a NA Group 1 molecule.

72. The method of claim 71, wherein the plurality is at least 2, at least 3, at least 4, or at least 5 such agents.

73. The method of claims 70-72, wherein the agent is an isolated polypeptide selected from the group consisting of PP Group 1, PP Group 2, PP Group 3, PP Group 4, and PP Group 5.

74. The method of claims 70-72, wherein the disorder is cancer.

75. The method of claims 73, wherein the disorder is cancer.

76. A method for treating a subject having a condition characterized by expression of a human cancer associated antigen precursor in cells of the subject, comprising:

- (i) removing an immunoreactive cell containing sample from the subject,
- (ii) contacting the immunoreactive cell containing sample to the host cell under conditions favoring production of cytolytic T cells against a human cancer associated antigen which is a fragment of the precursor,
- (iii) introducing the cytolytic T cells to the subject in an amount effective to lyse cells which express the human cancer associated antigen, wherein the host cell is transformed or transfected with an expression vector comprising an isolated nucleic acid molecule perably linked to a promoter, the isolated nucleic acid molecule being selected from the group of nucleic acid molecules consisting of NA Group 1, NA Group 2, NA Group 3, NA Group 4, and NA Group 5.

-266-

77. The method of claim 76, wherein the host cell recombinantly expresses an HLA molecule which binds the human cancer associated antigen.

78. The method of claim 76, wherein the host cell endogenously expresses an HLA molecule which binds the human cancer associated antigen.

79. A method for treating a subject having a condition characterized by expression of a human cancer associated antigen precursor in cells of the subject, comprising:

(i) identifying a nucleic acid molecule expressed by the cells associated with said condition, wherein said nucleic acid molecule is a NA Group 1 molecule;

(ii) transfecting a host cell with a nucleic acid selected from the group consisting of (a) the nucleic acid molecule identified, (b) a fragment of the nucleic acid identified which includes a segment coding for a human cancer associated antigen, (c) deletions, substitutions or additions to (a) or (b), and (d) degenerates of (a), (b), or (c);

(iii) culturing said transfected host cells to express the transfected nucleic acid molecule, and;

(iv) introducing an amount of said host cells or an extract thereof to the subject effective to increase an immune response against the cells of the subject associated with the condition.

80. The method of claim 79, further comprising identifying an MHC molecule which presents a portion of an expression product of the nucleic acid molecule, wherein the host cell expresses the same MHC molecule as identified and wherein the host cell presents an MHC binding portion of the expression product of the nucleic acid molecule.

81. The method of claim 79, wherein the immune response comprises a B-cell response or a T cell response.

82. The method of claim 81, wherein the response is a T-cell response which comprises generation of cytolytic T-cells specific for the host cells presenting the portion of the expression product of the nucleic acid molecule or cells of the subject expressing the human cancer associated antigen.

-267-

83. The method of claim 79, wherein the nucleic acid molecule is a NA Group 3 molecule.

84. The method of claims 79 or 80, further comprising treating the host cells to render
5 them non-proliferative.

85. A method for treating or diagnosing or monitoring a subject having a condition
characterized by expression of an abnormal amount of a protein encoded by a nucleic acid
molecule that is a NA Group 1 molecule, comprising
10 administering to the subject an antibody which specifically binds to the protein or a
peptide derived therefrom, the antibody being coupled to a therapeutically useful agent, in an
amount effective to treat the condition.

86. The method of claim 85, wherein the antibody is a monoclonal antibody.
15

87. The method of claim 86, wherein the monoclonal antibody is a chimeric antibody or a
humanized antibody.

88. A method for treating a condition characterized by expression in a subject of abnormal
20 amounts of a protein encoded by a nucleic acid molecule that is a NA Group 1 nucleic acid
molecule, comprising
administering to a subject a pharmaceutical composition of any one of claims 13-25
and 37-47 in an amount effective to prevent, delay the onset of, or inhibit the condition in the
subject.

89. The method of claim 88, wherein the condition is cancer.
25

90. The method of claim 88, further comprising first identifying that the subject expresses
in a tissue abnormal amounts of the protein.
30

91. The method of claim 89, further comprising first identifying that the subject expresses
in a tissue abnormal amounts of the protein.

92. A method for treating a subject having a condition characterized by expression of abnormal amounts of a protein encoded by a nucleic acid molecule that is a NA Group 1 nucleic acid molecule, comprising

- 5 (i) identifying cells from the subject which express abnormal amounts of the protein;
(ii) isolating a sample of the cells;
(iii) cultivating the cells, and
(iv) introducing the cells to the subject in an amount effective to provoke an immune response against the cells.

10

93. The method of claim 92, further comprising rendering the cells non-proliferative, prior to introducing them to the subject.

94. A method for treating a pathological cell condition characterized by aberrant
15 expression of a protein encoded by a nucleic acid molecule that is a NA Group 1 nucleic acid molecule, comprising

administering to a subject in need thereof an effective amount of an agent which inhibits the expression or activity of the protein.

- 20 95. The method of claim 94, wherein the agent is an inhibiting antibody which selectively binds to the protein and wherein the antibody is a monoclonal antibody, a chimeric antibody or a humanized antibody.

96. The method of claim 94, wherein the agent is an antisense nucleic acid molecule
25 which selectively binds to the nucleic acid molecule which encodes the protein.

97. The method of claim 94, wherein the nucleic acid molecule is a NA Group 3 nucleic acid molecule.

- 30 98. A composition of matter useful in stimulating an immune response to a plurality of a proteins encoded by nucleic acid molecules that are NA Group 1 molecules, comprising a plurality of peptides derived from the amino acid sequences of the proteins, wherein

-269-

the peptides bind to one or more MHC molecules presented on the surface of the cells which express an abnormal amount of the protein.

99. The composition of matter of claim 98, wherein at least a portion of the plurality of
5 peptides bind to MHC molecules and elicit a cytolytic response thereto.

100. The composition of matter of claim 99, further comprising an adjuvant.

101. The composition of matter of claim 100, wherein said adjuvant is a saponin, GM-CSF,
10 or an interleukin.

102. The composition of matter of claim 98, further comprising at least one peptide useful
in stimulating an immune response to at least one protein which is not encoded by nucleic
acid molecules that are NA Group 1 molecules, wherein the at least one peptide binds to one
15 or more MHC molecules.

103. An isolated antibody which selectively binds to a complex of:

- (i) a peptide derived from a protein encoded by a nucleic acid molecule that is a
NA Group 1 molecule and
- 20 (ii) and an MHC molecule to which binds the peptide to form the complex,
wherein the isolated antibody does not bind to (i) or (ii) alone.

104. The antibody of claim 103, wherein the antibody is a monoclonal antibody, a chimeric
antibody, a humanized antibody, or a fragment thereof.

25

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45 <210> 48
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<213> Homo sapiens

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5

<400> 49

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<400> 50

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 <212> DNA
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<400> 51

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781

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<211> 716
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20 <210> 56
 <211> 748
 <212> DNA
 <213> Homo sapiens

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 <213> Homo sapiens

 <400> 57
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60 <210> 58
 <211> 857
 <212> DNA
 <213> Homo sapiens

<400> 58

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<211> 739

<212> DNA

15 <213> Homo sapiens

<400> 61

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	tccccagctc	tgacgccaca	tactatccgt	ttgttcagga	accaccagtg	acagaaatgt	240
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<210> 62

<211> 665

<212> DNA

35 <213> Homo sapiens .

<400> 62

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	cctgaatctg	cggctgggtg	atcttaggga	aagggggtgt	gattggganc	aaagggggga	600
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<210> 63

<211> 1003

<212> DNA

55 <213> Homo sapiens

<400> 63

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	cttgctgaag	tactgaaata	ggataattca	tctaataaac	aaacaaacaa	aaaaaacaac	360
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	ggcttttttg	aanctcccnt	aattggncng	ggncctttan	ccttttttga	cgcccccccc	960
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<210> 64

<211> 765

<212> DNA

15 <213> Homo sapiens

<400> 64

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	gaaacatnnt	tgaccattct	ggttaaactg	cataaatngg	acatgggnng	naaaaaaaca	660
	aagggcgatc	tttttaccgg	tacctaaang	gcgggngggt	caaananaanc	anaaccgggg	720
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<210> 65

<211> 566

<212> DNA

35 <213> Homo sapiens

<400> 65

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<210> 66

50 <211> 445

<212> DNA

<213> Homo sapiens

<400> 66

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<210> 67
 <211> 976
 <212> DNA
 <213> Homo sapiens

5

<400> 67

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25

<210> 68
 <211> 487
 <212> DNA
 <213> Homo sapiens

30

<400> 68

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<210> 69
 <211> 826
 <212> DNA
 <213> Homo sapiens

45

<400> 69

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<210> 70
 <211> 1015

<212> DNA

<213> Homo sapiens

<400> 70

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	ctgttttaac ttntccaan cncngggtt gctggatttc cctgcttgan ctacnctggt	180
	ntttttnaanc ngntttctcc ncttctcctt ntnttttatt ttcanhcccn tttganattt	240
	ctttttccnt cncncncggt tcttggtggt agcnggtttt tcagcnnctg nttttatntc	300
10	nccncttta tttttcnccn tgancncnc nggggccng aaagctgcat nactaacnct	360
	cactggggct ncttcncca tggntatggn tgggaaattt gacncaactt taatctntgg	420
	gcaggcggt tagggataaa ggggaagtgt anaggcctc cnattttaaa naanaggga	480
	centcatctt ctgaatttct ncatgnccgg attttttctt ctgnggttt tggcgggga	540
	gttgaggnac nccngntcaa aaatttcnca agngcaaat ttactctttt tatggggcna	600
15	anggnaaacc ccttttatat tcntatgcn ccnttttagg gtttttttnc gactacataa	660
	ccccagccng acntttttct ttgnaaaaag aaattttcca ttgaangggg ggttcttttt	720
	aatacaaggg ccctnccgca aattgggaaa agggnggggn ttntcnaaaa gggntttntt	780
	gncccttttg ggcgggacct tccccngaag ggccnggggt tttttaanca cttttttttn	840
	aaaagaaant ttantant ttncnccgnt tttnaangng gttactntc aaattttttt	900
20	tattnaaacc nntttttagt tcccttattt gggaaanaag gccttttnaa ctttttatgg	960
	ggtatnggnc atttttgang ggaatttttt tcgttncaaa ataaantttg ttttt	1015

<210> 71

<211> 1140

<212> DNA

<213> Homo sapiens

<400> 71

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	tggggaccca gctgtacata tgtggataag ctgattaatg gttttgcaac tgtaatagta	120
	gctgtatcgt tctaatagcag acattggatt tggtgactgt ctcatgtgc catgaggtaa	180
	atgtaatgtt tcaggcattc tgcctgcaaa aaaatctatc atgtgctttt ctatagtgct	240
	ctggttctat agtgcaaatg cttttattag ccaataggaa ttttaaaata acatggaact	300
	tacacaaaaag gcttttcatg tgccttactt ttttaaaaag gagtttattg tattcattgg	360
35	aatatgtgac gtaagcaata aagggatgt tagacgtgtt aaaaaaaaaa acanaaaaca	420
	nnaaaacaaa aaaaatcctc gaaagtcttt tagagcgcc gngggccnat ngatttttcc	480
	ccccgggtgg ggtaccaggt aagtgncccc antttccct ataggagcc gtattacaat	540
	tactggccg tcgttttaca acgncngnga cttggnaaaa accntggcgt taccacaact	600
	taatcgctt tgnaaacatc cccctttcgc cagctgggnn taanaacgaa aaaggccccc	660
40	cgaatcncc tttccaaaca anttgcncca cntggatng ggnaatggga aannccaatt	720
	tttaaaaggg tntaatgggg gtnaaacnnc cggantncna attggnntng gggnttttaa	780
	aatcancaa cccnaaggc ttnntttang gccccnag tccnncagn tntggtaat	840
	ggncnttaan ncccccttnc cnaattttgt aaaagggtt ttcttggtt aaaaaaanc	900
	tcncanccnt tccccngaa cctganaaaa ttaaaaaaga naggccntt ggnngtgtgt	960
45	aaanttngtt tttncctt nttaaagggtc cccaaaaaan cttaccttcc aaattttccc	1020
	aaaataaann ttttttccn gentttnat gngggggng cccaccacac aaaggatttt	1080
	taccnanaat ntttncgna ntttttttaa aaacntaaa atttgttnan acacnttttt	1140

<210> 72

<211> 588

<212> DNA

<213> Homo sapiens

<400> 72

55	acacgtntaa cattcccttt attgcttacg tencatattc caatgaatac aataaactcc	60
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	tcctatnggc taataaaagc ntttgcacta tanaaccnga nacatntana aaagcncatg	180
	atngattttt ttgcaagcan aatgcctgaa acattacatt taccttatgg cacaatgaga	240
	cagtnacca atccaatgtn tgcattanaa cgatacagct acttttacag nngcgaaacc	300
60	attaattagn ttatccncat atgtacagnt gggccccac gtgacaaaat ctgnggccga	360
	attntttgga tccnctaata tgcacctgc aggcgcncga ngctccaagc ttttgnctcc	420
	cttttanng agggtnatt ttcnagctt gentnatnaa ggggaatagc ttgnttctng	480
	ngngaaantg ttattcnntc nccaatttnc acnchnataat accaagcccg ggnagttata	540

aaagtggatat aanccnnggg gtgccctaata tngnggtganc ttannctc

588

<210> 73
 <211> 526
 <212> DNA
 <213> Homo sapiens

5

<400> 73

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	tggaaaaatga ggaggctgag ccaggccgtg gagggctggg cgtgggggag ccagggcctc	120
	tgggcggagg tgggtcgggg gnnnaacnnn nnanattnnn cngnnngnnn nncctnnnt	180
	ttanangnn tnnnnngata nganctnctn ttangacgag gatnnataat nctaagtcta	240
	naactcctnc tanctngnnn ggaattgatc ntangatggc ntatgcaaata angaagtntc	300
	attctggntt gatgnntggg ggcntaacta nngnattanc angngnnaan ttttctctggg	360
15	tntnctanga nattnnngana aaatannggc ttngnannct anggcnatna nntntnatna	420
	cnananccta nnnngnnttt ntannnganaa gtntngnnng gaatgggatt ttgntctgnt	480
	nngangntan gcntncngng gntntngac cntttcnnga angaat	526

<210> 74
 <211> 608
 <212> DNA
 <213> Homo sapiens

20

<400> 74

25	ggcagattga tcttttatgt tcaagacagc aaattcagat acaaaaaccc accgccatcg	60
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	gaggagggtg cggggttcac agcaaaactn tgtcaaatgc ggaggtaaca ggctncacag	180
	ggagggggct cctctcagga ggggtgaggg cattattgca tttgctgggg ggaaggacaa	240
	ccctctcccc tgtattccct gcgtcaggaa actaggaagg ncatgacccc caaacagaac	300
30	ccaaggcccc agggagacag agggaccagt ttggcagctg atgggtggaaa gtgggtggagg	360
	cgggggtggc cccccaattt ggctgatccc tccccccct gtgcctgacc caactgaggt	420
	aggtggggaa cagggcacag gggggccggg gaccccgcc agactgggaa ccaggagggg	480
	gatgtccca ttggagcggg gcaaggggcc tggccaccc cccctnccatt gtccttgggc	540
35	tgcttancta gctcagctgg aggtcnggt cctgantnaa ngtcctgct gggggccccc	600
	ccagggtgc	608

<210> 75
 <211> 891
 <212> DNA
 <213> Homo sapiens

40

<400> 75

45	gtctgggtgcc agcagccgag gtaattccag ctccaatagc gtatattaaa gttgctgcag	60
	ttaaaaagct cgtagttgga tcttgggagc gggcgggagg tccgccgga ggcgagccac	120
	cgcccgctcc cgcccttgc ctctcggcgc cccctcgatg ctcttagctg agtgtccgc	180
	ggggcccgaa gcgtttactt tgaataaatt agagtgttca aagcaggccc gagccgctg	240
	gataccgag ctaggaataa tggaatagga ccgcggttct attttgttg ttttcggaac	300
	tgaggccatg attaagagg acggccgggg gcattcgtat tgcgccgcta gaggtgaaat	360
	tcttgaccg gcgcaagacg gaccagagcg aaagcatttg ccaagaatgt tttcattaat	420
50	caagaacgaa agtcggaggt tcgaagacga tcagataccg tcgtagttcc gaccataaac	480
	gatgccgacc ggcgatgcgg cggcggttatt cccatgaccc gccgggcagc tccccgaac	540
	cggtagcggg gtcgtggaac taagcccctg accagcggcg tgcacacctt nccgggtgtc	600
	ctacaagtct caggactcta ttcctcanca acgtgggtgac cgtgcccttc anagcttggg	660
	cacccaacc tacatntgca acgtgaatac aaaccagca acaccaangn gggcaagaaa	720
55	agttgaacc caatnttgta aaaaaactn acaacatgcc caccggggcc cagaacctga	780
	antcttgggg gggaccgtaa gtttctttt nccccaaac ccaaggacac ccttntgatt	840
	tcccggaacc tgagggtacat tctnngtggg ggaccnaacc nccaaaacct t	891

<210> 76
 <211> 1046
 <212> DNA
 <213> Homo sapiens

60

<400> 76
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 nccccngggg gangggccan cccnccncc nccnccataa anccccgggg gggggggggt 120
 ngccggcctt centnntttt tccccggaaa cggggngggg nntttttgag gnaaggggnt 180
 5 ggncaaacce tntcctttan ggggnnnnaa aaaattttcc cntggngccc cnnttttttc 240
 cccggggngn tnttttnaaa nnaaaaaggc cnnggggncn cncagcnggg nggggggggt 300
 ttantttttt nccngcnngc ctttgtnnnc ccactcnggg ngatgtnggt ngnaaaaaac 360
 nnttttcena ngcgggggaa ggcncancct tttttngnnn cncaccccca aagggggggg 420
 gggngngncc cntngggggg ncgggggngg nccttttggg tttnaaanana gnttttttan 480
 10 nnnngggggc ngggnggnnt ttttgggnnc cccatnnatt tntncntnn nccanttaac 540
 cannttggg ngcnggnng ggnaannccc ttccnccgg gnacnggcnn ttgnctcntn 600
 cccccnggct ttttttttgg ttttagacct nccgcccccc cccaccnnag ggaatnancc 660
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 gcnttttntt ttggggggaa anaaaaaac cgccccnaa aaaaatgntt tgccccgggg 780
 15 gccttanatt ttncccanat tggggccntt tttttcccn tngngtgn gnnggtggaa 840
 cccngcaaaa anggnngggc cccttttggg ggccccccc cctttngggg gcnatgnttt 900
 ggccngggcc cccngaagnt cccccngng gnccccnaa aaaaccccc tttttaancc 960
 cgggggaaaga aaaaccnccg ggnggggggn ntttngngnn nnangggaaa ttttccnccc 1020
 cctnttttta anaacctccc nctcct 1046

<210> 77
 <211> 636
 <212> DNA
 <213> Homo sapiens

<400> 77
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 aagagaactg ccgtcctgat ggaagagaac ttggtgaatt cagaaccaca actgtcaaca 120
 30 tcggttcaat tagtaccgca gatggttctg ctttagtgaa gttgggaaat nctacantna 180
 tctgtggagt taaagcagaa tttgcagcac catcaacaga tgcccctgat aaaggatacg 240
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 gagaagaggc ccaagtggct agccaattca ttgcagatgt cattgaaaat tcacagataa 360
 ttcagaaaaga ggacttatgc atttctccag gaaagcttgt ctgggttcta tactgtgatc 420
 tcatttgcct cgactacgat ggaaacattt tggatgcctg cacatttntt ttgctagcgg 480
 35 ctttaaaaaa tgtacaagtt gccttgaagt tactataaat gaagaaactg ctttagccag 540
 aagttaattt aaagnaagaa aagttatttg aatattaaga actcatncag ttggcaactt 600
 cccttttggc ggggttttgg atgacacttt tggcct 636

<210> 78
 <211> 687
 <212> DNA
 <213> Homo sapiens

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 aattacttca tccatcagtt ttttaacttc tttgtgtctt gtaactgtc ggctcataca 180
 gtcctgaagt ttagctccag ttagccact tccacctggt ttgtgaanac aacanagttt 240
 gccttcctca tccattacta ttgttaaggc tcctgttgcc agatgttcct cctctccagt 300
 50 aggttcaact ataagcaaag tgtcatcaaa cacagcaaag gaagttgcaa ctggatgagt 360
 tctaataatt aaataacttt tcttctttaa attaatctt gctaaagcag tttcttcatt 420
 tatagtaact tcaggcaact gtcatttttt aaagccgcta caaagcaaat gtgcaggcat 480
 ccaaaatgtt tccatcgtag tcgaggcaaa tgagatcaca gtatagaacc caaacaagct 540
 ttcctggaaa aatgcataag tccntctttc tgaaatatct ggngaatttt caatngacat 600
 55 ctgcaatgga attggctagc cccttgggcc tttctccnga nggccaaccg ggaatctnat 660
 gaaaccagg ggggggagat cncatt 687

<210> 79
 <211> 1235
 <212> DNA
 <213> Homo sapiens

<400> 79

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	gatgaacgan	ntntntggcag	agtcngctaa	ngaactccct	caagtttcat	ttgtgaagcc	120
	ggaagctgaa	ggtgttcctg	nagtatntga	aaaatatgag	attagctctg	tnnccacttt	180
	nntgtttttn	nagaattctn	acaaaatcca	ccgattgtat	ggcgtgcat	gcccnaaagn	240
5	nnnccctaan	tgacnttngn	ctgtgcattc	ctcggttcct	tcntacccag	cgctaataaa	300
	catcttanag	aagatctcaa	ccttcgcttg	aagaanttga	ctcatgctgc	cccctgcatg	360
	ctgctatnaa	aggaactcct	cagaaccacg	ctgtgggttc	ancangcaga	tggnggaaat	420
	tcttcacana	cataatatnc	agttttancg	tttttgnntt	catntcagat	gaaaagggtt	480
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10	agctnatang	aggactnnct	ttntttaagg	agcnggaagc	atntttnagn	aacttttatt	600
	ccaatttngn	nccnaaancn	ncccaanttt	tnngaaaaag	ctcaaacgtg	cttnacnaat	660
	aaaagctttc	cttgtggngg	cttttttttt	gnaaacggga	ncnanacngg	gaaccccaaa	720
	attgtggngt	tttctntaaa	accaaatttt	cgtggaaaana	tnctaaaant	nggtcctggg	780
	nggttngnaa	cnttgaaaaa	antttcnnan	tnntngggga	gggaaggaaa	taangttcng	840
15	accanggggt	taaaanaagct	tcantnaaaa	tnnggnccaa	aantacnncn	tcaangtttn	900
	tnntttttta	angggggnaa	ctttgggtgg	gnnaggantc	gggnnttgn	gggaaagggn	960
	nccttaaaaa	aaaangnggg	anatangccn	cnnttttcnc	gggangggga	aaaattatna	1020
	nattttttta	ncntcggggg	gcncnccnna	tttttngggg	ggngggcttt	tnaccnngn	1080
	ccnnttanaa	agaaaanggc	acctantntt	nggtcnattn	cnngccntaa	acctttttgc	1140
20	nggtccaaaa	aaaaaaaatt	ntggcnctna	tncttttcgg	gaaaaaaagn	gacncccgag	1200
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<210> 80

<211> 733

25 <212> DNA

<213> Homo sapiens

<400> 80

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	caagctccgg	agctcaagca	acccgcctgc	ctccgcctcc	caaagtgtct	ggatcacaa	120
	cacgagccat	tgtgccagc	ctggcactta	atgtgtgaaa	gccacaccat	ttctaacagg	180
	aacataaaaa	taccaggtca	tttcanaagc	cccagacttg	ggcaactcca	ctcactaact	240
	tgacgcgtgc	tacctcaaa	ccagtgtggc	acgaggcttc	aagcacagca	ctggggctgc	300
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	ttttaaaggta	cccatcctgg	tgaatgaggc	atcaggaaaac	ttctgcagct	ttgngtctga	600
	ttcaaaaang	ggggatacct	tttccttanc	catnacaang	gggcacaagn	ccgacacttc	660
40	tggtaaattn	caacactttt	ggggangctt	gaggcaagga	aaaccttatt	ttttttccaa	720
	gaaaataaaa	aaa					733

<210> 81

<211> 1058

45 <212> DNA

<213> Homo sapiens

<400> 81

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	aaattcagga	gctccaagag	aaactggaga	aggctgtaaa	agccagcacg	gaggccaccg	180
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	agaaccgaga	ggattcttct	gaaggcatca	gaaagaagct	ggtggaagct	gaggaacgcc	300
	gccattctct	ggagaacaag	gtaaaagagac	tagagacat	ggagcgtaga	gaaaacagac	360
55	tgaaggatga	catccagaca	aaatcccaac	agatccagca	gatggctgat	aaaattcttg	420
	agctcgaaag	gaaacatcgg	gaggcccaag	tctcagccca	gcacctagaa	gtgcacctga	480
	aacagaaaga	gcagcactat	gaggaaaaga	ttaaaagtgt	ggacaatcag	ataaagaaag	540
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	agaanggcaa	aattcttcag	cgaacagaag	gcgatgatca	atgctatgga	ttccaagatc	660
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	acnactgggg	aanataaacc	ccaagaaccc	agtgcacaaa	atcggttggt	ggactggaga	900

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 aaaaattttaa gttttcttgn ggaaccngat tacaatttna nccttcaggt ttacnngggg 1020
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5 <210> 82
 <211> 713
 <212> DNA
 <213> Homo sapiens

10 <400> 82
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 agcagttcac agatganaca cacaatatac attttcaggg ctcaagaagc ccatttntca 120
 tggagatcct aaatgaaatg ccaagactga aagaccatt ttcagtgacc tttccaaata 180
 ctgnggacca aganacaaaa cttcagcaaa cattcaatca aatntgccct ggggacggga 240
 15 ggggagggag taccaccca cagactccaa gcaacacata aaacgccaca gcaggacatt 300
 tgccaaagga gctaccacat ggaggtttgt aggcgtttca aacaagaaag cacttaggtt 360
 aanacaccan cnggaaggag ctgggatgca ggccaagtgt caatctggaa agggatctga 420
 actgtggaca cagttgaaaa cacggnctgt ttcacctgt gcgnggaaa cgggtctcct 480
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 caactgcaaa ncctntaggt gggtctgtnc nattgccag aatttctac ttttataaga 660
 nggnccncaa acccnatggg gagccnctt gnnctaaggc nttcccacc ttg 713

25 <210> 83
 <211> 771
 <212> DNA
 <213> Homo sapiens

30 <400> 83
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 tcccttcttg gttcaaagaa agtgatcctt ccaagctgca gttcaatact accaactgtc 120
 gtagtgatac cgtaattggag aaacggtcat ttaaggtgcc tctgggaaag ggaagacgct 180
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 35 cagatagtcc tgagaactgg gagaaagtct gggacaactg gaggctgctg acaatggccg 360
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45 <210> 84
 <211> 961
 <212> DNA
 <213> Homo sapiens

50 <400> 84
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 atccttccaa gctgcagttc aatactacca actgtcgtag tgataccgta atggagaaac 180
 ggtcatttaa ggtgcctctg ggaaagggaa gacgctgtgt cgttttagca gatggattct 240
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 55 aaatcaagac agagaagtca ggtagcattg gtgtgcaga tagtctgag aactgggaga 360
 aagtctggga caactggagg ctgtgacaa tggccgggat ctttgactgc tgggagcccc 420
 cagagggagg agatgtcctg tattcctata ccatcatcac agtggattcc tgcaaggct 480
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	ccacctcagc attaccgttt ggatgatag gccattggcc accactacag ggactcctat	480
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20 <213> Homo sapiens

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<212> DNA

40 <213> Homo sapiens

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<211> 833

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<211> 354
<212> DNA
<213> Homo sapiens

<400> 167

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50	tctacagaga acttcttgta attaaaagat ttcaattcat agcaaaactgg tgttttaaac	660
	tattgcagta gctggaactt tttagtgtaa ccagcattta ttggagaagt gaatcacaag	720
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	ttacgtctgc ctccagaata tgcctctact gtgagaaggg cagtacagtc tggctatgtc	840
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60	ttgaatctcc agatgttgaa aaagaagtga aacgatgctg agtacagatg ctgaaactgt	1260
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<210> 207

<211> 623

<212> DNA

<213> Homo sapiens

<400> 207

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	gtcacagcat	atthagagaa	aagacttggg	gcttaaataa	aaactaaggc	aaaatagacg	180
	cttagctgct	gatctacaga	gaacttcttg	taattaaag	atctcaattc	atagcaaaact	240
	ggtgttttaa	actattgcag	tagctggaac	tttttagtgt	aaccagcatt	tattggagaa	300
10	gtgaatcaca	aggaaataaa	gatgagtaaa	agcaaagatg	atgctcctca	cgaactggag	360
	agccagttta	tcttacgtct	gcctccagaa	tatgcctcta	ctgtgagaag	ggcagtacag	420
	tctggctatg	tcaacctcaa	ggacagactg	acaattgagt	tacatcctga	tgggcgtcat	480
	ggaatcgtca	gagtggaaccg	tgttccattg	gcctcaaaat	tagtagacct	gccctgtgtt	540
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<210> 208

<211> 979

<212> DNA

<213> Homo sapiens

<400> 208

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	tagcatcatt	gtctctagac	taggttcttc	ttattgatct	cacgtcatca	caaagcagca	180
	acagcagctt	ntanaaaatg	gagaaacagt	aaagtcctgc	aatgaagcta	taattaagggn	240
	tgaaccatac	attccgctaa	tcctgcaact	ttcctacaat	catttttctg	cctatacaat	300
	cctgcttctt	ataggatgaa	cacctagcaa	aacaatataa	atgtgctgaa	aaacaaaatt	360
30	acaaacaaat	gaaagaactt	aacagaacac	acagcattaa	aaggactagg	aagagcaagg	420
	tcttaatacc	cagtacaata	aagccaagaa	ttttctaatt	ctgaccagtc	tgaagactga	480
	aattaaatat	cagttctttt	tacttctcta	ggagtgtatc	tagctcctct	tgcaaagagc	540
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	tcttgagagc	cagattttcc	actttcatga	tgagacctct	tgncgttttg	ccctgtcctg	660
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	tncccaaaac	ttcctcgggg	naagaaggtn	atatcttctt	atctgggagg	cnnggggctat	840
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<210> 209

<211> 780

<212> DNA

<213> Homo sapiens

<400> 209

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50	gaagaattaa	ggaaacgaca	aggagacgct	cggtctcttc	ccgcttggct	ccttgccggc	180
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	taccggaggg	gaagagagct	cgctgagccc	tgattttttg	agtgtctttg	ttccgggaga	300
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	attaaaagat	ttcaattcat	aagcaaactg	gtgttttaaa	ctattgcagt	aanctgggac	660
	tttttagtgg	taaccagcat	ttanttgagg	aagtgaatc	acaagggaaa	tnaagatgaa	720
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<210> 210

<211> 859

<212> DNA

<213> H mo sapiens

<400> 210

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	caaacta	gca	tcattgt	cctc	tagactaggt	tcttcttatt	gatctcacgt	catcaca	aag	180
	cagcaac	agc	agcttct	aga	aaatggagaa	acagtaaagt	cctgcaatga	agctata	aatt	240
	aagggtg	aac	catacat	tcc	gctaatecctg	caactttcct	acaatcattt	ttctgc	ctat	300
	acaatc	cctgc	ttcttat	agg	atgaacacct	agcaaaacaa	tacaaatttg	ctgaaaa	aca	360
10	aaattaca	aaa	caaatgaa	ag	aacttaacag	aacacacagc	attaaaagga	ctaggaag	ag	420
	caagggt	cctta	ataccag	ta	caataaagcc	aagaattttc	taatgctgac	cagtctga	ag	480
	actgaa	atta	aatatc	agtt	ctttttactt	ctctaggagt	gattctagct	cctcttg	caa	540
	agagctg	agt	tgctcct	ttt	ctcggncctt	cttttggttg	agctcatcca	gtacagc	ctg	600
	aaatctg	ttc	ttgagag	cca	gatttccact	ttcatgatga	gacctcttgn	cggtttg	ccc	660
15	tgctcct	gggc	tcttggg	agc	ttggctttat	gggtggcaatc	tgcttntgaa	atnccata	aac	720
	cngctgg	atn	gggtcct	tca	ntttcctggg	gctggctatc	tggtatcaatt	aacttggn	ct	780
	ggaactg	ncct	tttccaa	acn	ttcttcgggn	caaagaaggt	tatatcttct	tnatcttg	ga	840
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<210> 211

<211> 771

<212> DNA

<213> Homo sapiens

<400> 211

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	cagtagctgg	aactttt	tag	taaccagc	atttattgga	gaagtgaatc	acaaggaaat	180
30	aaagatgagt	aaaag	caaag	atgatgtcc	tcacgaactg	gagagccagt	ttatcttacg	240
	tctgcctcca	gaatag	cct	ctactgtgag	aagggcagta	cagtctggtc	atgtcaacct	300
	caaggacaga	ctgaca	attg	agttacatcc	tgatgggctg	catggaatcg	tcagagtggg	360
	ccgtgttcca	ttggc	cctcaa	aattagtaga	cctgccctgt	gttatggaaa	gcttgaaaac	420
	cattgataaa	aaaact	tttt	acaagacagc	tgatatctgt	cagatgcttg	tatccacagt	480
35	tgatgggtgat	ctctat	cctc	ctgtggagga	gccagttgct	agcactgatc	ctaaagcaag	540
	caagaaaaag	gataag	gaca	aagagaaaaa	gtttatctgg	aaccacggaa	ttactctgcc	600
	tctaaagaat	gtcang	gaag	aaaaagggtc	cggagacagc	ccaaagaaga	aatntnttga	660
	atctncagat	gttgaaa	aaag	aagtgaacg	atgctgagta	canatgctga	aactgtaata	720
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<210> 212

<211> 855

<212> DNA

<213> Homo sapiens

<400> 212

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	caaacta	gca	tcattgt	cctc	tagactaggt	tcttcttatt	gatctcacgt	catcaca	aag	180
50	cagcaac	agc	agcttct	aga	aaatggagaa	acagtaaagt	cctgcaatga	agctata	aatt	240
	aaggntg	aac	catacat	tcc	gctaatecctg	caactttcct	acaatcattt	ttctgc	ctat	300
	acaatc	cctgc	ttcttat	agg	atgaacacct	agcaaaacaa	tataaatttg	ctgaaaa	aca	360
	aaattaca	aaa	caaatgaa	ag	aacttaacag	aacacacagc	attaaaagga	ctaggaag	ag	420
	caagggt	cctta	ataccag	ta	caataaagcc	aagaattttc	taatgctgac	cagtctga	ag	480
	actgaa	atta	aatatc	agtt	ctttttactt	ctctaggagt	gattctagct	cctcttg	caa	540
55	agagctg	agt	tgctcct	ttt	ctcggncctt	cttttggttg	agctcatccc	agtacaag	ccc	600
	tggaatntg	ttcttg	agaa	gccagatttt	ccactttcat	ggatgaganc	cctcttgctg			660
	tttttgcc	cct	gtcctgg	gtc	ttttggagcc	ttgccctttc	atgggtgncaa	tctggctt	ct	720
	tgaattccc	a	taacccc	gct	ggntnngggc	ccttcatttt	tccnggggcn	ggtcattttg		780
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<210> 213

<211> 679

<212> DNA

<213> Homo sapiens

<400> 213

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	caaaactagca	tcattgtctc	tagactaggt	tcttcttatt	gatctcacgt	catcacaaag	180
	cagcaacagc	agcttctaga	aaatggagaa	acagtaaagt	cctgcaatga	agctataaatt	240
	aagggttgaa	catacattcc	gctaactctg	caactttcct	acaatcattt	ttctgcctat	300
10	acaatcctgc	ttcttatagg	atgaacacct	agcaaaaaca	tataaatttg	ctgaaaaaca	360
	aaattacaaa	caaatgaaa	aacttaacag	aacacacagc	attaaaagga	ctaggaagag	420
	caaggtctta	ataccagta	caataaagcc	aagaattttc	taatgctgac	cagtctgaag	480
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	agagctgagt	tgctcctttt	ctcggncttc	cttttgttg	agctcatccc	agtacaagcc	600
15	ctgaaaatct	gtcttgagag	ccagatttcc	actttcatga	tgaganccct	cttgctgggt	660
	ttgcctgtc	cctggggtc					679

<210> 214

<211> 672

<212> DNA

<213> Homo sapiens

<400> 214

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	gatcactctg	ccaagcggca	ggaagaatta	aggaaacgac	aaggagacgc	tcggctctct	180
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	ctctccgcgt	tgctccggcag	cggcacctag	aggttgggac	ttggcattgc	atctgattta	480
	atgaacttaa	gtctgtgaat	aagcctttgt	gttaacgact	ggatttcggg	cacagcatat	540
	ttagagaaaa	gacttggagc	ttaaataaaa	actaaggcaa	aatanacgct	tagctgctga	600
	tctacaaaaa	aacttntttg	taattaaaag	atttcaattc	atagccaact	gggtgtttta	660
35	actattgcag	ta					672

<210> 215

<211> 779

<212> DNA

<213> Homo sapiens

<400> 215

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	ctctgccaa	cgccaggaag	aattaaggaa	acgacaagga	gacgctcgcc	tctctccgc	180
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	tctttgttcc	gggagagt	gtgagttgaa	agtatctctg	ctgggcttcc	tgggcccga	360
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	ctanttgcaa	gtaacttggg	actttttaat	tgtaaccncg	catttttttt	gggagaagt	720
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<210> 216

<211> 734

<212> DNA

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<400> 216

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<400> 291

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<211> 900

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<212> DNA

<213> Homo sapiens

<400> 292

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<211> 824

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<212> DNA

<213> Homo sapiens

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<213> Homo sapiens

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<210> 298

<211> 800

<212> DNA

15 <213> Homo sapiens

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25 <400> 385

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<212> DNA

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25

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11

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664
720
768

10> 391

11> 650

12> DNA

13> Homo sapiens

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212> DNA

213> Homo sapiens

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5

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45

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<213> Homo sapiens

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<211> 665

<212> DNA

<213> Homo sapiens

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<212> DNA

<213> Homo sapiens

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<211> 717

<212> DNA

<213> Homo sapiens

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<212> DNA

<213> Homo sapiens

<400> 437

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<212> DNA

<213> Homo sapiens

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<210> 439

<211> 733

<212> DNA

<213> Homo sapiens

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<400> 439

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<212> DNA
45 <213> Homo sapiens

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<211> 728
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<213> Homo sapiens

<400> 485

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<211> 742

<212> DNA

<213> Homo sapiens

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<211> 757

<212> DNA

<213> Homo sapiens

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	Leu Lys Glu Glu Glu Arg Val Leu Lys Glu Thr Cys Asp Gln Lys Asp	
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 35 40 45
 Ala His Tyr Asp Ala Val Glu Ala Glu Leu Lys Ser Ser Thr Val Gly
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 Leu Val Thr Leu Asn Asp Met Lys Ala Lys Gln Glu Ala Leu Val Lys
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 Met Lys Leu Glu Lys Leu Arg Glu Lys Glu Arg Lys Lys Glu Ala Lys
 100 105 110
 60 Arg Lys Ile Ser Ser Leu Ser Phe Thr Leu Glu Glu Glu Glu Glu Gly
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Glu Glu Ile Thr Thr Lys Lys Arg Lys Leu Gly Lys Asn Pro Asp Val
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 35 40 45
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 115 120 125
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 Gly Phe Leu Leu Thr Leu Leu Leu Ser Lys Leu Leu Gln Leu His Leu
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 40 Gln Leu Leu Gly Leu Leu Leu Gly Gln Leu Leu Leu Pro Leu Leu
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 His Gln Ser Leu Leu Leu Gly Leu His Val Ile Gln Gly His Glu Thr
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 His Gly Ala Gly Leu Glu Leu Cys Leu His Arg Val Val Val Arg Arg
 195 200 205
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	Pro	Gly	Pro	Gly	Ala	Arg	Ala	Gly	Arg	Ser	Ser	Thr	Ser	Met	Cys	Thr
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 225 230 235 240
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 Val Lys Asp Cys Thr Glu Ala Leu Lys Leu Asp Gly Lys Asn Val Lys
 15 260 265 270
 Ala Phe Tyr Arg Arg Ala Gln Ala His Lys Ala Leu Lys Asp Tyr Lys
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 35 40 45
 35 Arg Leu Ala Gln Glu Asn Glu Val Asp Phe Ile Leu Leu Gly Gly Asp
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 Leu Phe His Glu Asn Lys Pro Ser Arg Lys Thr Leu His Thr Cys Leu
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 Val Asn Tyr Gln Asp Gly Asn Leu Asn Ile Ser Ile Pro Val Phe Ser
 115 120 125
 45 Ile His Gly Asn His Asp Asp Pro Thr Gly Ala Asp Ala Leu Cys Ala
 130 135 140
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 Gln Trp Leu Trp Glu Lys Ile Asp Ile Xaa Ser Gly Phe Cys Phe Lys
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 Phe Xaa Glu
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 35 40 45
 5 Ala Ile Thr Tyr Thr Tyr Asp Leu Met Ala Asn Leu Ala Phe Ile Arg
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 Gly Gln Leu Glu Asn Ala Glu Gln Leu Phe Lys Ala Thr Met Ser Tyr
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 10 Leu Leu Gly Gly Gly Met Lys Gln Glu Asp Asn Ala Ile Ile Glu Ile
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 Ser Leu Lys Leu Ala Ser Ile Tyr Ala Ala Gln Asn Arg Gln Glu Phe
 100 105 110
 Ala Val Ala Gly Tyr Glu Phe Cys Ile Ser Thr Leu Glu Glu Lys Ile
 115 120 125
 15 Glu Arg Glu Lys Glu Leu Ala Glu Asp Ile Met Ser Val Glu Glu Lys
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25 <213> Homo sapiens

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 115 120 125
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 245 250 255
 60 Lys Tyr Leu Asp Ile Pro Lys Met Leu Asp Ala Glu Asp Ile Val Asn
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 Thr Ala Arg Pro Asp Glu Lys Ala Ile Met Thr Tyr Val Ser Ser Phe
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 305 310 315 320
 5 Ser Met Glu Asp Tyr Glu Lys Leu Ala Ser Asp Leu Leu Glu Trp Ile
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 10 Gln Glu Met Gln Gln Lys Leu Glu Asp Phe Arg Asp Tyr Arg Arg Val
 355 360 365
 His Lys Pro Pro Lys Val Gln Glu Lys Cys Gln Leu Glu Ile Asn Phe
 370 375 380
 Asn Ser Val Gln Thr Lys Leu Arg Leu Ser Asn Arg Pro Ala Phe Met
 385 390 395 400
 15 Pro Ser Glu Gly Lys Met Val Ser Asp Ile Asn Asn Gly Trp Gln His
 405 410 415
 Leu Glu Gln Ala Glu Lys Gly Tyr Glu Glu Trp Leu Leu Asn Glu Ile
 420 425 430
 20 Arg Arg Leu Glu Arg Leu Asp His Leu Ala Glu Lys Phe Arg Gln Lys
 435 440 445
 Ala Ser Ile His Glu Ala Trp Thr Asp Gly Lys Glu Ala Met Leu Lys
 450 455 460
 His Arg Asp Tyr Glu Thr Ala Thr Leu Ser Asp Ile Lys Ala Leu Ile
 465 470 475 480
 25 Arg Lys His Glu Ala Phe Glu Ser Asp Leu Ala Ala His Gln Asp Arg
 485 490 495
 Val Glu Gln Ile Ala Ala Ser Ala Gln Glu Leu Asn Glu Leu Asp Tyr
 500 505 510
 30 Tyr Asp Ser His Asn Val Asn Thr Arg Cys Gln Lys Ile Cys Asp Gln
 515 520 525
 Trp Asp Ala Leu Gly Ser Leu Thr His Ser Arg Arg Glu Ala Leu Glu
 530 535 540
 Lys Thr Glu Lys Gln Leu Glu Ala Ile Ile Asp Gln Leu His Leu Glu
 545 550 555 560
 35 Tyr Ala Lys Pro Ala Ala Pro Phe Asn Asn Trp Met Glu Ser Ala Met
 565 570 575
 Glu Asp Leu Gln Asp Met Phe Ile Val His Thr Ile Glu Glu Ile Glu
 580 585 590
 40 Gly Leu Ile Ser Ala His Asp Gln Phe Lys Ser Thr Leu Pro Asp Ala
 595 600 605
 Asp Arg Glu Arg Glu Ala Ile Leu His Pro Gln Gly Gly Gln Arg Ile
 610 615 620
 Ala Glu Ser Asn His Ile Lys Leu Ser Gly Ser Asn Pro Tyr Thr Thr
 625 630 635 640
 45 Val Thr Pro Gln Ile Ile Asn Ser Lys Trp Glu Lys Val Gln Gln Leu
 645 650 655
 Val Pro Lys Arg Asp His Ala Leu Leu Glu Glu Gln Ser Lys Gln Gln
 660 665 670
 50 Gln Ser Asn Glu His Leu Arg Arg Gln Phe Ala Ser Gln Ala Asn Val
 675 680 685
 Val Gly Pro Trp Ile Gln Thr Lys Met Glu Glu Ile Ala Ile Ser Ile
 690 695 700
 Glu Met Asn Gly Thr Leu Glu Asp Gln Leu Ser His Leu Lys Gln Tyr
 705 710 715 720
 55 Glu Arg Ser Ile Val Asp Tyr Lys Pro Asn Leu Asp Leu Leu Glu Gln
 725 730 735
 Gln His Gln Leu Ile Gln Glu Ala Leu Ile Phe Asp Asn Lys His Thr
 740 745 750
 60 Asn Tyr Thr Met Glu His Ile Arg Val Gly Trp Glu Gln Leu Leu Thr
 755 760 765
 Thr Ile Ala Arg Thr Ile Asn Glu Val Glu Asn Gln Ile Leu Thr Arg
 770 775 780
 Asp Ala Lys Gly Ile Ser Gln Glu Gln Met Gln Glu Phe Arg Ala Ser

785 790 795 800
 Phe Asn His Phe Asp Lys Asp His Gly Gly Ala Leu Gly Arg Gly Val
 805 810 815
 5 Gln Gly Leu Pro His Gln Pro Gly Leu Arg Arg Gly Glu Arg Pro Ala
 820 825 830
 Gly Glu Ala Glu Phe Asn Arg Ile Met Ser Leu Val Asp Pro Asn His
 835 840 845
 Ser Gly Leu Val Thr Phe Gln Ala Phe Ile Asp Phe Met Ser Arg Glu
 850 855 860
 10 Thr Thr Asp Thr Asp Thr Ala Asp Gln Val Ile Thr Ser Phe Lys Val
 865 870 875 880
 Leu Ala Gly Asp Lys Asn Phe Ile Thr Ala Glu Glu Leu Arg Arg Glu
 885 890 895
 Leu Pro Pro Asp Gln Ala Glu Tyr Cys Ile Ala Arg Met Ala Pro Tyr
 900 905 910
 15 Gln Gly Pro Asp Gly Val Arg Gly Ala Leu Asp Tyr Lys Ser Phe Ser
 915 920 925
 Thr Ala Leu Tyr Gly Glu Ser Asp Leu
 930 935
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 <211> 1884
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 <213> Homo sapiens
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 <400> 603
 Val Ala Gly Cys Arg Arg Arg Gly Ala Gly Asp Pro Asn Met Ala Asn
 1 5 10 15
 30 Leu Glu Glu Ser Phe Pro Arg Gly Gly Thr Arg Lys Ile His Lys Pro
 20 25 30
 Glu Lys Ala Phe Gln Gln Ser Val Glu Gln Asp Asn Leu Phe Asp Ile
 35 40 45
 Ser Thr Glu Glu Gly Ser Thr Lys Arg Lys Lys Ser Gln Lys Gly Pro
 50 55 60
 35 Ala Lys Thr Lys Lys Leu Lys Ile Glu Lys Arg Glu Ser Ser Lys Ser
 65 70 75 80
 Ala Arg Glu Lys Phe Glu Ile Leu Ser Val Glu Ser Leu Cys Glu Gly
 85 90 95
 Met Arg Ile Leu Gly Cys Val Lys Glu Val Asn Glu Leu Glu Leu Val
 100 105 110
 40 Ile Ser Leu Pro Asn Gly Leu Gln Gly Phe Val Gln Val Thr Glu Ile
 115 120 125
 Cys Asp Ala Tyr Thr Lys Lys Leu Asn Glu Gln Val Thr Gln Glu Gln
 130 135 140
 45 Pro Leu Lys Asp Leu Leu His Leu Pro Glu Leu Phe Ser Pro Gly Met
 145 150 155 160
 Leu Val Arg Cys Val Val Ser Ser Leu Gly Ile Thr Asp Arg Gly Lys
 165 170 175
 Lys Ser Val Lys Leu Ser Leu Asn Pro Lys Asn Val Asn Arg Val Leu
 180 185 190
 50 Ser Ala Glu Ala Leu Lys Pro Gly Met Leu Leu Thr Gly Thr Val Ser
 195 200 205
 Ser Leu Glu Asp His Gly Tyr Leu Val Asp Ile Gly Val Asp Gly Thr
 210 215 220
 55 Arg Ala Phe Leu Pro Leu Lys Ala Gln Glu Tyr Ile Arg Gln Lys
 225 230 235 240
 Asn Lys Gly Ala Lys Leu Lys Val Gly Gln Tyr Leu Asn Cys Ile Val
 245 250 255
 Glu Lys Val Lys Gly Asn Gly Gly Val Val Ser Leu Ser Val Gly His
 260 265 270
 60 Ser Glu Val Ser Thr Ala Ile Ala Thr Glu Gln Gln Ser Trp Asn Leu
 275 280 285
 Asn Asn Leu Leu Pro Gly Leu Val Lys Ala Gln Val Gln Lys Val

[illegible]

	Glu	Glu	Lys	Gln	Arg	Met	Leu	Leu	Ser	Leu	Arg	Leu	Ser	Asp	Cys	Gly
					805					810					815	
	Leu	Gly	Asp	Leu	Ala	Ile	Thr	Ser	Leu	Leu	Leu	Leu	Asn	Gln	Cys	Leu
				820				825						830		
5	Glu	Glu	Leu	Gln	Gly	Val	Arg	Ser	Leu	Met	Ser	Asn	Arg	Asp	Ser	Val
			835				840					845				
	Leu	Ile	Gln	Thr	Leu	Ala	Glu	Met	Thr	Pro	Gly	Met	Phe	Leu	Asp	Leu
		850					855					860				
10	Val	Val	Gln	Glu	Val	Leu	Glu	Asp	Gly	Ser	Val	Val	Phe	Ser	Gly	Gly
	865					870					875				880	
	Pro	Val	Pro	Asp	Leu	Val	Leu	Lys	Ala	Ser	Arg	Tyr	His	Arg	Ala	Gly
				885					890						895	
	Gln	Glu	Val	Glu	Ser	Gly	Gln	Lys	Lys	Lys	Val	Val	Ile	Leu	Asn	Val
				900					905					910		
15	Asp	Leu	Leu	Lys	Leu	Glu	Val	His	Val	Ser	Leu	His	Gln	Asp	Leu	Val
			915					920					925			
	Asn	Arg	Lys	Ala	Arg	Lys	Leu	Arg	Lys	Gly	Ser	Glu	His	Gln	Ala	Ile
		930					935					940				
20	Val	Gln	His	Leu	Glu	Lys	Ser	Phe	Ala	Ile	Ala	Ser	Leu	Val	Glu	Thr
	945					950					955				960	
	Gly	His	Leu	Ala	Ala	Phe	Ser	Leu	Thr	Ser	His	Leu	Asn	Asp	Thr	Phe
				965						970					975	
	Arg	Phe	Asp	Ser	Glu	Lys	Leu	Gln	Val	Gly	Gln	Gly	Val	Ser	Leu	Thr
				980					985					990		
25	Leu	Lys	Thr	Thr	Glu	Pro	Gly	Val	Thr	Gly	Leu	Leu	Leu	Ala	Val	Glu
			995				1000						1005			
	Gly	Pro	Ala	Ala	Lys	Arg	Thr	Met	Arg	Pro	Thr	Gln	Lys	Asp	Ser	Glu
		1010					1015					1020				
30	Thr	Val	Asp	Glu	Asp	Glu	Glu	Val	Asp	Pro	Ala	Leu	Thr	Val	Gly	Thr
	1025					1030					1035				104	
	Ile	Lys	Lys	His	Thr	Leu	Ser	Ile	Gly	Asp	Met	Val	Thr	Gly	Thr	Val
				1045						1050					1055	
	Lys	Ser	Ile	Lys	Pro	Thr	His	Val	Val	Val	Thr	Leu	Glu	Asp	Gly	Ile
				1060					1065					1070		
35	Ile	Gly	Cys	Ile	His	Ala	Ser	His	Ile	Leu	Asp	Asp	Val	Pro	Glu	Gly
			1075					1080					1085			
	Thr	Ser	Pro	Thr	Thr	Lys	Leu	Lys	Val	Gly	Lys	Thr	Val	Thr	Ala	Arg
		1090					1095					1100				
40	Val	Ile	Gly	Gly	Arg	Asp	Met	Lys	Thr	Phe	Lys	Tyr	Leu	Pro	Ile	Ser
	1105					1110					1115				112	
	His	Pro	Arg	Phe	Val	Arg	Thr	Ile	Pro	Glu	Leu	Ser	Val	Arg	Pro	Ser
				1125				</								

		1300		1305		1310										
	Ser	Arg	Thr	Asn	Pro	Glu	Thr	Lys	Ser	Lys	Val	Glu	Asp	Pro	Glu	Ile
		1315		1320		1325										
5	Asn	Ser	Ile	Gln	Asp	Ile	Lys	Glu	Gly	Gln	Leu	Leu	Arg	Gly	Tyr	Val
		1330		1335		1340										
	Gly	Ser	Ile	Gln	Pro	His	Gly	Val	Phe	Phe	Arg	Leu	Gly	Pro	Ser	Val
	1345			1350		1355									136	
	Val	Gly	Leu	Ala	Arg	Tyr	Ser	His	Val	Ser	Gln	His	Ser	Pro	Ser	Lys
				1365		1370									1375	
10	Lys	Ala	Leu	Tyr	Asn	Lys	His	Leu	Pro	Glu	Gly	Lys	Leu	Leu	Thr	Ala
				1380		1385									1390	
	Arg	Val	Leu	Arg	Leu	Asn	His	Gln	Lys	Asn	Leu	Val	Glu	Leu	Ser	Phe
				1395		1400									1405	
	Leu	Pro	Gly	Asp	Thr	Gly	Lys	Pro	Asp	Val	Leu	Ser	Ala	Ser	Leu	Glu
15		1410				1415							1420			
	Gly	Gln	Leu	Thr	Lys	Gln	Glu	Glu	Arg	Lys	Thr	Glu	Ala	Glu	Glu	Arg
	1425					1430						1435				144
	Asp	Gln	Lys	Gly	Glu	Lys	Lys	Asn	Gln	Lys	Arg	Asn	Glu	Lys	Lys	Asn
				1445						1450					1455	
20	Gln	Lys	Gly	Gln	Glu	Glu	Val	Glu	Met	Pro	Ser	Lys	Glu	Lys	Gln	Gln
				1460						1465					1470	
	Pro	Gln	Lys	Pro	Gln	Ala	Gln	Lys	Arg	Gly	Gly	Arg	Glu	Cys	Arg	Glu
				1475						1480					1485	
	Ser	Gly	Ser	Glu	Gln	Glu	Arg	Val	Ser	Lys	Lys	Pro	Lys	Lys	Ala	Gly
25		1490				1495						1500				
	Leu	Ser	Glu	Glu	Asp	Asp	Ser	Leu	Val	Asp	Val	Tyr	Tyr	Arg	Glu	Gly
	1505					1510						1515				152
	Lys	Glu	Glu	Ala	Glu	Glu	Thr	Asn	Val	Leu	Pro	Lys	Glu	Lys	Gln	Thr
				1525						1530					1535	
30	Lys	Pro	Ala	Glu	Ala	Pro	Arg	Leu	Gln	Leu	Ser	Ser	Gly	Phe	Ala	Trp
				1540						1545					1550	
	Asn	Val	Gly	Leu	Asp	Ser	Leu	Thr	Pro	Ala	Leu	Pro	Pro	Leu	Ala	Glu
				1555						1560					1565	
	Ser	Ser	Asp	Ser	Glu	Glu	Asp	Glu	Lys	Pro	His	Gln	Ala	Thr	Ile	Lys
35		1570				1575						1580				
	Lys	Ser	Lys	Lys	Glu	Arg	Glu	Leu	Glu	Lys	Gln	Lys	Ala	Glu	Lys	Glu
	1585					1590						1595				160
	Leu	Ser	Arg	Ile	Glu	Glu	Ala	Leu	Met	Asp	Pro	Gly	Arg	Gln	Pro	Glu
				1605						1610					1615	
40	Ser	Ala	Asp	Asp	Phe	Asp	Arg	Leu	Val	Leu	Ser	Ser	Pro	Asn	Ser	Ser
				1620						1625					1630	
	Ile	Leu	Trp	Leu	Gln	Tyr	Met	Ala	Phe	His	Leu	Gln	Ala	Thr	Glu	Ile
				1635						1640					1645	
	Glu	Lys	Ala	Arg	Ala	Val	Ala	Glu	Arg	Ala	Leu	Lys	Thr	Ile	Ser	Phe
45		1650				1655						1660				
	Arg	Glu	Glu	Gln	Glu	Lys	Leu	Asn	Val	Trp	Val	Ala	Leu	Leu	Asn	Leu
	1665					1670						1675				168
	Glu	Asn	Met	Tyr	Gly	Ser	Gln	Glu	Ser	Leu	Thr	Lys	Val	Phe	Glu	Arg
				1685						1690					1695	
50	Ala	Val	Gln	Tyr	Asn	Glu	Pro	Leu	Lys	Val	Phe	Leu	His	Leu	Ala	Asp
				1700						1705					1710	
	Ile	Tyr	Ala	Lys	Ser	Glu	Lys	Phe	Gln	Glu	Ala	Gly	Glu	Leu	Tyr	Asn
				1715						1720					1725	
	Arg	Met	Leu	Lys	Arg	Phe	Arg	Gln	Glu	Lys	Ala	Val	Trp	Ile	Lys	Tyr
55		1730				1735						1740				
	Gly	Ala	Phe	Leu	Leu	Arg	Ser	Gln	Ala	Ala	Ala	Ser	His	Arg	Val	
	1745					1750						1755				176
	Leu	Gln	Arg	Ala	Leu	Glu	Cys	Leu	Pro	Ser	Lys	Glu	His	Val	Asp	Val
				1765						1770					1775	
60	Ile	Ala	Lys	Phe	Ala	Gln	Leu	Glu	Phe	Gln	Leu	Gly	Asp	Ala	Glu	Arg
				1780						1785					1790	
	Ala	Lys	Ala	Ile	Phe	Glu	Asn	Thr	Leu	Ser	Thr	Tyr	Pro	Lys	Arg	Thr
				1795						1800					1805	

Asp Val Trp Ser Val Tyr Ile Asp Met Thr Ile Lys His Gly Ser Gln
 1810 1815 1820
 Lys Asp Val Arg Asp Ile Phe Glu Arg Val Ile His Leu Ser Leu Ala
 1825 1830 1835 184
 5 Pro Lys Arg Met Lys Phe Phe Phe Lys Arg Tyr Leu Asp Tyr Glu Lys
 1845 1850 1855
 Gln His Gly Thr Glu Lys Asp Val Gln Ala Val Lys Ala Lys Ala Leu
 1860 1865 1870
 10 Glu Tyr Val Glu Ala Lys Ser Ser Val Leu Glu Asp
 1875 1880

<210> 604

<211> 192

<212> PRT

15 <213> Homo sapiens

<400> 604

Asp Ala Leu Leu Arg Glu Phe Gln Glu Glu Ile Ala Arg Leu Lys Ala
 1 5 10 15
 20 Gln Leu Glu Lys Arg Ser Ile Glu Glu Lys Met Arg Leu Leu Lys Glu
 20 25 30
 Lys Glu Lys Lys Met Glu Asp Leu Arg Arg Glu Lys Asp Ala Ala Glu
 35 40 45
 25 Met Leu Gly Ala Lys Ile Lys Ala Met Glu Ser Lys Leu Leu Val Gly
 50 55 60
 Gly Lys Asn Ile Val Asp His Thr Asn Glu Gln Gln Lys Ile Leu Glu
 65 70 75 80
 Gln Lys Arg Gln Glu Ile Ala Glu Gln Lys Arg Xaa Glu Arg Glu Ile
 85 90 95
 30 Gln Gln Gln Met Glu Ser Arg Asp Glu Glu Thr Leu Glu Leu Lys Glu
 100 105 110
 Thr Tyr Ser Ser Leu Gln Gln Glu Val Asp Ile Lys Thr Lys Lys Leu
 115 120 125
 35 Lys Lys Leu Phe Xaa Lys Leu Gln Ala Val Lys Ala Glu Ile His Asp
 130 135 140
 Leu Gln Glu Glu His Xaa Lys Glu Arg Gln Glu Leu Xaa Gln Thr Gln
 145 150 155 160
 Asn Glu Leu Thr Arg Glu Leu Lys Leu Lys His Leu Ile Ile Glu Asn
 165 170 175
 40 Phe Ile Pro Leu Glu Glu Lys Ser Lys Ile Met Asn Arg Ala Phe Phe
 180 185 190

<210> 605

<211> 186

<212> PRT

45 <213> Homo sapiens

<400> 605

Lys Pro Gly Arg Glu Lys Gln Glu Gly Thr Met Ala Ser Ser Ser Gly
 1 5 10 15
 50 Asn Asp Asp Asp Leu Thr Ile Pro Arg Ala Ala Ile Asn Lys Met Ile
 20 25 30
 Lys Glu Thr Leu Pro Asn Val Arg Val Ala Asn Asp Ala Arg Glu Leu
 35 40 45
 55 Val Val Asn Cys Cys Thr Glu Phe Ile His Leu Ile Ser Ser Glu Ala
 50 55 60
 Asn Glu Ile Cys Asn Lys Ser Glu Lys Lys Thr Ile Ser Pro Glu His
 65 70 75 80
 Val Ile Gln Ala Leu Glu Ser Leu Gly Phe Gly Ser Tyr Ile S r Glu
 85 90 95
 60 Val Lys Glu Val Leu Gln Glu Cys Lys Thr Val Ala Leu Lys Arg Arg
 100 105 110
 Lys Ala Ser Ser Arg Leu Glu Asn Leu Gly Ile Pro Glu Glu Glu Leu

115 120 125
 Leu Arg Gln Gln Gln Glu Leu Phe Ala Lys Ala Arg Gln Gln Gln Ala
 130 135 140
 Glu Leu Ala Gln Gln Glu Trp Leu Gln Met Gln Gln Ala Ala Gln Gln
 145 150 155 160
 Ala Gln Leu Ala Ala Ala Ser Ala Ser Ala Ser Asn Gln Ala Gly Ser
 165 170 175
 Ser Gln Asp Glu Glu Asp Asp Asp Asp Ile
 180 185
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 <211> 328
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 <213> Homo sapiens
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 <400> 606
 Glu Pro Val Val Leu Arg Phe Met Ile Phe Cys Arg Leu Leu Ala Lys
 1 5 10 15
 Met Ala Asn Asn Asp Ala Val Leu Lys Arg Leu Glu Gln Lys Gly Ala
 20 20 25 30
 Glu Ala Asp Gln Ile Ile Glu Tyr Leu Lys Gln Gln Val Ser Leu Leu
 35 40 45
 Lys Glu Lys Ala Ile Leu Gln Ala Thr Leu Arg Glu Glu Lys Lys Leu
 50 55 60
 25 Arg Val Glu Asn Ala Lys Leu Lys Lys Glu Ile Glu Glu Leu Lys Gln
 65 70 75 80
 Glu Leu Ile Gln Ala Glu Ile Gln Asn Gly Val Lys Gln Ile Ala Phe
 85 90 95
 Pro Ser Gly Thr Pro Leu His Ala Asn Ser Met Val Ser Glu Asn Val
 100 105 110
 30 Ile Gln Ser Thr Ala Val Thr Thr Val Ser Ser Gly Thr Lys Glu Gln
 115 120 125
 Ile Lys Gly Gly Thr Gly Asp Glu Lys Lys Ala Lys Glu Lys Ile Glu
 130 135 140
 35 Lys Lys Gly Glu Lys Lys Glu Lys Lys Gln Gln Ser Ile Ala Gly Ser
 145 150 155 160
 Ala Asp Ser Lys Pro Ile Asp Val Ser Arg Leu Asp Leu Arg Ile Gly
 165 170 175
 Cys Ile Ile Thr Ala Arg Lys His Pro Asp Ala Asp Ser Leu Tyr Val
 180 185 190
 40 Glu Glu Val Asp Val Gly Glu Ile Ala Pro Arg Thr Val Val Ser Gly
 195 200 205
 Leu Val Asn His Val Pro Leu Glu Gln Met Gln Asn Arg Met Val Ile
 210 215 220
 45 Leu Leu Cys Asn Leu Lys Pro Ala Lys Met Arg Gly Val Leu Ser Gln
 225 230 235 240
 Ala Met Val Met Cys Ala Ser Ser Pro Glu Lys Ile Glu Ile Leu Ala
 245 250 255
 Pro Pro Asn Gly Ser Val Pro Gly Asp Arg Ile Thr Phe Asp Ala Phe
 260 265 270
 50 Pro Gly Glu Pro Asp Lys Glu Leu Asn Pro Lys Lys Lys Ile Trp Glu
 275 280 285
 Gln Ile Gln Pro Asp Leu His Thr Asn Asp Glu Cys Val Ala Thr Tyr
 290 295 300
 55 Lys Gly Val Pro Phe Glu Val Lys Gly Lys Gly Val Cys Arg Ala Gln
 305 310 315 320
 Thr Met Ser Asn Ser Gly Ile Lys
 325
 60
 <210> 607
 <211> 347
 <212> PRT
 <213> Homo sapiens

	Arg	Arg	Glu	Ala	Val	Lys	Gln	Tyr	Ser	Ser	Tyr	Asn	Phe	Phe	Arg	Pro
					85					90					95	
	Asp	Asn	Glu	Glu	Ala	Met	Lys	Val	Arg	Lys	Gln	Cys	Ala	Leu	Ala	Ala
				100					105					110		
5	Leu	Arg	Asp	Val	Lys	Ser	Tyr	Leu	Ala	Lys	Glu	Gly	Gly	Gln	Ile	Ala
			115					120					125			
	Val	Phe	Asp	Ala	Thr	Asn	Thr	Thr	Arg	Glu	Arg	Arg	His	Met	Ile	Leu
			130				135					140				
10	His	Phe	Ala	Lys	Glu	Asn	Asp	Phe	Lys	Ala	Phe	Phe	Ile	Glu	Ser	Val
	145					150					155				160	
	Cys	Asp	Asp	Pro	Thr	Val	Val	Ala	Ser	Asn	Ile	Met	Glu	Val	Lys	Ile
				165						170					175	
	Ser	Ser	Pro	Asp	Tyr	Lys	Asp	Cys	Asn	Ser	Ala	Glu	Ala	Met	Asp	Asp
			180						185					190		
15	Phe	Met	Lys	Arg	Ile	Ser	Cys	Tyr	Glu	Ala	Ser	Tyr	Gln	Pro	Leu	Asp
			195					200					205			
	Pro	Asp	Lys	Cys	Asp	Arg	Asp	Leu	Ser	Leu	Ile	Lys	Val	Ile	Asp	Val
			210				215					220				
20	Gly	Arg	Arg	Phe	Leu	Val	Asn	Arg	Val	Gln	Asp	His	Ile	Gln	Ser	Arg
	225					230					235					240
	Ile	Val	Tyr	Tyr	Leu	Met	Asn	Ile	His	Val	Gln	Pro	Arg	Thr	Ile	Tyr
				245						250					255	
	Leu	Cys	Arg	His	Gly	Glu	Asn	Glu	His	Asn	Leu	Gln	Gly	Arg	Ile	Gly
			260					265					270			
25	Gly	Asp	Ser	Gly	Leu	Ser	Ser	Arg	Gly	Lys	Lys	Phe	Ala	Ser	Ala	Leu
		275						280					285			
	Ser	Lys	Phe	Val	Glu	Glu	Gln	Asn	Leu	Lys	Asp	Leu	Arg	Val	Trp	Thr
		290					295					300				
30	Ser	Gln	Leu	Lys	Ser	Thr	Ile	Gln	Thr	Ala	Glu	Ala	Leu	Arg	Leu	Pro
	305					310					315					320
	Tyr	Glu	Gln	Trp	Lys	Ala	Leu	Asn	Glu	Ile	Asp	Ala	Gly	Val	Cys	Glu
				325						330					335	
	Glu	Leu	Thr	Tyr	Glu	Glu	Ile	Arg	Asp	Thr	Tyr	Pro	Glu	Glu	Tyr	Ala
			340						345				350			
35	Leu	Arg	Glu	Gln	Asp	Lys	Tyr	Tyr	Arg	Tyr	Pro	Thr	Gly	Glu	Ser	
		355						360				365				
	Tyr	Gln	Asp	Leu	Val	Gln	Arg	Leu	Glu	Pro	Val	Ile	Met	Glu	Leu	Glu
		370					375					380				
40	Arg	Gln	Glu	Asn	Val	Leu	Val	Ile	Cys	His	Gln	Ala	Val	Leu	Arg	Cys
	385					390					395				400	
	Leu	Leu	Ala	Tyr	Phe	Leu	Asp	Lys	Ser	Ala	Glu	Glu	Met	Pro	Tyr	Leu
				405						410					415	
	Lys	Cys	Pro	Leu	His	Thr	Val	Leu	Lys	Leu	Thr	Pro	Val	Ala	Tyr	Gly
			420						425				430			
45	Cys	Arg	Val	Glu	Ser	Ile	Tyr	Leu	Asn	Val	Glu	Ser	Val	Cys	Thr	His
		435						440					445			
	Arg	Glu	Arg	Ser	Glu	Asp	Ala	Lys	Lys	Gly	Pro	Asn	Pro	Leu	Met	Arg
		450					455					460				
50	Arg	Asn	Ser	Val	Thr	Pro	Leu	Ala	Ser	Pro	Glu	Pro	Thr	Lys	Lys	Pro
	465					470					475					480
	Arg	Ile	Asn	Ser	Phe	Glu	Glu	His	Val	Ala	Ser	Thr	Ser	Ala	Ala	Leu
				485						490					495	
	Pro	Ser	Cys	Leu	Pro	Pro	Glu	Val	Pro	Thr	Gln	Leu	Pro	Gly	Gln	Asn
			500						505					510		
55	Met	Lys	Gly	Ser	Arg	Ser	Ser	Ala	Asp	Ser	Ser	Arg	Lys	His		
		515						520					525			

<210> 609

<211> 205

60 <212> PRT

<213> Homo sapiens

<400> 609

Asn Ile Ser Cys Asn Leu Leu Asn Ile Val Leu Lys Val Lys Asn Arg
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 Met Val Val Trp Glu Leu Glu Ala Leu Phe Pro Leu Leu Gln Asn Ala
 20 25 30
 5 Tyr Leu Ser Cys Ile Ile Val Lys Trp Lys Cys His Lys Leu Pro Ile
 35 40 45
 Ile His Trp Xaa Pro Leu Tyr Phe Thr Gln Leu Thr Leu Thr Trp Glu
 50 55 60
 10 Ile Pro His Asn His Ser Ile Arg Glu Ala Ser Xaa Ser Pro Gln Gln
 65 70 75 80
 Leu Arg Leu Ile Gly Leu Phe Gln Pro Gly Ile Ile Arg Ser Arg Leu
 85 90 95
 Pro Gln Ser Gln Lys Gly Glu Glu Ala Xaa Pro Val Trp Ala Pro Gly
 100 105 110
 15 Cys Leu Val Gln Pro Arg Val His Ser Trp Met Pro Arg Ser Pro Xaa
 115 120 125
 Trp Val Ser Xaa Glu Cys Ser Ala Leu Gln Gly Ala Gly Leu Val Ala
 130 135 140
 20 Gln Gly Pro Phe Gln Glu Phe His Ser Leu Thr Leu Val Gln Ala Ala
 145 150 155 160
 Ala Trp Ala Pro Pro Gly Ala Gly Ser Trp Ala Gly Arg Pro Xaa Trp
 165 170 175
 Arg Pro Met Leu Leu Lys Ala Val Asp Ala Arg Leu Phe Trp Trp Val
 180 185 190
 25 Arg Gly Leu Ala Xaa Arg Gly Asp Thr Ile Xaa Val Ser
 195 200 205

<210> 610

<211> 199

<212> PRT

<213> Homo sapiens

<400> 610

Val Ile Pro Ser Thr Gly Ile Lys Leu Pro Ser Ser Val Phe Ala Ser
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 Glu Phe Glu Glu Asp Val Gly Leu Leu Asn Lys Ala Ala Pro Val Ser
 20 25 30
 Gly Pro Arg Leu Asp Phe Asp Pro Asp Ile Val Ala Ala Leu Asp Asp
 35 40 45
 40 Asp Phe Asp Phe Asp Asp Pro Asp Asn Leu Leu Glu Asp Asp Phe Ile
 50 55 60
 Leu Gln Ala Asn Lys Ala Thr Gly Glu Glu Glu Gly Met Asp Ile Gln
 65 70 75 80
 Lys Ser Glu Asn Glu Asp Asp Ser Glu Trp Glu Asp Val Asp Asp Glu
 85 90 95
 45 Lys Gly Asp Ser Asn Asp Asp Tyr Asp Ser Ala Gly Leu Leu Ser Asp
 100 105 110
 Glu Asp Cys Met Ser Val Pro Gly Lys Thr His Arg Ala Ile Ala Asp
 115 120 125
 50 His Leu Phe Trp Ser Glu Glu Thr Lys Ser Arg Phe Thr Glu Tyr Ser
 130 135 140
 Met Thr Ser Ser Val Met Arg Arg Asn Glu Gln Leu Thr Leu His Asp
 145 150 155 160
 Glu Arg Phe Glu Lys Phe Tyr Glu Gln Tyr Asp Asp Asp Glu Ile Gly
 165 170 175
 55 Ala Leu Asp Asn Ala Glu Leu Glu Gly Ser Ile Gln Val Gly Gln Gln
 180 185 190
 Ser Leu Thr Gly Ser Phe Glu
 195

<210> 611

<211> 117

<212> PRT

<213> Homo sapiens

<400> 611

5 Ser Cys Ser Gly Ala Gly Thr Pro Arg Thr Gly Thr Arg Ser Pro Met
 1 5 10 15
 Glu Ala Trp His Ala Gly Arg Gly Asn Arg Pro Thr Pro Pro Ser Ala
 20 25 30
 Leu Ser Pro Ala Arg Lys Arg Gly Lys Asn Cys Asn Ser Ser Gly Lys
 35 40 45
 10 Leu Ser Ser Lys Ser Leu Pro Thr Ser Asp Asp Tyr Glu Leu Gly Ala
 50 55 60
 Gly Ile Arg Lys Arg His Lys Gly Pro Lys Glu Glu His Asn Ala Leu
 65 70 75 80
 Ile Gly Thr Gly Lys Ala Arg Glu Arg Asn Gln Thr Trp Asp Glu His
 85 90 95
 15 Glu Ala Ser Ser Lys Phe Ile Ser Gln Leu Lys Ile Lys Lys Lys Lys
 100 105 110
 Met Asp Ser Asp Gln
 115

20

<210> 612

<211> 128

<212> PRT

<213> Homo sapiens

25

<400> 612

Ser Leu Leu Ala Ala Gly Ser His Met Leu Arg Glu Val Leu Asp Gly
 1 5 10 15
 Pro Val Val Gly Pro Ala Gln Glu Pro Ala Ala Pro Thr Gly Ala Glu
 20 25 30
 Ala His Asn Lys Tyr Ser Trp Met Arg Lys Lys Glu Glu Arg Met Tyr
 35 40 45
 Pro Met Lys Ser Ser Val Glu Asp Met Asp Val Leu Glu Leu Asp Phe
 50 55 60
 35 Arg Met Trp Arg Ala Glu Val Gln His Gln Tyr Lys Glu Lys Gln His
 65 70 75 80
 Glu Leu Val Lys Leu Gln Arg Arg Arg Asp Ser Glu Asp Arg His Glu
 85 90 95
 Glu Ser His Gly Ser Leu Ala Arg Arg Pro Trp Lys Gln Thr His Ala
 100 105 110
 40 Pro Glu Arg Pro Val Ala Arg Pro Gln Glu Gly Glu Glu Leu Gln Gln
 115 120 125

45

<210> 613

<211> 197

<212> PRT

<213> Homo sapiens

<400> 613

50 Ala Arg Ala Leu Glu Lys Leu Glu Ala Ala Glu Ser Leu Val Leu Glu
 1 5 10 15
 Gln Ser Phe Leu His Gly Ile Thr Leu Leu Ser Glu Ile Ala Glu Leu
 20 25 30
 Glu Leu Glu Arg Arg Ser Gln Glu Met Gly Gly Ala Glu Arg Ala Leu
 35 40 45
 Val Ala Arg Pro Ser Leu Glu Ser Leu Leu Ala Ala Gly Ser His Met
 50 55 60
 Leu Arg Glu Val Leu Asp Gly Pro Val Val Asp Pro Leu Lys Asn Leu
 65 70 75 80
 60 Arg Leu Pro Arg Glu Leu Lys Pro Asn Lys Lys Tyr Ser Trp Met Arg
 85 90 95
 Lys Lys Glu Glu Arg Met Tyr Ala Met Lys Ser Ser Leu Glu Asp Met
 100 105 110

Asp Ala Leu Glu Leu Asp Phe Arg Met Arg Leu Ala Glu Val Gln Arg
 115 120 125
 Gln Tyr Lys Glu Lys Gln Arg Glu Leu Val Lys Leu Gln Arg Arg Arg
 130 135 140
 5 Asp S r Glu Asp Arg Arg Glu Glu Pro His Arg Ser Leu Ala Arg Arg
 145 150 155 160
 Gly Pro Gly Arg Pro Arg Lys Arg Thr His Ala Pro Ser Ala Leu Ser
 165 170 175
 10 Pro Pro Arg Lys Arg Gly Lys Ser Gly His Ser Ser Gly Lys Leu Ser
 180 185 190
 Ser Lys Val Ser Cys
 195

15 <210> 614
 <211> 184
 <212> PRT
 <213> Homo sapiens

20 <400> 614
 Leu Lys Met Asn Ser Ile Cys Leu Ile Lys Leu Gly Ile Thr Lys Ile
 1 5 10 15
 Ala Val Gln Thr Ser Ser His Thr Pro Thr Arg Gln Asn Ser Ile Tyr
 20 25 30
 25 Lys Met Phe Xaa Gly Lys Pro Xaa Pro Asn Pro Cys Pro Lys Arg Ala
 35 40 45
 Arg Thr Lys Pro Gly Val Ser Gly Trp Ala Xaa Asn Val Ser Ala Gly
 50 55 60
 Val Gly Gly Thr Arg Gly Arg Gly Arg Arg Ala Gly Arg Arg Ala Ser
 65 70 75 80
 30 Gly Xaa Lys Arg Arg Xaa Lys Ser Ser His Ile Thr Ala Gln Lys Glu
 85 90 95
 Pro Ala Gly Asp Ile Ile Thr Met Ile Gln Ser Asn Xaa Ser Lys Asn
 100 105 110
 Gln Asn His Ser Ala Asp Asn Ser Lys Leu Arg Cys Gln Glu Pro Ile
 115 120 125
 35 Trp Gln Pro Ser Cys Xaa His Ser His Gly Pro Phe Thr His His Xaa
 130 135 140
 Ser Arg Ala Pro Thr Arg Phe Pro Phe Ala Tyr Leu His Ala Phe Phe
 145 150 155 160
 40 Ala Arg Lys His Gly Arg Phe Phe Gly Phe Gly Ala Ser Asn Leu Gly
 165 170 175
 Lys Pro Phe Pro Pro Xaa Ser Cys
 180

45 <210> 615
 <211> 188
 <212> PRT
 <213> Homo sapiens

50 <400> 615
 Ala Arg Ala Glu Val Gln Glu Lys Lys Lys Lys Met Lys Asn Glu Asn
 1 5 10 15
 Ala Asp Lys Leu Leu Lys Ser Glu Lys Gln Met Lys Lys Ser Glu Lys
 20 25 30
 55 Lys Ser Lys Gln Glu Lys Glu Lys Ser Lys Lys Lys Lys Gly Gly Lys
 35 40 45
 Thr Glu Gln Asp Gly Tyr Gln Lys Pro Thr Asn Lys His Phe Thr Gln
 50 55 60
 Ser Pro Lys Lys Ser Val Ala Asp Leu Leu Gly Ser Phe Glu Gly Lys
 65 70 75 80
 60 Arg Arg Leu Leu Leu Ile Thr Ala Pro Lys Ala Glu Asn Asn Met Tyr
 85 90 95
 Val Gln Gln Arg Asp Glu Tyr Leu Glu Ser Phe Cys Lys Met Ala Thr

100 105 110
 Arg Lys Ile Ser Val Ile Thr Ile Phe Gly Pro Val Asn Asn Ser Thr
 115 120 125
 Met Lys Ile Asp His Phe Gln Leu Asp Asn Glu Lys Pro Met Arg Val
 130 135 140
 Val Asp Asp Glu Asp Leu Val Asp Gln Arg Leu Ile Ser Glu Leu Arg
 145 150 155 160
 Lys Glu Tyr Gly Met Thr Tyr Asn Asp Phe Phe Met Val Leu Thr Asp
 165 170 175
 10 Val Asp Leu Arg Val Lys Gln Tyr Tyr Glu Val Gln
 180 185

 <210> 616
 <211> 129
 15 <212> PRT
 <213> Homo sapiens

 <400> 616
 20 Ala Arg Gly Gly Gly Ala Arg Leu Arg Arg Gly Asp Ala Ser Pro
 1 5 10 15
 Val Arg Pro Arg Arg Gly Leu His Ala Pro Leu Ala Arg Ser Leu Pro
 20 25 30
 Pro Pro Ala Pro Arg Pro Ala Met Ala Glu Pro Ser Ser Ala Arg Arg
 35 40 45
 25 Pro Val Pro Leu Ile Glu Ser Glu Leu Tyr Phe Leu Ile Ala Arg Tyr
 50 55 60
 Leu Ser Ala Gly Pro Cys Arg Arg Ala Ala Gln Val Leu Val Gln Glu
 65 70 75 80
 Leu Glu Gln Tyr Gln Leu Leu Pro Lys Arg Leu Asp Trp Glu Gly Asn
 85 90 95
 30 Glu His Asn Arg Ser Tyr Xaa Glu Leu Val Leu Ser Asn Lys His Val
 100 105 110
 Ala Pro Asp His Leu Leu Gln Ile Cys Glu Arg Ile Gly Ser Tyr Val
 115 120 125
 35 Gly

 <210> 617
 <211> 215
 40 <212> PRT
 <213> Homo sapiens

 <400> 617
 45 Arg Arg Gly Arg Pro Gly Pro Gly Gly Ala Ala Leu His Ala Gly His
 1 5 10 15
 Val Gly Val Gly Pro Leu Arg Pro Pro Ala Leu His Gly Pro Gln Ala
 20 25 30
 Gly Pro Pro Gly Ala Gly Ala Leu Pro Ala Pro Gly Pro Gln Ile Arg
 35 40 45
 50 Arg Ser Gly Ala Glu Pro Arg Gly Gln Ala Val Arg Val Pro Arg Arg
 50 55 60
 Gln Thr Ala Gly Gly Ala Val Trp Gly Arg Arg His Arg Leu Leu Leu
 65 70 75 80
 Gly Gln Ala Gly Arg Asp Thr Val Trp Glu Asp Ala Arg Glu Pro Leu
 85 90 95
 55 Ala Pro Val Ala Leu Pro Gly Gly Arg Asn Pro Val Asn Tyr Gly Arg
 100 105 110
 Pro Tyr Arg Leu Ser Cys Val Glu Xaa Phe Ala Ala Thr Phe Leu His
 115 120 125
 60 Xaa Arg Leu Xaa Gln Thr Leu Leu Ser Phe Cys Cys Gly Lys Phe Lys
 130 135 140
 Trp Gly Lys Gly Leu Leu Gly Pro Glu Xaa Ala Lys Xaa Leu Asp Lys
 145 150 155 160

Xaa Pro Val Leu Xaa Xaa Pro Arg Xaa Lys Cys Phe Lys Ala Xaa Gln
 165 170 175
 Xaa Phe Leu Gly Lys Leu Pro Met Glu Lys Pro Pro Arg Xaa Glu Glu
 180 185 190
 5 Asn Arg Ile Pro Xaa Asn Val Gly Phe Lys Gly Lys Lys Ile Leu Glu
 195 200 205
 Asn Pro Lys Arg Xaa Phe Trp
 210 215

 10 <210> 618
 <211> 137
 <212> PRT
 <213> Homo sapiens

 15 <400> 618
 Pro Arg His Leu Pro Thr Arg Ser Leu Glu Ala Phe Ala Glu Glu Val
 1 5 10 15
 Gly Ala Ala Leu Gln Ala Ser Val Glu Pro Gly Ala Ala Asp Gly Glu
 20 25 30
 20 Gly Gly Pro Gly Pro Ala Ala Leu Pro Cys Thr Leu Ala Met Trp Glu
 35 40 45
 Leu Gly His Cys Asp Pro Arg Arg Cys Thr Gly Arg Lys Leu Ala Arg
 50 55 60
 Leu Gly Leu Val Arg Cys Leu Arg Leu Gly His Arg Phe Gly Gly Leu
 25 65 70 75 80
 Val Leu Ser Pro Val Gly Lys Gln Tyr Ala Ser Pro Ala Asp Arg Gln
 85 90 95
 Leu Val Ala Gln Ser Gly Val Ala Val Ile Asp Cys Ser Trp Ala Arg
 100 105 110
 30 Leu Asp Glu Thr Pro Phe Gly Lys Met Arg Gly Ser His Leu Arg Leu
 115 120 125
 Leu Pro Tyr Leu Val Ala Ala Thr Pro
 130 135

 35 <210> 619
 <211> 227
 <212> PRT
 <213> Homo sapiens

 40 <400> 619
 Gly Thr Ser Ile Tyr Ser Gly Arg Leu Leu Ser Arg Ala Asn Thr Glu
 1 5 10 15
 Lys Ser Tyr Gly Ile Asp Glu Asn Gly Arg Asp Glu Asn Thr Met Lys
 20 25 30
 45 Asn Ile Phe Ser Lys Lys Arg Lys Leu Glu Val Ala Cys Ser Asp Cys
 35 40 45
 Glu Val Glu Val Leu Pro Leu Gly Leu Glu Thr His Pro Arg Thr Ala
 50 55 60
 Lys Thr Glu Lys Cys Pro Pro Lys Phe Ser Asn Asn Pro Lys Glu Leu
 50 65 70 75 80
 Thr Met Glu Thr Lys Tyr Asp Asn Ile Ser Arg Ile Gln Tyr His Ser
 85 90 95
 Val Ile Arg Asp Pro Glu Ser Lys Thr Ala Ile Phe Gln His Asn Gly
 100 105 110
 55 Lys Lys Met Glu Phe Val Ser Ser Glu Ser Val Thr Pro Glu Asp Asn
 115 120 125
 Asp Gly Phe Lys Pro Pro Arg Glu His Leu Asn Ser Lys Thr Lys Gly
 130 135 140
 Ala Gln Lys Asp Ser Ser Ser Asn His Val Asp Glu Phe Glu Asp Asn
 60 145 150 155 160
 Leu Leu Ile Glu S r Asp Val Ile Asp Ile Thr Lys Tyr Arg Glu Glu
 165 170 175
 Thr Pro Pro Arg Ser Arg Cys Asn Gln Ala Thr Thr Leu Asp Asn Gln
 215

180 185 190
 Asn Ile Lys Lys Ala Ile Glu Val Gln Ile Gln Lys Pro Pro Arg Gly
 195 200 205
 Thr Ile Tyr Ser Met Ser Lys Thr Ser Xaa Tyr Phe Val Met Lys Lys
 5 210 215 220
 Leu Leu Lys
 225

 <210> 620
 10 <211> 227
 <212> PRT
 <213> Homo sapiens

 <400> 620
 15 Ile Pro Xaa Gln Pro Phe Phe Lys Pro Asn Gly Lys Lys Met Glu Phe
 1 5 10 15
 Val Ser Ser Glu Ser Val Thr Pro Glu Asp Asn Asp Gly Phe Lys Pro
 20 20 25 30
 Pro Arg Glu His Leu Asn Ser Lys Thr Lys Gly Ala Gln Lys Asp Ser
 35 40 45
 Ser Ser Asn His Val Asp Glu Phe Glu Asp Asn Leu Leu Ile Glu Ser
 50 55 60
 Asp Val Ile Asp Ile Thr Lys Tyr Arg Glu Glu Thr Pro Pro Arg Ser
 65 70 75 80
 25 Arg Cys Asn Gln Ala Thr Thr Leu Asp Asn Gln Asn Ile Lys Lys Ala
 85 90 95
 Ile Glu Val Gln Ile Gln Lys Pro Gln Glu Gly Arg Ser Thr Ala Cys
 100 105 110
 Gln Arg Gln Gln Val Phe Cys Asp Glu Glu Leu Leu Ser Glu Thr Lys
 115 120 125
 30 Asn Thr Ser Ser Asp Ser Leu Thr Lys Phe Asn Lys Gly Asn Val Phe
 130 135 140
 Leu Leu Asp Ala Thr Lys Glu Gly Asn Val Gly Arg Phe Leu Asn His
 145 150 155 160
 35 Ser Cys Cys Pro Asn Leu Leu Val Gln Asn Val Phe Val Glu Thr His
 165 170 175
 Asn Arg Asn Phe Pro Leu Val Ala Phe Phe Thr Asn Arg Tyr Val Lys
 180 185 190
 Ala Arg Thr Glu Leu Thr Trp Asp Tyr Gly Tyr Glu Ala Gly Thr Val
 195 200 205
 40 Pro Glu Lys Glu Ile Phe Cys Gln Cys Gly Val Asn Lys Cys Arg Lys
 210 215 220
 Lys Ile Leu
 225
 45
 <210> 621
 <211> 204
 <212> PRT
 <213> Homo sapiens
 50
 <400> 621
 Leu Asn Thr Leu Ser Thr Pro Glu Glu Lys Leu Ala Ala Leu Cys Lys
 1 5 10 15
 Lys Tyr Ala Asp Leu Leu Glu Glu Ser Arg Ser Val Gln Lys Gln Met
 20 25 30
 Lys Ile Leu Gln Lys Lys Gln Ala Gln Ile Val Lys Glu Lys Val His
 35 40 45
 Leu Gln Ser Glu His Ser Lys Ala Ile Leu Ala Arg Ser Lys Leu Glu
 50 55 60
 60 Ser Leu Cys Arg Glu Leu Gln Arg His Asn Lys Thr Leu Lys Glu Glu
 65 70 75 80
 Asn Met Gln Gln Ala Arg Glu Glu Glu Glu Arg Arg Lys Glu Ala Thr
 85 90 95

Ala His Ph Gln Il Thr Leu Asn Glu Ile Gln Ala Gln Leu Glu Gln
 100 105 110
 His Asp Ile His Asn Ala Lys Leu Arg Gln Glu Asn Ile Glu Leu Gly
 115 120 125
 5 Glu Lys Leu Lys Lys Leu Ile Glu Gln Tyr Ala Leu Arg Glu Glu His
 130 135 140
 Ile Asp Lys Val Phe Lys His Lys Glu Leu Gln Gln Gln Leu Val Asp
 145 150 155 160
 10 Ala Lys Leu Gln Gln Thr Thr Gln Leu Ile Lys Glu Ala Asp Glu Lys
 165 170 175
 His Gln Arg Glu Arg Glu Phe Leu Leu Lys Glu Ala Thr Glu Ser Arg
 180 185 190
 His Lys Tyr Glu Gln Met Lys Gln Gln Glu Val His
 195 200
 15
 <210> 622
 <211> 187
 <212> PRT
 <213> Homo sapiens
 20
 <400> 622
 Glu Leu Gly Pro Glu Thr Arg Gly Arg Ala Val Gly Pro Arg Asn Glu
 1 5 10 15
 25 Ala Lys Met Leu Glu Gly Asp Leu Val Ser Lys Met Leu Arg Ala Val
 20 25 30
 Leu Gln Ser His Lys Asn Gly Val Ala Leu Pro Arg Leu Gln Gly Glu
 35 40 45
 Tyr Arg Ser Leu Thr Gly Asp Trp Ile Pro Phe Lys Gln Leu Gly Phe
 50 55 60
 30 Pro Thr Leu Glu Ala Tyr Leu Arg Ser Val Pro Ala Val Val Arg Ile
 65 70 75 80
 Glu Thr Ser Arg Ser Gly Glu Ile Thr Cys Tyr Ala Met Ala Cys Thr
 85 90 95
 35 Glu Thr Ala Arg Ile Ala Gln Leu Val Ala Arg Gln Arg Ser Ser Lys
 100 105 110
 Arg Lys Thr Gly Arg Gln Val Asn Cys Gln Met Arg Val Lys Lys Thr
 115 120 125
 Met Pro Phe Phe Leu Glu Gly Lys Pro Lys Ala Thr Leu Arg Gln Pro
 130 135 140
 40 Gly Phe Ala Ser Asn Phe Ser Val Gly Lys Lys Pro Asn Pro Ala Pro
 145 150 155 160
 Leu Arg Asp Lys Gly Asn Ser Ala Gly Val Lys Pro Asp Ala Glu Met
 165 170 175
 45 Ser Pro Tyr Met Leu His Thr Thr Leu Trp Lys
 180 185
 <210> 623
 <211> 141
 <212> PRT
 50 <213> Homo sapiens
 <400> 623
 Gln Trp Arg Lys Thr Lys Cys Met Leu Gln Lys Trp Lys Ile Ser Gly
 1 5 10 15
 55 Thr Gly Cys Phe Leu Lys Gly Ile Leu Thr Asn Gly Leu Val Ser Val
 20 25 30
 Tyr Glu Leu Asp Tyr Gly Lys His Glu Leu Val Asn Ile Arg Lys Val
 35 40 45
 Gln Pro Leu Val Asp Met Phe Arg Lys Leu Pro Phe Gln Ala Val Thr
 50 55 60
 60 Ala Gln Leu Ala Gly Val Lys Cys Asn Gln Trp Ser Glu Glu Ala S r
 65 70 75 80
 Met Val Phe Arg Asn His Val Glu Lys Lys Pro Leu Val Ala Leu Val
 217

85 90 95
 Gln Thr Val Ile Glu Asn Ala Asn Pro Trp Asp Arg Lys Val Val Val
 100 105 110
 Tyr Leu Val Asp Thr Ser Leu Pro Asp Thr Asp Thr Trp Ile His Asp
 115 120 125
 Phe Met Ser Glu Tyr Leu Ile Glu Leu Ser Lys Val Asn
 130 135 140

10
 <210> 624
 <211> 201
 <212> PRT
 <213> Homo sapiens

15
 Met Val Ser Gly Asn Val Arg Val Met Ser Glu Met Leu Thr Glu Leu
 1 5 10 15
 Val Pro Thr Gln Ala Glu Pro Ala Asp Leu Glu Leu Leu Gln Glu Leu
 20 25 30
 Asn Arg Thr Cys Arg Ala Met Gln Gln Arg Val Leu Glu Leu Ile Pro
 35 40 45
 Gln Ile Ala Asn Glu Gln Leu Thr Glu Glu Leu Leu Ile Val Asn Asp
 50 55 60
 Asn Leu Asn Asn Val Phe Leu Arg His Glu Arg Phe Glu Arg Phe Arg
 65 70 75 80
 25 Thr Gly Gln Thr Thr Lys Ala Pro Ser Glu Ala Glu Pro Ala Ala Asp
 85 90 95
 Leu Ile Asp Met Gly Pro Asp Pro Ala Ala Thr Gly Asn Leu Ser Ser
 100 105 110
 Gln Leu Ala Gly Met Asn Leu Gly Ser Ser Ser Val Arg Ala Gly Leu
 115 120 125
 30 Gln Ser Leu Glu Ala Ser Gly Arg Leu Glu Asp Glu Phe Asp Met Phe
 130 135 140
 Ala Leu Thr Arg Gly Ser Ser Leu Ala Asp Gln Arg Lys Glu Val Lys
 145 150 155 160
 35 Tyr Glu Ala Pro Gln Ala Thr Asp Gly Leu Ala Gly Ala Leu Asp Ala
 165 170 175
 Arg Gln Gln Ser Thr Gly Arg Asp Pro Ser His Pro Gly Leu Pro His
 180 185 190
 40 Gly Gly His Xaa Ala Val Ala Val His
 195 200

45
 <210> 625
 <211> 244
 <212> PRT
 <213> Homo sapiens

50
 Glu Ala Arg Ser Ala Ala Gln Val Ala Leu Cys Ile Gln Gln Leu Gln
 1 5 10 15
 Lys Ser Ile Ala Trp Glu Lys Ser Ile Met Lys Val Tyr Cys Gln Ile
 20 25 30
 Cys Arg Lys Gly Asp Asn Glu Glu Leu Leu Leu Leu Cys Asp Gly Cys
 35 40 45
 Asp Lys Gly Cys His Thr Tyr Cys His Arg Pro Lys Ile Thr Thr Ile
 50 55 60
 Pro Asp Gly Asp Trp Phe Cys Pro Ala Cys Ile Ala Lys Ala Ser Gly
 65 70 75 80
 Gln Thr Leu Lys Ile Lys Lys Leu His Val Lys Gly Lys Lys Thr Asn
 85 90 95
 60 Glu Ser Lys Lys Gly Lys Lys Val Thr Leu Thr Gly Asp Thr Glu Asp
 100 105 110
 Glu Asp Ser Ala Ser Thr Ser Ser Ser Leu Lys Arg Gly Asn Lys Asp
 115 120 125

Leu Lys Lys Arg Lys Met Glu Glu Asn Thr Ser Ile Asn Leu Ser Lys
 130 135 140
 Gln Glu Ser Phe Thr Ser Val Lys Lys Pro Lys Arg Asp Asp Ser Lys
 145 150 155 160
 5 Asp Leu Ala Leu Cys Ser Met Ile Leu Thr Glu Met Glu Thr His Glu
 165 170 175
 Asp Ala Trp Pro Phe Leu Leu Pro Val Asn Leu Lys Leu Val Pro Gly
 180 185 190
 Tyr Lys Lys Val Ile Lys Lys Pro Met Asp Phe Ser Thr Ile Arg Glu
 195 200 205
 10 Lys Leu Ser Ser Gly Gln Tyr Pro Asn Leu Glu Thr Phe Ala Leu Asp
 210 215 220
 Val Arg Leu Val Phe Asp Thr Val Lys His Leu Met Glu Asp Asp Ser
 225 230 235 240
 15 Asp Ile Gly Arg

<210> 626
 <211> 208
 20 <212> PRT
 <213> Homo sapiens

<400> 626
 25 Ala Arg Gly Lys Pro Ser Leu Val Arg Glu Thr Ser Arg Ile Thr Val
 1 5 10 15
 Leu Glu Ala Leu Arg His Pro Ile Gln Val Ser Arg Arg Leu Leu Ser
 20 25 30
 Arg Pro Gln Asp Ala Leu Glu Gly Val Val Leu Ser Pro Ser Leu Glu
 35 40 45
 30 Ala Arg Val Arg Asp Ile Ala Ile Ala Thr Arg Asn Thr Lys Lys Asn
 50 55 60
 Arg Ser Leu Tyr Arg Asn Ile Leu Met Tyr Gly Pro Pro Gly Thr Gly
 65 70 75 80
 Lys Thr Leu Phe Ala Lys Lys Leu Ala Leu His Ser Gly Met Asp Tyr
 85 90 95
 35 Ala Ile Met Thr Gly Gly Asp Val Ala Pro Met Gly Arg Glu Gly Val
 100 105 110
 Thr Ala Met His Lys Leu Phe Asp Trp Ala Asn Thr Ser Arg Arg Gly
 115 120 125
 40 Leu Leu Leu Phe Val Asp Glu Ala Asp Ala Phe Leu Arg Lys Arg Ala
 130 135 140
 Thr Glu Lys Ile Ser Glu Asp Leu Arg Ala Thr Leu Asn Ala Phe Leu
 145 150 155 160
 Tyr Arg Thr Gly Gln His Ser Asn Lys Phe Met Leu Val Leu Ala Ser
 165 170 175
 45 Asn Gln Pro Glu Gln Phe Asp Trp Ala Ile Asn Asp Arg Xaa Asn Glu
 180 185 190
 Met Val His Phe Asp Leu Xaa Arg Ala Xaa Arg Asn Gly Ser Ala Trp
 195 200 205

50 <210> 627
 <211> 230
 <212> PRT
 <213> Homo sapiens

55 <400> 627
 Val Asn Arg Pro Gln Leu Gln Pro Gln Ala Trp Thr Gly Gln Leu Thr
 1 5 10 15
 Val Arg Pro Xaa Thr Pro Pro Pro Gly Ser Leu Leu Pr Pro Xaa Ser
 20 25 30
 60 Gly Ser Pro Val Cys Glu Xaa Ser Gly His Ala Gly His Arg Gly Lys
 35 40 45
 Gln Gly Ser Gly Cys Pro Thr Trp Val Trp Pro Trp Gln Ala Pro Pro
 219

50 55 60
 His Leu Ala Leu Leu Trp Glu Pro Arg Thr Lys Thr Ser Pro Ala Trp
 65 70 75 80
 Leu Leu Leu Pro Arg Gly Xaa Xaa Gln His Pro Pro Xaa Gln Xaa Pro
 85 90 95
 Gly Gln Gly Leu Gly Cys Lys Ala Ser Pro Ser Pro Cys Glu Pro Xaa
 100 105 110
 Gly Lys Cys Ile Ser Gln Xaa Cys Leu Glu Gly Gln Glu Gly Gly Leu
 115 120 125
 10 Pro Leu Pro Ser Gln Xaa Leu Gln Gln Gly Val Pro Trp Gly Ala Lys
 130 135 140
 Arg Pro Thr Ala Thr Thr Arg His Pro Gly Gly Gln Arg Pro Trp Ala
 145 150 155 160
 Gln Pro Asn Pro His Pro Gly Ala Xaa Pro Lys Cys Ala Gly Ala Gly
 165 170 175
 15 Lys Ala Gly Val Gly Xaa Gly Pro Xaa Pro Gly Phe Arg Glu Leu Trp
 180 185 190
 Ile Ser Leu Xaa Thr Ser Xaa Xaa Gly Gly Leu Arg Xaa His Ala Gln
 195 200 205
 20 Ala Leu Ser Leu Xaa Pro Ala Gln Ser Ser Xaa Gly Ala Xaa Gly Gln
 210 215 220
 Tyr Phe Ser Pro Gly Cys
 225 230
 25 <210> 628
 <211> 215
 <212> PRT
 <213> Homo sapiens
 30 <400> 628
 Gln Cys Gly Leu Xaa His Pro Arg Gln Val Pro Ser Ser Leu Xaa Xaa
 1 5 10 15
 Gln Gly His Gln Cys Val Lys Xaa Arg Gly Met Pro Ala Thr Gly Gly
 20 25 30
 35 Ser Arg Val Gln Ala Ala Pro Pro Gly Ser Gly Pro Gly Arg Arg Pro
 35 40 45
 Leu Thr Trp Leu Cys Cys Gly Ser Arg Glu Gln Arg His His Leu Pro
 50 55 60
 Gly Ser Cys Cys Pro Gly Gly Xaa Xaa Ser Thr His Pro Xaa Xaa Gly
 65 70 75 80
 40 Leu Gly Arg Gly Trp Gly Ala Lys Pro His Pro Pro Pro Val Ser Xaa
 85 90 95
 Thr Glu Asn Ala Phe Pro Xaa Ser Val Ser Arg Gly Arg Lys Glu Ala
 100 105 110
 45 Cys Pro Ser Leu Ala Xaa Ala Tyr Asn Arg Gly Cys Pro Gly Gly Gln
 115 120 125
 Asn Asp Arg Pro Pro Pro Gln Asp Ile Leu Gly Asp Lys Gly Pro Gly
 130 135 140
 50 His Ser Pro Ile Pro Ile Gln Glu Xaa Ile Leu Asn Val Gln Gly Pro
 145 150 155 160
 Ala Arg Gln Gly Trp Xaa Gly Val Arg Xaa Gln Ala Ser Val Ser Cys
 165 170 175
 Gly Ser Pro Xaa Gly Leu Xaa Asp Xaa Glu Gly Phe Xaa Pro Thr Pro
 180 185 190
 55 Arg Pro Phe Arg Xaa Xaa Gln His Asn Leu Leu Xaa Val Leu Xaa Asp
 195 200 205
 Ser Ile Phe His Pro Gly Val
 210 215
 60 <210> 629
 <211> 236
 <212> PRT
 <213> Homo sapiens

<400> 629

	Ala	Arg	Ala	Glu	Val	Glu	Lys	Gln	Thr	Ser	Leu	Thr	Pro	Arg	Glu	Leu
	1				5					10					15	
5	Glu	Ile	Arg	Arg	Arg	Glu	Asp	Glu	Tyr	Arg	Phe	Thr	Lys	Leu	Leu	Gln
			20				25						30			
	Ile	Ala	Gly	Ile	Ser	Pro	His	Gly	Asn	Ala	Leu	Gly	Ala	Ser	Met	Gln
		35					40						45			
10	Gln	Gln	Val	Asn	Gln	Gln	Ile	Pro	Gln	Glu	Lys	Arg	Gly	Gly	Glu	Val
		50				55						60				
	Leu	Asp	Ser	Ser	His	Asp	Asp	Ile	Lys	Leu	Glu	Lys	Ser	Asn	Ile	Leu
	65				70						75				80	
	Leu	Leu	Gly	Pro	Thr	Gly	Ser	Gly	Lys	Thr	Leu	Leu	Ala	Gln	Thr	Leu
					85					90					95	
15	Ala	Lys	Cys	Leu	Asp	Val	Pro	Phe	Ala	Ile	Cys	Asp	Cys	Thr	Thr	Leu
			100						105					110		
	Thr	Gln	Ala	Gly	Tyr	Val	Gly	Glu	Asp	Ile	Glu	Ser	Val	Ile	Ala	Lys
		115						120					125			
20	Leu	Leu	Gln	Asp	Ala	Asn	Tyr	Asn	Val	Glu	Lys	Ala	Gln	Gln	Gly	Ile
		130					135					140				
	Val	Phe	Leu	Asp	Glu	Val	Asp	Lys	Ile	Gly	Ser	Val	Pro	Gly	Ile	His
	145				150						155				160	
	Gln	Leu	Arg	Asp	Val	Gly	Gly	Glu	Gly	Val	Gln	Gln	Gly	Leu	Leu	Lys
				165						170					175	
25	Leu	Leu	Glu	Gly	Thr	Ile	Val	Asn	Val	Pro	Glu	Lys	Asn	Ser	Arg	Lys
			180						185					190		
	Leu	Arg	Gly	Glu	Thr	Val	Gln	Val	Asp	Thr	Thr	Asn	Ile	Leu	Phe	Val
		195						200					205			
30	Ala	Ser	Gly	Ala	Phe	Asn	Gly	Phe	Arg	Gln	Asn	His	Gln	Xaa	Gly	Gly
		210					215					220				
	Lys	Asn	Glu	Lys	Tyr	Leu	Gly	Phe	Xaa	Thr	Pro	Ile				
	225					230					235					

35 <210> 630
 <211> 285
 <212> PRT
 <213> Homo sapiens

<400> 630

40	Ser	Arg	Ala	Cys	Arg	Ser	Thr	Leu	Val	Asp	Pro	Lys	Glu	Asn	Met	Asp
	1				5					10					15	
	Thr	Ser	Asn	Thr	Ser	Ile	Ser	Lys	Met	Lys	Arg	Ser	Arg	Pro	Thr	Ser
			20					25						30		
45	Glu	Gly	Ser	Asp	Ile	Glu	Ser	Thr	Glu	Pro	Gln	Lys	Gln	Cys	Ser	Lys
		35					40						45			
	Lys	Lys	Lys	Lys	Arg	Asp	Arg	Val	Glu	Ala	Ser	Ser	Ser	Leu	Pro	Glu
		50					55					60				
	Arg	Thr	Gly	Lys	Arg	Lys	Arg	Ser	Ser	Ser	Glu	Asp	Ala	Glu	Ser	Leu
	65				70						75				80	
50	Ala	Pro	Arg	Ser	Lys	Val	Lys	Lys	Ile	Ile	Gln	Lys	Asp	Ile	Ile	Lys
				85						90					95	
	Glu	Ala	Ser	Glu	Ala	Ser	Lys	Glu	Asn	Arg	Asp	Ile	Glu	Ile	Ser	Thr
			100						105					110		
55	Glu	Glu	Glu	Lys	Asp	Thr	Gly	Asp	Leu	Lys	Asp	Ser	Ser	Leu	Leu	Lys
		115						120						125		
	Thr	Lys	Arg	Lys	His	Lys	Lys	Lys	His	Lys	Glu	Arg	His	Lys	Met	Gly
		130					135					140				
	Glu	Glu	Val	Ile	Pro	Leu	Arg	Val	Leu	Ser	Lys	Ser	Glu	Trp	Met	Asp
	145				150						155				160	
60	Leu	Lys	Lys	Glu	Tyr	Leu	Ala	Leu	Gln	Lys	Ala	Ser	Met	Ala	Ser	Leu
				165						170					175	
	Lys	Lys	Thr	Ile	Ser	Gln	Xaa	Lys	Ser	Glu	Ser	Glu	Met	Glu	Thr	Asp
			180						185					190		

Ser Gly Val Pro Gln Asn Thr Gly Met Lys Asn Glu Lys Thr Ala Asn
 195 200 205
 Arg Glu Glu Cys Arg Thr Gln Glu Lys Val Asn Ala Thr Gly Pro Gln
 210 215 220
 5 Phe Val Ser Gly Val Ile Val Lys Ile Ile Ser Thr Glu Pr Leu Leu
 225 230 235 240
 Ala Gly Asn Lys Ser Gly Ile Phe Gly Ser Asn Leu Arg Lys Phe Phe
 245 250 255
 Tyr Val Asp Leu Leu Glu Xaa Glu Pro Xaa Trp Pro Ala Arg Leu Lys
 10 260 265 270
 Thr Xaa Glu Asp Ala Gln Xaa Val Ile Asn Ala Phe Pro
 275 280 285

 <210> 631
 15 <211> 593
 <212> PRT
 <213> Homo sapiens

 <400> 631
 20 Leu Asp Met Ala Pro Glu Ile Asn Leu Pro Gly Pro Met Ser Leu Ile
 1 5 10 15
 Asp Asn Thr Lys Gly Gln Leu Val Val Asn Pro Glu Ala Leu Lys Ile
 20 25 30
 25 Leu Ser Ala Ile Thr Gln Pro Val Val Val Ala Ile Val Gly Leu
 35 40 45
 Tyr Arg Thr Gly Lys Ser Tyr Leu Met Asn Lys Leu Ala Gly Lys Lys
 50 55 60
 Asn Gly Phe Ser Leu Gly Ser Thr Val Lys Ser His Thr Lys Gly Ile
 65 70 75 80
 30 Trp Met Trp Cys Val Pro His Pro Lys Lys Pro Glu His Thr Leu Val
 85 90 95
 Leu Leu Asp Thr Glu Gly Leu Gly Asp Ile Glu Lys Gly Asp Asn Glu
 100 105 110
 Asn Asp Ser Trp Ile Phe Ala Leu Ala Ile Leu Leu Ser Ser Thr Phe
 115 120 125
 35 Val Tyr Asn Ser Met Gly Thr Ile Asn Gln Gln Ala Met Asp Gln Leu
 130 135 140
 His Tyr Val Thr Glu Leu Thr Asp Arg Ile Lys Ala Asn Ser Ser Pro
 145 150 155 160
 40 Gly Asn Asn Ser Val Asp Asp Ser Ala Asp Phe Val Ser Phe Phe Pro
 165 170 175
 Ala Phe Val Trp Thr Leu Arg Asp Phe Thr Leu Glu Leu Glu Val Asp
 180 185 190
 Gly Glu Pro Ile Thr Ala Asp Asp Tyr Leu Glu Leu Ser Leu Lys Leu
 195 200 205
 45 Arg Lys Gly Thr Asp Lys Lys Ser Lys Ser Phe Asn Asp Pro Arg Leu
 210 215 220
 Cys Ile Arg Lys Phe Phe Pro Lys Arg Lys Cys Phe Val Phe Asp Trp
 225 230 235 240
 50 Pro Ala Pro Lys Lys Tyr Leu Ala His Leu Glu Gln Leu Lys Glu Glu
 245 250 255
 Glu Leu Asn Pro Asp Phe Ile Glu Gln Val Ala Glu Phe Cys Ser Tyr
 260 265 270
 Ile Leu Ser His Ser Asn Val Lys Thr Leu Ser Gly Gly Ile Ala Val
 275 280 285
 55 Asn Gly Pro Arg Leu Glu Ser Leu Val Leu Thr Tyr Val Asn Ala Ile
 290 295 300
 Ser Ser Gly Asp Leu Pro Cys Met Glu Asn Ala Val Leu Ala Leu Ala
 305 310 315 320
 60 Gln Ile Glu Asn Ser Ala Ala Val Glu Lys Ala Ile Ala His Tyr Glu
 325 330 335
 Gln Gln Met Gly Gln Lys Val Gln Leu Pro Thr Glu Thr Leu Gln Glu
 340 345 350

Leu Leu Asp Leu His Arg Asp Ser Glu Arg Glu Ala Ile Glu Val Phe
 355 360 365
 Met Lys Asn Ser Phe Lys Asp Val Asp Gln Met Phe Gln Arg Lys Leu
 370 375 380
 5 Gly Ala Gln Leu Glu Ala Arg Arg Asp Asp Phe Cys Lys Gln Asn Ser
 385 390 395 400
 Lys Ala Ser Ser Asp Cys Cys Met Ala Leu Leu Gln Asp Ile Phe Gly
 405 410 415
 10 Pro Leu Glu Glu Asp Val Lys Gln Gly Thr Phe Ser Lys Pro Gly Gly
 420 425 430
 Tyr Arg Leu Phe Thr Gln Lys Leu Gln Glu Leu Lys Asn Lys Tyr Tyr
 435 440 445
 Gln Val Pro Arg Lys Gly Ile Gln Ala Lys Glu Val Leu Lys Lys Tyr
 450 455 460
 15 Leu Glu Ser Lys Glu Asp Val Ala Asp Ala Leu Leu Gln Thr Asp Gln
 465 470 475 480
 Ser Leu Ser Glu Lys Glu Lys Ala Ile Glu Val Glu Arg Ile Lys Ala
 485 490 495
 20 Glu Ser Ala Glu Ala Ala Lys Lys Met Leu Glu Glu Ile Gln Lys Lys
 500 505 510
 Asn Glu Glu Met Met Glu Gln Lys Glu Lys Ser Tyr Gln Glu His Val
 515 520 525
 Lys Gln Leu Thr Glu Lys Met Glu Arg Asp Arg Ala Gln Leu Met Ala
 530 535 540
 25 Glu Gln Glu Lys Thr Leu Ala Leu Lys Leu Gln Glu Gln Glu Arg Leu
 545 550 555 560
 Leu Lys Glu Gly Phe Glu Asn Glu Ser Lys Arg Leu Gln Lys Asp Ile
 565 570 575
 30 Trp Asp Ile Gln Met Arg Ser Lys Ser Leu Glu Pro Ile Cys Asn Ile
 580 585 590
 Leu

35 <210> 632
 <211> 191
 <212> PRT
 <213> Homo sapiens

40 <400> 632
 Arg Arg Pro Ala Ala Gly Leu Arg Asp Xaa Val Xaa Ser Ala Pro Arg
 1 5 10 15
 Gly Met Ala Ser Glu Gly Pro Xaa Glu Pro Glu Ser Glu Gly Ile Lys
 20 25 30
 45 Leu Ser Gly Ile Cys Gln Thr Ile Cys Pro Gln Ile Cys Arg Ala Gln
 35 40 45
 Cys Gly Met Val Arg Val Leu Arg Ser Met Cys Leu Pro Gln Leu Cys
 50 55 60
 Ser His Ile Leu Ser Val Cys Ser Gly Thr Thr Ser Asp Arg Asn Xaa
 65 70 75 80
 50 Tyr Ser Val Pro Gly Ser Gln Tyr Leu Tyr Asn Gln Pro Ser Cys Tyr
 85 90 95
 Arg Gly Phe Gln Thr Xaa Lys His Arg Asn Glu Asn Thr Cys Pro Leu
 100 105 110
 55 Pro Gln Glu Met Lys Ala Leu Phe Lys Lys Lys Thr Xaa Asp Glu Lys
 115 120 125
 Lys Thr Tyr Asp Gln Gln Lys Phe Asp Ser Glu Arg Ala Asp Gly Thr
 130 135 140
 Ile Ser Ser Glu Ile Lys Ser Ala Arg Gly Ser His His Leu Ser Ile
 145 150 155 160
 60 Tyr Ala Glu Asn Ser Leu Lys Ser Asp Gly Tyr His Lys Arg Thr Asp
 165 170 175
 Arg Lys Ser Arg Ile Ile Cys Lys Lys Trp Ile Tyr Leu Gln Thr
 180 185 190

5 <210> 633
 <211> 149
 <212> PRT
 <213> Homo sapiens

 <400> 633
 Leu Gln Val Cys Leu Pro Ala Gly Gly Pro Cys Xaa Val Cys Pro Gln
 1 5 10 15
 10 Lys Val Met Xaa Leu Leu Pro Ile Phe Xaa Leu Xaa Lys Met Xaa Pro
 20 25 30
 Pro Val Xaa Arg Ala Val Val Thr Ser Pro Trp Xaa Gly Phe Thr Ser
 35 40 45
 15 Leu Leu Xaa Xaa Xaa Asn Phe Gln Thr Asn Xaa Xaa Leu Gly Asn Pro
 50 55 60
 Pro Gly Gly Leu Glu Lys Pro Xaa Gln Val Ala Val Pro Pro Pro Pro
 65 70 75 80
 Leu Pro Phe Xaa Ala Xaa Gly Glu Pro Xaa Pro Ser Ile Phe Trp Ala
 85 90 95
 20 Pro Phe Xaa Trp Gly Asn Xaa Val Gly Gly Leu Phe Xaa Ser Pro Leu
 100 105 110
 Lys Lys Xaa Gly Phe Leu Glu Xaa Pro Xaa Ile Xaa Xaa Xaa Pro Leu
 115 120 125
 25 Xaa Phe Leu Asp Gly Pro Pro Lys Phe Phe Phe Gln Xaa Phe Phe Gly
 130 135 140
 Pro Phe Phe Lys Xaa
 145

30 <210> 634
 <211> 124
 <212> PRT
 <213> Homo sapiens

 <400> 634
 Val Asn Ser Thr Leu Thr Ile Glu Glu Phe His Ser Lys Leu Gln Glu
 1 5 10 15
 Ala Thr Asn Phe Pro Leu Arg Pro Phe Val Ile Pro Phe Leu Lys Ala
 20 25 30
 40 Asn Leu Pro Leu Leu Gln Arg Glu Leu Leu His Cys Ala Arg Leu Ala
 35 40 45
 Lys Gln Asn Pro Ala Gln Tyr Leu Ala Gln His Glu Gln Leu Leu Leu
 50 55 60
 Asp Ala Ser Thr Thr Ser Pro Val Asp Ser Ser Glu Leu Leu Leu Asp
 65 70 75 80
 45 Val Asn Glu Asn Gly Lys Arg Arg Thr Pro Asp Arg Thr Lys Glu Asn
 85 90 95
 Gly Phe Asp Arg Glu Pro Leu His Ser Glu His Pro Ser Lys Arg Pro
 100 105 110
 50 Cys Thr Ile Ser Pro Gly Gln Arg Tyr Lys Ser Lys
 115 120

55 <210> 635
 <211> 187
 <212> PRT
 <213> Homo sapiens

 <400> 635
 Arg Thr Lys Ala Lys Lys Asp Lys Ala Gln Arg Xaa Xaa Xaa Xaa Xaa
 1 5 10 15
 60 Xaa Xaa Gly Xaa Ala Pro His Ser Glu Ser Asp Leu Pro Glu Gln Glu
 20 25 30
 Glu Glu Ile Leu Gly Ser Asp Asp Glu Gln Glu Asp Pro Asn Asp
 35 40 45

Tyr Cys Lys Gly Gly Tyr His Leu Val Lys Ile Gly Asp Leu Phe Asn
 50 55 60
 Gly Arg Tyr His Val Ile Arg Lys Leu Gly Trp Gly His Phe Ser Thr
 65 70 75 80
 5 Val Trp Leu Ser Trp Asp Ile Gln Gly Lys Lys Phe Val Ala Met Lys
 85 90 95
 Xaa Val Lys Ser Ala Glu His Tyr Thr Glu Thr Ala Leu Asp Glu Ile
 100 105 110
 10 Xaa Leu Leu Lys Ser Val Arg Asn Ser Asp Pro Asn Asp Pro Asn Arg
 115 120 125
 Glu Met Val Val Gln Leu Leu Asp Asp Phe Lys Ile Ser Gly Val Asn
 130 135 140
 Gly Thr His Ile Cys Met Val Phe Glu Val Leu Gly His His Leu Leu
 145 150 155 160
 15 Lys Trp Ile Ile Lys Ser Asn Tyr Xaa Gly Leu Pro Leu Pro Cys Xaa
 165 170 175
 Lys Lys Ile Ile Xaa Xaa Val Phe Thr Gly Xaa
 180 185
 20 <210> 636
 <211> 275
 <212> PRT
 <213> Homo sapiens
 25 <400> 636
 Ser Arg Ala Cys Arg Ser Thr Leu Val Asp Pro Lys Arg Val Cys Lys
 1 5 10 15
 Gly Ile Leu Glu Tyr Leu Thr Val Ala Glu Val Val Glu Thr Met Glu
 20 25 30
 30 Asp Leu Val Thr Tyr Thr Lys Asn Leu Gly Pro Gly Met Thr Lys Met
 35 40 45
 Ala Lys Met Ile Asp Glu Arg Gln Gln Glu Leu Thr His Gln Glu His
 50 55 60
 Arg Val Met Leu Val Asn Ser Met Asn Thr Val Lys Glu Leu Leu Pro
 65 70 75 80
 35 Val Leu Ile Ser Ala Met Lys Ile Phe Val Thr Thr Lys Asn Ser Lys
 85 90 95
 Asn Gln Gly Ile Glu Glu Ala Leu Lys Asn Arg Asn Phe Thr Val Glu
 100 105 110
 40 Lys Met Ser Ala Glu Ile Asn Glu Ile Ile Arg Val Leu Gln Leu Thr
 115 120 125
 Ser Trp Asp Glu Asp Ala Trp Ala Ser Lys Asp Thr Glu Ala Met Lys
 130 135 140
 Arg Ala Leu Ala Ser Ile Asp Ser Lys Leu Asn Gln Ala Lys Gly Trp
 145 150 155 160
 45 Leu Arg Asp Pro Ser Ala Ser Pro Gly Asp Ala Gly Glu Gln Ala Ile
 165 170 175
 Arg Gln Ile Leu Asp Glu Ala Gly Lys Val Gly Glu Leu Cys Ala Gly
 180 185 190
 50 Lys Lys Arg Arg Glu Xaa Leu Gly Asn Leu Gln Asn Ala Xaa Ala Asp
 195 200 205
 Asp Cys Gln Ser Gly Leu Thr Ser Val Pro Arg Gly Gln Gly Ser Leu
 210 215 220
 Pro Xaa Gly Pro Cys Xaa Lys Ser Xaa Thr Xaa Tyr Xaa Gln Gly Leu
 225 230 235 240
 55 Gly Xaa Cys Ser Pro Ala Lys Xaa Glu Lys Ala Ser Phe Gln Ser Trp
 245 250 255
 Glu Ser Leu Ala His Xaa Lys Pro Lys His Leu Xaa Xaa Lys Xaa Thr
 260 265 270
 60 Met Leu Val
 275

<210> 637

<211> 162
 <212> PRT
 <213> Homo sapiens

5 <400> 637
 Gln Lys Leu Val Ile Glu Asn Phe Asp Asp Glu Gln Ile Trp Gln Gln
 1 5 10 15
 Leu Glu Leu Gln Asn Glu Pro Ile Leu Gln Tyr Phe Gln Asn Ala Val
 20 25 30
 10 Ser Glu Thr Ile Asn Asp Glu Asp Ile Ser Leu Leu Pro Glu Ser Glu
 35 40 45
 Glu Gln Glu Arg Glu Glu Asp Gly Ser Glu Ile Glu Ala Asp Asp Lys
 50 55 60
 Glu Asp Leu Glu Asp Leu Glu Glu Glu Glu Val Ser Asp Met Gly Asn
 15 65 70 75 80
 Asp Asp Pro Glu Met Gly Glu Arg Ala Glu Asn Ser Ser Lys Ser Asp
 85 90 95
 Leu Arg Lys Ser Pro Val Phe Ser Asp Glu Asp Ser Asp Leu Asp Phe
 100 105 110
 20 Asp Ile Ser Lys Leu Glu Gln Gln Ser Lys Val Gln Asn Lys Gly Gln
 115 120 125
 Gly Lys Pro Arg Glu Lys Ser Ile Val Asp Asp Lys Phe Phe Lys Leu
 130 135 140
 Ser Glu Met Glu Ala Tyr Leu Glu Asn Ile Glu Lys Glu Glu Glu Pro
 25 145 150 155 160
 Lys Arg

30 <210> 638
 <211> 171
 <212> PRT
 <213> Homo sapiens

 <400> 638
 35 Lys Met Ala Ala Gly Phe Lys Thr Val Glu Pro Xaa Glu Tyr Tyr Arg
 1 5 10 15
 Arg Phe Leu Lys Glu Asn Cys Arg Pro Asp Gly Arg Glu Leu Gly Glu
 20 25 30
 Phe Arg Thr Thr Thr Val Asn Ile Gly Ser Ile Ser Thr Ala Asp Gly
 40 35 40 45
 Ser Ala Leu Val Lys Leu Gly Asn Xaa Thr Xaa Ile Cys Gly Val Lys
 50 55 60
 Ala Glu Phe Ala Ala Pro Ser Thr Asp Ala Pro Asp Lys Gly Tyr Val
 65 70 75 80
 45 Val Pro Asn Val Asp Leu Pro Pro Leu Cys Ser Ser Arg Phe Arg Ser
 85 90 95
 Gly Pro Pro Gly Glu Glu Ala Gln Val Ala Ser Gln Phe Ile Ala Asp
 100 105 110
 Val Ile Glu Asn Ser Gln Ile Ile Gln Lys Glu Asp Leu Cys Ile Ser
 50 115 120 125
 Pro Gly Lys Leu Val Trp Val Leu Tyr Cys Asp Leu Ile Cys Leu Asp
 130 135 140
 Tyr Asp Gly Asn Ile Leu Asp Ala Cys Thr Phe Xaa Leu Leu Ala Ala
 145 150 155 160
 55 Leu Lys Asn Val Gln Val Ala Leu Lys Leu Leu
 165 170

60 <210> 639
 <211> 230
 <212> PRT
 <213> Homo sapiens

<400> 639

Xaa Ser Arg Ala Cys Arg Ser Thr Leu Val Asp Pro Lys Leu Lys Ala
 1 5 10 15
 Lys Asp Gln Gly Lys Pro Glu Val Gly Glu Tyr Ala Lys Leu Glu Lys
 20 25 30
 5 Ile Asn Ala Glu Gln Gln Leu Lys Ile Gln Glu Leu Gln Glu Lys Leu
 35 40 45
 Glu Lys Ala Val Lys Ala Ser Thr Glu Ala Thr Glu Leu Leu Gln Asn
 50 55 60
 Ile Arg Gln Ala Lys Glu Arg Ala Glu Arg Glu Leu Glu Lys Leu Gln
 65 70 75 80
 10 Asn Arg Glu Asp Ser Ser Glu Gly Ile Arg Lys Lys Leu Val Glu Ala
 85 90 95
 Glu Glu Arg Arg His Ser Leu Glu Asn Lys Val Lys Arg Leu Glu Thr
 100 105 110
 15 Met Glu Arg Arg Glu Asn Arg Leu Lys Asp Asp Ile Gln Thr Lys Ser
 115 120 125
 Gln Gln Ile Gln Gln Met Ala Asp Lys Ile Leu Glu Leu Glu Glu Lys
 130 135 140
 His Arg Glu Ala Gln Val Ser Ala Gln His Leu Glu Val His Leu Lys
 145 150 155 160
 20 Gln Lys Glu Gln His Tyr Glu Glu Lys Ile Lys Val Leu Asp Asn Gln
 165 170 175
 Ile Lys Lys Asp Leu Ala Asp Lys Glu Thr Leu Glu Asn Met Met Gln
 180 185 190
 25 Arg His Glu Glu Ala His Glu Xaa Gly Lys Ile Leu Gln Arg Thr
 195 200 205
 Glu Gly Asp Asp Gln Cys Tyr Gly Phe Gln Asp Gln Ile Pro Gly Thr
 210 215 220
 Xaa Asp Cys Gly Thr Val
 225 230
 30

<210> 640

<211> 256

<212> PRT

35 <213> Homo sapiens

<400> 640

Phe Glu Lys Asp Ala Asp Ser Ser Glu Arg Ile Ile Ala Pro Met Arg
 1 5 10 15
 40 Trp Gly Leu Val Pro Ser Trp Phe Lys Glu Ser Asp Pro Ser Lys Leu
 20 25 30
 Gln Phe Asn Thr Thr Asn Cys Arg Ser Asp Thr Val Met Glu Lys Arg
 35 40 45
 Ser Phe Lys Val Pro Leu Gly Lys Gly Arg Arg Cys Val Val Leu Ala
 50 55 60
 45 Asp Gly Phe Tyr Glu Trp Gln Arg Cys Gln Gly Thr Asn Gln Arg Gln
 65 70 75 80
 Pro Tyr Phe Ile Tyr Phe Pro Gln Ile Lys Thr Glu Lys Ser Gly Ser
 85 90 95
 50 Ile Gly Ala Ala Asp Ser Pro Glu Asn Trp Glu Lys Val Trp Asp Asn
 100 105 110
 Trp Arg Leu Leu Thr Met Ala Gly Ile Phe Asp Cys Trp Glu Pro Pro
 115 120 125
 Glu Gly Gly Asp Val Leu Tyr Ser Tyr Thr Ile Ile Thr Val Asp Ser
 130 135 140
 55 Cys Lys Gly Leu Ser Asp Ile His His Arg Met Pro Ala Ile Leu Asp
 145 150 155 160
 Gly Glu Glu Ala Val Ser Lys Trp Leu Asp Phe Gly Glu Val Ser Thr
 165 170 175
 60 Xaa Glu Ala Leu Lys Leu Ile His Pro Thr Glu Asn Ile Thr Phe His
 180 185 190
 Ala Val Ser Ser Val Xaa Asn Asn Ser Arg Asn Asn Thr Ser Glu Cys
 195 200 205

Leu Ala Xaa Val Asp Leu Val Val Lys Xaa Glu Leu Lys Ala Ser Gly
 210 215 220
 Asn Xaa Pro Lys Asp Val Ala Met Gly Trp Xaa Gln Ser Xaa Pro Lys
 225 230 235 240
 5 Lys Glu Asp Ser Lys Thr Leu Gln Lys Glu Lys Val Arg Cys Xaa Pro
 245 250 255

<210> 641
 <211> 178
 10 <212> PRT
 <213> Homo sapiens

<400> 641
 Gln Ser Asn Ser Pro Val Leu Leu Ser Arg Leu His Phe Glu Lys Asp
 1 5 10 15
 Ala Asp Ser Ser Glu Arg Ile Ile Ala Pro Met Arg Trp Gly Leu Val
 20 25 30
 Pro Ser Trp Phe Lys Glu Ser Asp Pro Ser Lys Leu Gln Phe Asn Thr
 35 40 45
 20 Thr Asn Cys Arg Ser Asp Thr Val Met Glu Lys Arg Ser Phe Lys Val
 50 55 60
 Pro Leu Gly Lys Gly Arg Arg Cys Val Val Leu Ala Asp Gly Phe Tyr
 65 70 75 80
 Glu Trp Gln Arg Cys Gln Gly Thr Asn Gln Arg Gln Pro Tyr Phe Ile
 85 90 95
 25 Tyr Phe Pro Gln Ile Lys Thr Glu Lys Ser Gly Ser Ile Gly Ala Ala
 100 105 110
 Asp Ser Pro Glu Asn Trp Glu Lys Val Trp Asp Asn Trp Arg Leu Leu
 115 120 125
 30 Thr Met Ala Gly Ile Phe Asp Cys Trp Glu Pro Pro Glu Gly Gly Asp
 130 135 140
 Val Leu Tyr Ser Tyr Thr Ile Ile Thr Val Asp Ser Cys Lys Gly Leu
 145 150 155 160
 Ser Asp Ile His His Arg Met Pro Ala Ile Leu Asp Gly Glu Glu Ala
 165 170 175
 35 Ser Phe

<210> 642
 40 <211> 235
 <212> PRT
 <213> Homo sapiens

<400> 642
 Ala Val Ser Val Ser Cys Ile Thr Tyr Leu Arg Gly Ile Phe Pro Glu
 1 5 10 15
 Cys Ala Tyr Gly Thr Arg Tyr Leu Asp Asp Leu Cys Val Lys Ile Leu
 20 25 30
 Arg Glu Asp Lys Asn Cys Pro Gly Ser Thr Gln Leu Val Lys Trp Met
 35 40 45
 50 Leu Gly Cys Tyr Asp Ala Leu Gln Lys Lys Tyr Leu Arg Met Val Val
 50 55 60
 Leu Ala Val Tyr Thr Asn Pro Glu Asp Pro Gln Thr Ile Ser Glu Cys
 65 70 75 80
 55 Tyr Gln Phe Lys Phe Lys Tyr Thr Asn Asn Gly Pro Leu Met Asp Phe
 85 90 95
 Ile Ser Lys Asn Gln Ser Asn Glu Ser Ser Met Leu Ser Thr Asp Thr
 100 105 110
 Lys Lys Ala Ser Ile Leu Leu Ile Arg Lys Ile Tyr Ile Leu Met Gln
 115 120 125
 60 Asn Leu Gly Pro Leu Pro Asn Asp Val Cys Leu Thr Met Lys Leu Phe
 130 135 140
 Tyr Tyr Asp Glu Val Thr Pro Pro Asp Tyr Gln Pro Pro Gly Phe Lys

	145				150				155				160				
	Asp	Gly	Asp	Cys	Glu	Gly	Val	Ile	Phe	Glu	Gly	Glu	Pro	Met	Tyr	Leu	
					165					170					175		
5	Asn	Val	Gly	Glu	Val	Ser	Thr	Pro	Phe	His	Ile	Phe	Lys	Val	Lys	Val	
				180					185					190			
	Thr	Thr	Glu	Arg	Glu	Arg	Met	Glu	Asn	Ile	Asp	Ser	Thr	Xaa	Leu	Ser	
			195					200					205				
	Pro	Lys	Gln	Ile	Lys	Thr	Pro	Phe	Gln	Lys	Ile	Leu	Arg	Asp	Lys	Asp	
		210					215					220					
10	Val	Xaa	Xaa	Glu	Gln	Asp	Xaa	Tyr	Ile	Ser	Gly						
		225				230					235						

15 <210> 643
 <211> 301
 <212> PRT
 <213> Homo sapiens

				<400>	643												
20	Thr	Xaa	Leu	Ala	Arg	Xaa	Gln	Val	Asp	Thr	Ser	Gly	Ser	Lys	Ala	Met	
	1				5				10					15			
	Met	Leu	Pro	Val	Leu	Thr	His	His	Ile	Arg	Tyr	His	Gln	Cys	Leu	Met	
				20					25					30			
	His	Leu	Asp	Lys	Leu	Ile	Gly	Tyr	Thr	Phe	Gln	Asp	Arg	Cys	Leu	Leu	
				35				40					45				
25	Gln	Leu	Ala	Met	Thr	His	Pro	Ser	His	His	Leu	Asn	Phe	Gly	Met	Asn	
	50						55					60					
	Pro	Asp	His	Ala	Arg	Asn	Ser	Leu	Ser	Asn	Cys	Gly	Ile	Arg	Gln	Pro	
	65					70					75				80		
	Lys	Tyr	Gly	Asp	Arg	Lys	Val	His	His	Met	His	Met	Arg	Lys	Lys	Gly	
					85					90					95		
30	Ile	Asn	Thr	Leu	Ile	Asn	Ile	Met	Ser	Arg	Leu	Gly	Gln	Asp	Asp	Pro	
				100					105					110			
	Thr	Pro	Ser	Arg	Ile	Asn	His	Asn	Glu	Arg	Leu	Glu	Phe	Leu	Gly	Asp	
				115				120					125				
35	Ala	Val	Val	Glu	Phe	Leu	Thr	Ser	Val	His	Leu	Tyr	Tyr	Leu	Phe	Pro	
	130						135					140					
	Ser	Leu	Glu	Glu	Gly	Gly	Leu	Ala	Thr	Tyr	Arg	Thr	Ala	Ile	Val	Gln	
	145				150						155				160		
	Asn	Gln	His	Leu	Ala	Met	Leu	Ala	Lys	Lys	Leu	Glu	Leu	Asp	Arg	Phe	
					165				170					175			
40	Met	Leu	Tyr	Ala	His	Gly	Pro	Asp	Leu	Cys	Arg	Glu	Ser	Asp	Leu	Arg	
				180					185					190			
	His	Ala	Met	Ala	Asn	Cys	Phe	Glu	Ala	Leu	Ile	Gly	Ala	Val	Tyr	Leu	
				195				200				205					
45	Glu	Gly	Ser	Leu	Glu	Glu	Ala	Lys	Gln	Leu	Phe	Gly	Arg	Leu	Leu	Phe	
	210						215					220					
	Asn	Asp	Pro	Asp	Leu	Arg	Glu	Val	Trp	Leu	Asn	Tyr	Pro	Leu	His	Pro	
	225				230						235				240		
	Leu	Gln	Leu	Gln	Glu	Pro	Asn	Thr	Asp	Arg	Gln	Leu	Ile	Gly	Asn	Phe	
					245				250					255			
50	Phe	Gln	Phe	Tyr	Lys	Lys	Leu	Thr	Glu	Phe	Glu	Arg	Asn	Gln	Leu	Gly	
				260					265					270			
	Val	Asn	Phe	Leu	Leu	Ile	Gly	Ser	Asp	Phe	Xaa	Ala	Xaa	Gly	Xaa	Ser	
				275				280					285				
55	His	Leu	Arg	Asn	Trp	Gly	Asp	Leu	Thr	Xaa	Xaa	Thr	Pro				
	290						295					300					

60 <210> 644
 <211> 163
 <212> PRT
 <213> Homo sapiens

<400> 644

Pro Ile Met Ser Xaa Xaa Thr Xaa Ser Thr Leu Val Asp Pro Lys Leu
 1 5 10 15
 Cys Leu Val Tyr Val Tyr Met Pro Asn Gly Ser Leu Leu Asp Arg Leu
 20 25 30
 5 Ser Cys Leu Asp Gly Thr Pro Pro Leu Ser Trp His Met Arg Cys Lys
 35 40 45
 Ile Ala Gln Gly Ala Ala Asn Gly Ile Asn Phe Leu His Glu Asn His
 50 55 60
 His Ile His Arg Asp Ile Lys Ser Ala Asn Ile Leu Leu Asp Glu Ala
 65 70 75 80
 10 Phe Thr Ala Lys Ile Ser Asp Phe Gly Leu Ala Arg Ala Ser Glu Lys
 85 90 95
 Phe Ala Gln Thr Val Met Thr Ser Arg Ile Val Gly Thr Thr Ala Tyr
 100 105 110
 15 Met Ala Pro Glu Ala Leu Arg Gly Glu Ile Thr Pro Lys Ser Asp Ile
 115 120 125
 Tyr Ser Phe Gly Val Val Leu Leu Glu Ile Ile Thr Gly Leu Pro Ala
 130 135 140
 Val Asp Glu His Arg Glu Pro Gln Leu Leu Leu Asp Ile Lys Arg Arg
 145 150 155 160
 20 Asn Xaa Arg

25 <210> 645
 <211> 155
 <212> PRT
 <213> Homo sapiens

<400> 645
 30 Asp Tyr Arg Xaa Ile Glu Ile Thr Ile Cys Lys Asn Asp Glu Cys Val
 1 5 10 15
 Leu Glu Asp Asn Ser Gln Arg Thr Lys Trp Lys Val Ile Ser Pro Thr
 20 25 30
 Gly Asn Glu Ala Xaa Val Pro Xaa Val Cys Phe Leu Ile Pro Pro Pro
 35 35 40 45
 Asn Lys Asp Ala Ile Xaa Met Ala Ser Arg Val Glu Gln Ser Tyr Xaa
 50 55 60
 Lys Val Met Ala Leu Trp His Gln Leu His Val Asn Thr Lys Ser Leu
 65 70 75 80
 40 Xaa Ser Trp Asn Tyr Leu Arg Lys Asp Leu Asp Leu Val Gln Thr Trp
 85 90 95
 Asn Leu Glu Lys Leu Arg Ser Ser Ala Pro Gly Glu Cys His Gln Ile
 100 105 110
 Met Xaa Asn Leu Gln Ala His Tyr Glu Asp Phe Xaa Gln Asp Ser Arg
 115 120 125
 45 Asp Ser Val Leu Val Ser Val Ala Asp Arg Leu Arg Leu Glu Glu Glu
 130 135 140
 Xaa Glu Ala Cys Lys Ala Arg Phe Gln His Leu
 145 150 155

50 <210> 646
 <211> 200
 <212> PRT
 <213> Homo sapiens

<400> 646
 Arg Gly Asn Xaa Gln Gly Lys Ala Xaa Ser Ser Glu Thr Lys Glu Ser
 1 5 10 15
 Thr Asp Ile Glu Lys Ala Ile Leu Glu Gln Gln Val Leu Ser Glu Glu
 20 25 30
 60 Leu Thr Thr Lys Lys Glu Gln Val Phe Glu Ala Ile Lys Thr Ser Gln
 35 40 45
 Ile Phe Leu Ala Lys His Gly His Lys Leu Ser Glu Lys Glu Lys Lys
 236

50 55 60
 Gln Ile Ser Glu Gln Leu Asn Ala Leu Asn Lys Ala Tyr His Asp Leu
 65 70 75 80
 Cys Asp Gly Ser Ala Asn Gln Leu Gln Gln Leu Gln Ser Gln Leu Ala
 85 90 95
 5 His Gln Thr Glu Gln Lys Glu Cys Arg Ala Val Ala Gly Val Ile Asp
 100 105 110
 Leu Gly Thr Val Glu Ile Phe Pro Ile Phe Lys Ala Met Gln Lys Gly
 115 120 125
 10 Leu Leu Asp Gln Asp Thr Gly Leu Val Leu Leu Glu Ser Gln Val Ile
 130 135 140
 Met Ser Gly Leu Ile Ala Pro Glu Thr Gly Glu Asn Leu Ser Leu Glu
 145 150 155 160
 Glu Gly Val Ala Arg Asn Leu Ile Asn Pro Gln Met Tyr Gln Gln Leu
 15 165 170 175
 Arg Glu Leu Gln Asp Ala Leu Ala Leu Ile Ser Arg Leu Thr Glu Ser
 180 185 190
 Arg Gly Pro Leu Ser Val Val Glu
 195 200
 20
 <210> 647
 <211> 169
 <212> PRT
 <213> Homo sapiens
 25
 <400> 647
 Lys Glu Gln Arg Lys Glu Asn Glu Pro Glu Ala Glu Lys Thr His Leu
 1 5 10 15
 Phe Ala Lys Gln Glu Lys Ala Phe Tyr Pro Lys Ser Phe Lys Ser Lys
 20 25 30
 30 Lys Gln Lys Pro Ser Arg Val Leu Tyr Ser Ser Thr Glu Ser Ser Asp
 35 40 45
 Glu Glu Ala Leu Gln Asn Lys Lys Ile Ser Thr Ser Cys Ser Val Ile
 50 55 60
 35 Pro Glu Thr Ser Asn Ser Asp Met Gln Thr Lys Lys Glu Tyr Val Val
 65 70 75 80
 Ser Gly Glu His Lys Gln Lys Gly Lys Val Lys Arg Lys Leu Lys Asn
 85 90 95
 Gln Asn Lys Asn Lys Glu Asn Gln Glu Leu Lys Gln Glu Lys Glu Gly
 100 105 110
 40 Lys Glu Asn Thr Arg Ile Thr Asn Leu Thr Val Asn Thr Gly Leu Asp
 115 120 125
 Cys Ser Glu Lys Thr Arg Glu Glu Gly Asn Phe Arg Lys Ser Phe Ser
 130 135 140
 45 Pro Lys Asp Asp Thr Ser Leu His Leu Phe His Ile Ser Thr Gly Lys
 145 150 155 160
 Ser Pro Lys His Ser Cys Gly Leu Lys
 165
 50
 <210> 648
 <211> 139
 <212> PRT
 <213> Homo sapiens
 55
 <400> 648
 Ala Phe Leu Phe Pro Ser Xaa Tyr Ala Ser Ile Tyr Val Phe Leu Met
 1 5 10 15
 Xaa Tyr Leu Xaa Tyr Pro Phe Phe Ser Xaa Gly Asn Leu Asn Phe Gln
 20 25 30
 60 Met Xaa Asp Tyr Asp Leu His Pro Leu Phe Trp His Leu Ile Phe His
 35 40 45
 Gln Ile Leu Xaa Gly Asn Leu Ser Asp Val Xaa Phe Phe Pro Tyr Ala
 50 55 60
 121

Tyr Xaa Ile Leu Xaa Leu Asn Phe Xaa Ala Xaa Ile Gln Ile Leu Xaa
 65 70 75 80
 Tyr His Xaa Xaa Gln Xaa Gln Ala Val Met Thr Phe Gln Asn Phe Leu
 85 90 95
 5 Gly Ile Asn Met Phe Xaa Tyr Val Leu Xaa Leu Gly Gly Xaa Thr Xaa
 100 105 110
 Phe His Leu Ile Xaa Xaa Asn Val Trp Xaa Ile Tyr Xaa Xaa Lys Tyr
 115 120 125
 Glu Ile Asn Val Met Lys Xaa His Xaa Leu Gly
 10 130 135

<210> 649

<211> 321

<212> PRT

15 <213> Homo sapiens

<400> 649

Gly Lys Asp Leu Leu Asn Met Tyr Ile Glu Thr Glu Gly Lys Met Ile
 1 5 10 15
 20 Met Gln Asp Lys Leu Glu Lys Glu Arg Asn Asp Ala Lys Asn Ala Val
 20 25 30
 Glu Glu Tyr Val Tyr Glu Phe Arg Asp Lys Leu Cys Gly Pro Tyr Glu
 35 40 45
 25 Lys Phe Ile Cys Glu Gln Asp His Gln Asn Phe Leu Arg Leu Leu Thr
 50 55 60
 Glu Thr Glu Asp Trp Leu Tyr Glu Glu Gly Glu Asp Gln Ala Lys Gln
 65 70 75 80
 Ala Tyr Val Asp Lys Leu Glu Glu Leu Met Lys Ile Gly Thr Pro Val
 85 90 95
 30 Lys Val Arg Phe Gln Glu Ala Glu Glu Arg Pro Lys Met Phe Glu Glu
 100 105 110
 Leu Gly Gln Arg Leu Gln His Tyr Ala Lys Ile Ala Ala Asp Phe Arg
 115 120 125
 Asn Lys Asp Glu Lys Tyr Asn His Ile Asp Glu Ser Glu Met Lys Lys
 130 135 140
 35 Val Glu Ala Lys Gln Ala Tyr Val Asp Lys Leu Glu Glu Leu Met Lys
 145 150 155 160
 Ile Gly Thr Pro Val Lys Val Arg Phe Gln Glu Ala Glu Glu Arg Pro
 165 170 175
 40 Lys Met Phe Glu Glu Leu Gly Gln Arg Leu Gln His Tyr Ala Lys Ile
 180 185 190
 Ala Ala Asp Phe Arg Asn Lys Asp Glu Lys Tyr Asn His Ile Asp Glu
 195 200 205
 Ser Glu Met Lys Lys Val Glu Lys Ser Val Asn Glu Val Met Glu Trp
 210 215 220
 45 Met Asn Asn Val Met Asn Ala Gln Ala Lys Lys Ser Leu Asp Gln Asp
 225 230 235 240
 Pro Val Val Arg Ala Gln Glu Ile Lys Thr Lys Ile Lys Glu Leu Asn
 245 250 255
 50 Asn Thr Cys Glu Pro Val Val Thr Gln Pro Lys Pro Lys Ile Glu Ser
 260 265 270
 Pro Lys Leu Glu Arg Thr Pro Asn Gly Pro Asn Ile Asp Lys Lys Glu
 275 280 285
 Glu Asp Leu Glu Asp Lys Asn Asn Phe Gly Ala Glu Pro Pro His Gln
 290 295 300
 55 Asn Gly Glu Cys Tyr Pro Asn Glu Lys Asn Ser Val Asn Met Asp Leu
 305 310 315 320
 Asp

60

<210> 650

<211> 188

<212> PRT

<213> Homo sapiens

<400> 650

5 Cys Ala Ile Leu Ser Pro Ala Phe Lys Val Arg Glu Phe Ser Val Thr
 1 5 10 15
 Asp Ala Val Pro Phe Pro Ile Ser Leu Ile Trp Asn His Asp Ser Glu
 20 25 30
 Asp Thr Glu Gly Val His Glu Val Phe Ser Arg Asn His Ala Ala Pro
 35 40 45
 10 Phe Ser Lys Val Leu Thr Phe Leu Arg Arg Gly Pro Phe Glu Leu Glu
 50 55 60
 Ala Phe Tyr Ser Asp Pro Gln Gly Val Pro Tyr Pro Glu Ala Lys Ile
 65 70 75 80
 Gly Arg Phe Val Val Gln Asn Val Ser Ala Gln Lys Asp Gly Glu Lys
 85 90 95
 15 Ser Arg Val Lys Val Lys Val Arg Val Asn Thr His Gly Ile Phe Thr
 100 105 110
 Ile Ser Thr Ala Ser Met Val Glu Lys Val Pro Thr Glu Glu Asn Glu
 115 120 125
 20 Met Ser Ser Glu Ala Asp Met Glu Cys Leu Asn Gln Arg Pro Pro Glu
 130 135 140
 Asn Pro Asp Thr Asp Ala Asn Glu Lys Lys Val Asp Gln Pro Pro Glu
 145 150 155 160
 Ala Lys Lys Pro Lys Ile Lys Val Val Asn Val Glu Leu Pro Ile Glu
 165 170 175
 25 Ala Asn Leu Val Trp Gln Leu Gly Glu Arg Pro Ser
 180 185

<210> 651

30 <211> 174

<212> PRT

<213> Homo sapiens

<400> 651

35 Xaa Ile Xaa Lys Xaa Ile Gly Lys Xaa Xaa Xaa Gly Leu Lys Pro Val
 1 5 10 15
 Gly Asn Leu Val Xaa Val Xaa Xaa Xaa Leu Xaa Gly Xaa Tyr Glu Lys
 20 25 30
 Phe Ile Cys Glu Xaa Val Phe Lys Xaa Xaa Asp Asp Ala Xaa Gln Xaa
 35 40 45
 40 Leu Xaa Xaa Ala Val Ser Gly Xaa Gly Gly Xaa Ser Xaa Xaa Xaa
 50 55 60
 Arg Cys Xaa Val Ala Gly Leu Arg Xaa Xaa Gly Xaa Pro Val Lys Val
 65 70 75 80
 45 Xaa Phe Xaa Glu His Xaa Asn Gly Gln Lys Cys Phe Xaa Thr Xaa Gln
 85 90 95
 Xaa Leu Gln Xaa Tyr Pro Lys Ile Ala Ala Asp Phe Arg Asn Lys Xaa
 100 105 110
 Xaa Lys Ser Xaa Xaa Ile Asp Glu Phe Glu Met Lys Lys Val Glu Lys
 115 120 125
 50 Xaa Val Asn Glu Val Met Glu Trp Met Asn Asn Val Met Asn Ala Gln
 130 135 140
 Ala Lys Xaa Ser Phe Asp Gln Asp Pro Val Xaa Arg Ala Gln Glu Ile
 145 150 155 160
 55 Lys Thr Lys Ile Lys Glu Leu Xaa Thr His Val Asn Pro Leu
 165 170

<210> 652

60 <211> 150

<212> PRT

<213> Homo sapiens

<400> 652

Gly Asn Ile Xaa His Ser Asp Xaa Xaa Val Xaa Xaa Gln Asn Xaa Phe
 1 5 10 15
 Trp Leu Leu Asn Leu Leu Pro Phe Xaa Gln Tyr Xaa Gly His Leu Glu
 20 25 30
 5 Phe Phe Pro Val Xaa Xaa Ile Gln Phe Leu Val Ser Xaa Gly Leu Gln
 35 40 45
 Arg Val His Met Cys Xaa Gln Phe Leu Asp Phe Cys Phe Asn Phe Leu
 50 55 60
 Ser Pro Xaa Asn Trp Ile Leu Ile Lys Thr Xaa Phe Ser Leu Ser Ile
 10 65 70 75 80
 His Asp Ile Ile His Pro Phe His His Phe Ile Asn Xaa Leu Leu His
 85 90 95
 Phe Phe His Phe Lys Leu Ile Asn Xaa Xaa Gly Phe Xaa Xaa Leu Ile
 100 105 110
 15 Ser Glu Val Ser Cys Tyr Leu Gly Ile Xaa Leu Gln Xaa Leu Xaa Ser
 115 120 125
 Xaa Lys Thr Phe Leu Ala Val Xaa Met Phe Xaa Lys Xaa Asn Phe His
 130 135 140
 Trp Xaa Ala Xaa Xaa Pro
 20 145 150

<210> 653

<211> 155

<212> PRT

25 <213> Homo sapiens

<400> 653

Ala Glu Xaa Ala Ala Leu Cys Gln Asp Ser Ser Cys Phe Arg Asn Lys
 1 5 10 15
 30 Asp Glu Lys Xaa Thr His Ile Asp Glu Xaa Glu Met Lys Lys Val Glu
 20 25 30
 Lys Ser Val Asn Glu Val Met Glu Trp Met Asn Asn Val Met Asn Ala
 35 35 40 45
 Gln Ala Lys Lys Ser Leu Asp Gln Asp Pro Val Val Arg Ala Gln Glu
 50 55 60
 35 Ile Lys Pro Lys Ile Lys Glu Leu Asn Asn Thr Cys Glu Pro Val Val
 65 70 75 80
 Thr Xaa Pro Lys Pro Lys Ile Glu Xaa Pro Lys Leu Glu Arg Thr Pro
 85 90 95
 40 Asn Gly Pro Asn Ile Asp Lys Lys Glu Glu Asp Leu Glu Xaa Lys Xaa
 100 105 110
 Asn Phe Gly Xaa Glu Pro Pro His Gln Asn Gly Glu Cys Tyr Pro Asn
 115 120 125
 Glu Lys Asn Ser Val Asn Met Asp Leu Asp Xaa Ile Xaa Leu Asn Trp
 130 135 140
 45 Pro Ile Pro Ser Ile Asn Lys Ile Phe Leu Pro
 145 150 155

<210> 654

50 <211> 188

<212> PRT

<213> Homo sapiens

<400> 654

Cys Ala Ile Leu Ser Pro Ala Phe Lys Val Arg Glu Phe Ser Val Thr
 1 5 10 15
 Asp Ala Val Pro Phe Pro Ile Ser Leu Ile Trp Asn His Asp Ser Glu
 20 25 30
 60 Asp Thr Glu Gly Val His Glu Val Phe Ser Arg Asn His Ala Ala Pro
 35 40 45
 Phe Ser Lys Val Leu Thr Phe Leu Arg Arg Gly Pro Phe Glu Leu Glu
 50 55 60
 Ala Phe Tyr Ser Asp Pro Gln Gly Val Pro Tyr Pro Glu Ala Lys Ile
 234

	65					70					75					80
	Gly	Arg	Phe	Val	Val	Gln	Asn	Val	Ser	Ala	Gln	Lys	Asp	Gly	Glu	Lys
					85					90					95	
5	Ser	Arg	Val	Lys	Val	Lys	Val	Arg	Val	Asn	Thr	His	Gly	Ile	Phe	Thr
				100					105					110		
	Ile	Ser	Thr	Ala	Ser	Met	Val	Glu	Lys	Val	Pro	Thr	Glu	Glu	Asn	Glu
				115				120					125			
	Met	Ser	Ser	Glu	Ala	Asp	Met	Glu	Cys	Leu	Asn	Gln	Arg	Pro	Pro	Glu
				130			135						140			
10	Asn	Pro	Asp	Thr	Asp	Ala	Asn	Glu	Lys	Lys	Val	Asp	Gln	Pro	Pro	Glu
	145					150					155					160
	Ala	Lys	Lys	Pro	Lys	Ile	Lys	Val	Val	Asn	Val	Glu	Leu	Pro	Ile	Glu
					165					170					175	
	Ala	Asn	Leu	Val	Trp	Gln	Leu	Gly	Glu	Arg	Pro	Ser				
15				180					185							

20 <210> 655
 <211> 138
 <212> PRT
 <213> Homo sapiens

	<div> <div><400> 655</div> <div>Ala Glu Ala Ala Ala Leu Cys Gln Asp Ser Ser Cys Phe Arg Asn Lys</div> <div>1 5 10 15</div> </div>															
25	<div> <div>Asp Glu Lys Xaa Thr His Ile Asp Glu Ser Glu Met Lys Lys Val Glu</div> <div>20 25 30</div> </div>															
	<div> <div>Lys Ser Val Asn Glu Val Met Glu Trp Met Asn Asn Val Met Asn Ala</div> <div>35 40 45</div> </div>															
30	<div> <div>Gln Ala Lys Lys Ser Leu Asp Gln Asp Pro Val Val Arg Ala Gln Glu</div> <div>50 55 60</div> </div>															
	<div> <div>Ile Lys Thr Lys Ile Lys Glu Leu Thr Asn Thr Cys Glu Pro Val Val</div> <div>65 70 75 80</div> </div>															
	<div> <div>Thr Xaa Pro Lys Pro Lys Ile Glu Ser Pro Lys Leu Glu Arg Thr Pro</div> <div>85 90 95</div> </div>															
35	<div> <div>Asn Gly Pro Asn Ile Asp Lys Lys Glu Glu Asp Leu Glu Asp Lys Asn</div> <div>100 105 110</div> </div>															
	<div> <div>Asn Phe Gly Ala Xaa Pro Pro His Gln Asn Gly Glu Cys Tyr Pro Asn</div> <div>115 120 125</div> </div>															
40	<div> <div>Glu Lys Asn Ser Val Asn Met Asp Leu Asp</div> <div>130 135</div> </div>															

45 <210> 656
 <211> 110
 <212> PRT
 <213> Homo sapiens

		<400> 656															
	Arg	Xaa	Arg	Gln	Arg	Leu	Gln	His	Tyr	Ala	Lys	Ile	Ala	Ala	Xaa	Phe	
	1				5					10					15		
50	Arg	Asn	Lys	Asp	Glu	Lys	Ser	Pro	Xaa	Ile	Asp	Glu	Phe	Glu	Met	Lys	
				20					25					30			
	Lys	Val	Glu	Lys	Xaa	Val	Asn	Glu	Val	Met	Glu	Trp	Met	Asn	Asn	Val	
			35					40					45				
	Met	Asn	Ala	Gln	Xaa	Lys	Xaa	Ser	Xaa	Asp	Gln	Asp	Pro	Val	Val	Arg	
55		50					55					60					
	Ala	Gln	Glu	Ile	Asn	Xaa	Lys	Ser	Arg	Asn	Xaa	Xaa	Thr	His	Val	Xaa	
	65					70					75				80		
	Xaa	Xaa	Xaa	Pro	Asn	Arg	Xaa	Xaa	Lys	Leu	Asn	Xaa	Pro	Xaa	Xaa	Lys	
					85					90					95		
60	Glu	Leu	Gln	Met	Ala	Gln	Ile	Leu	Ile	Lys	Arg	Lys	Lys	Ile			
				100					105					110			

<210> 657

<211> 138
 <212> PRT
 <213> Homo sapiens

5 <400> 657
 Ala Glu Ala Ala Ala Leu Cys Gln Asp Ser Ser Cys Phe Arg Asn Lys
 1 5 10 15
 Asp Glu Lys Ser Pro His Ile Asp Glu Phe Glu Met Lys Lys Val Xaa
 20 25 30
 10 Lys Xaa Val Asn Glu Val Met Glu Trp Met Asn Asn Val Met Asn Ala
 35 40 45
 Gln Ala Lys Xaa Ser Phe Asp Gln Asp Pro Val Val Xaa Ala Gln Glu
 50 55 60
 Ile Lys Xaa Lys Ile Lys Glu Leu Xaa Xaa Xaa Cys Glu Pro Val Val
 15 65 70 75 80
 Thr Xaa Pro Lys Xaa Lys Ile Glu Xaa Pro Xaa Leu Glu Arg Thr Xaa
 85 90 95
 Asn Gly Pro Asn Ile Asp Lys Lys Glu Glu Asp Leu Glu Xaa Xaa Xaa
 100 105 110
 20 Xaa Phe Xaa Xaa Glu Xaa Xaa His Gln Asn Xaa Glu Cys Tyr Pro Asn
 115 120 125
 Glu Lys Asn Xaa Val Asn Met Asp Leu Asp
 130 135

25 <210> 658
 <211> 133
 <212> PRT
 <213> Homo sapiens

30 <400> 658
 Gly Lys Met Ile Met Gln Asp Lys Leu Glu Lys Glu Arg Asn Asp Ala
 1 5 10 15
 Lys Asn Ala Val Glu Glu Tyr Val Tyr Glu Phe Arg Asp Lys Leu Cys
 20 25 30
 35 Gly Pro Tyr Glu Lys Phe Ile Cys Glu Gln Asp His Gln Asn Phe Leu
 35 40 45
 Arg Leu Leu Thr Glu Thr Glu Asp Trp Leu Tyr Glu Glu Gly Glu Asp
 50 55 60
 Gln Ala Lys Gln Ala Tyr Val Asp Lys Leu Glu Glu Leu Met Lys Ile
 40 65 70 75 80
 Gly Thr Pro Val Lys Val Arg Phe Gln Glu Ala Glu Glu Arg Pro Lys
 85 90 95
 Met Phe Glu Glu Leu Gly Gln Arg Leu Gln His Tyr Ala Lys Ile Ala
 100 105 110
 45 Ala Asp Phe Arg Asn Lys Asp Glu Lys Tyr Asn His Ile Asp Glu Ser
 115 120 125
 Glu Met Lys Lys Val
 130

50 <210> 659
 <211> 118
 <212> PRT
 <213> Homo sapiens

55 <400> 659
 Phe Leu Phe Ile Asn Ile Xaa Ala Ile Trp Ser Ser Phe Gln Xaa Gly
 1 5 10 15
 Xaa Phe Asn Phe Trp Phe Arg Leu Gly Tyr Asn Gly Xaa Thr Cys Xaa
 20 25 30
 60 Gly Gln Phe Leu Asp Phe Xaa Phe Asn Phe Leu Ser Xaa Tyr Asn Trp
 35 40 45
 Ile Leu Ile Lys Thr Xaa Phe Ser Leu Ser Ile His Asp Ile Ile His
 50 55 60

Pro Phe His His Phe Ile Asn Arg Leu Xaa Xaa Phe Phe His Phe Xaa
 65 70 75 80
 Leu Ile Asn Met Xaa Gly Phe Leu Ile Leu Ile Xaa Glu Val Ser Cys
 85 90 95
 5 Xaa Leu Gly Ile Met Leu Xaa Pro Xaa Pro Ser Xaa Ser Asn Ile Leu
 100 105 110
 Gly Arg Ser Ser Ala Ser
 115
 10 <210> 660
 <211> 141
 <212> PRT
 <213> Homo sapiens
 15 <400> 660
 Xaa Thr Arg Xaa Arg Xaa Gln His Tyr Ala Lys Xaa Ala Ala Asp Phe
 1 5 10 15
 Xaa Asn Lys Asp Glu Lys Ser Xaa His Ile Asp Glu Xaa Glu Met Lys
 20 25 30
 Lys Xaa Xaa Lys Ser Val Asn Glu Val Met Glu Trp Met Asn Asn Val
 35 40 45
 Met Asn Ala Gln Ala Lys Xaa Ser Leu Asp Gln Asp Pro Val Val Xaa
 50 55 60
 Ala Gln Glu Ile Lys Xaa Lys Ile Lys Glu Leu Thr Xaa Thr Cys Xaa
 25 65 70 75 80
 Pro Val Val Thr Gln Pro Lys Pro Lys Ile Glu Xaa Pro Xaa Leu Glu
 85 90 95
 Arg Thr Pro Asn Gly Xaa Asn Ile Asp Lys Lys Glu Glu Asp Leu Glu
 100 105 110
 30 Xaa Lys Xaa Asn Phe Xaa Gly Glu Pro Pro His Gln Asn Gly Glu Cys
 115 120 125
 Tyr Pro Asn Glu Lys Asn Ser Val Asn Met Asp Leu Asp
 130 135 140
 35 <210> 661
 <211> 175
 <212> PRT
 <213> Homo sapiens
 40 <400> 661
 Ala Lys Gln Ala Tyr Val Asp Lys Leu Glu Glu Leu Met Lys Ile Gly
 1 5 10 15
 Thr Pro Val Lys Val Arg Phe Gln Glu Ala Glu Glu Arg Pro Lys Met
 20 25 30
 45 Phe Glu Glu Leu Gly Gln Arg Leu Gln His Tyr Ala Lys Ile Ala Ala
 35 40 45
 Asp Phe Arg Asn Lys Asp Glu Lys Tyr Asn His Ile Asp Glu Ser Glu
 50 55 60
 Met Lys Lys Val Glu Lys Ser Val Asn Glu Val Met Glu Trp Met Asn
 65 70 75 80
 Asn Val Met Asn Ala Gln Ala Lys Lys Ser Leu Asp Gln Asp Pro Val
 85 90 95
 Val Arg Ala Gln Glu Ile Lys Thr Lys Ile Lys Glu Leu Asn Asn Thr
 100 105 110
 55 Cys Glu Pro Val Val Thr Gln Pro Lys Pro Lys Ile Glu Ser Pro Lys
 115 120 125
 Leu Glu Arg Thr Pro Asn Gly Pro Asn Ile Asp Lys Lys Glu Glu Asp
 130 135 140
 Leu Glu Asp Lys Asn Asn Phe Gly Ala Glu Pro Pro His Gln Asn Gly
 60 145 150 155 160
 Glu Cys Tyr Pro Asn Glu Lys Asn Ser Val Asn Met Asp Leu Asp
 165 170 175

<210> 662
 <211> 120
 <212> PRT
 <213> Homo sapiens

5

<400> 662
 Glu Thr Glu Gly Lys Met Ile Met Gln Asp Lys Leu Glu Lys Glu Arg
 1 5 10 15
 Asn Asp Ala Lys Asn Ala Val Glu Glu Tyr Val Tyr Glu Phe Arg Asp
 10 20 25 30
 Lys Leu Cys Gly Pro Tyr Glu Lys Phe Ile Cys Glu Gln Asp His Gln
 35 40 45
 Asn Phe Leu Arg Leu Leu Thr Glu Thr Glu Asp Trp Leu Tyr Glu Glu
 50 55 60
 Xaa Glu Asp Gln Ala Lys Gln Xaa Xaa Val Asp Xaa Leu Glu Xaa Leu
 15 65 70 75 80
 Met Lys Xaa Xaa Thr Pro Val Lys Val Arg Phe Gln Glu Ala Glu Glu
 85 90 95
 Arg Pro Lys Met Phe Glu Glu Leu Gly Gln Arg Leu Xaa His Tyr Ala
 100 105 110
 20 Lys Ile Ala Ala Asp Phe Lys Lys
 115 120

<210> 663
 <211> 79
 <212> PRT
 <213> Homo sapiens

25

<400> 663
 Xaa Phe Gln Xaa Val Asp Xaa Xaa Leu Phe Ser Leu Val Leu Xaa Phe
 1 5 10 15
 Phe Ile Gln Pro Val Phe Ser Phe Cys Glu Glu Ser Gln Lys Ile Leu
 20 25 30
 Met Ile Leu Leu Thr Tyr Lys Phe Phe Ile Trp Ser Thr Gln Leu Val
 35 35 40 45
 Ser Glu Leu Ile His Ile Phe Leu Asn Cys Ile Phe Ser Ile Ile Pro
 50 55 60
 Phe Phe Phe Gln Phe Ile Leu His Tyr His Leu Thr Leu Cys Leu
 65 70 75

<210> 664
 <211> 97
 <212> PRT
 <213> Homo sapiens

40

45

<400> 664
 Met Asn Asn Val Met Asn Ala Gln Ala Lys Lys Ser Leu Asp Gln Asp
 1 5 10 15
 Pro Val Val Arg Ala Gln Glu Ile Lys Thr Lys Ile Lys Glu Leu Asn
 20 25 30
 Asn Thr Cys Glu Pro Val Val Thr Gln Pro Lys Pro Lys Ile Glu Ser
 35 40 45
 Pro Lys Leu Glu Arg Thr Pro Asn Gly Pro Asn Ile Asp Lys Lys Glu
 50 55 60
 Glu Asp Leu Glu Asp Lys Asn Asn Phe Gly Ala Glu Pro Pro His Gln
 55 65 70 75 80
 Asn Gly Glu Cys Tyr Pro Asn Glu Lys Asn Ser Val Asn Met Asp Leu
 85 90 95
 Asp

60

<210> 665
 <211> 178

<212> PRT

<213> Homo sapiens

<400> 665

5 Glu Asp Gln Ala Lys Gln Ala Tyr Val Asp Lys Leu Glu Glu Leu Met
 1 5 10 15
 Lys Ile Gly Thr Pro Val Lys Val Arg Phe Gln Glu Ala Glu Glu Arg
 20 25 30
 Pro Lys Met Phe Glu Glu Leu Gly Gln Arg Leu Gln His Tyr Ala Lys
 35 40 45
 10 Ile Ala Ala Asp Phe Arg Asn Lys Asp Glu Lys Tyr Asn His Ile Asp
 50 55 60
 Glu Ser Glu Met Lys Lys Val Glu Lys Ser Val Asn Glu Val Met Glu
 65 70 75 80
 15 Trp Met Asn Asn Val Met Asn Ala Gln Ala Lys Lys Ser Leu Asp Gln
 85 90 95
 Asp Pro Val Val Arg Ala Gln Glu Ile Lys Thr Lys Ile Lys Glu Leu
 100 105 110
 Asn Asn Thr Cys Glu Pro Val Val Thr Gln Pro Lys Pro Lys Ile Glu
 115 120 125
 20 Ser Pro Lys Leu Glu Arg Thr Pro Asn Gly Pro Asn Ile Asp Lys Lys
 130 135 140
 Glu Glu Asp Leu Glu Asp Lys Asn Asn Phe Gly Ala Glu Pro Pro His
 145 150 155 160
 25 Gln Asn Gly Glu Cys Tyr Pro Asn Glu Lys Asn Ser Val Asn Met Asp
 165 170 175
 Leu Asp

30 <210> 666
 <211> 198
 <212> PRT
 <213> Homo sapiens

35 <400> 666
 Gly Arg Gln Pro Glu Val Arg Ser Asp Leu Arg Arg Leu Ser Pro Ala
 1 5 10 15
 Phe Ser Gln Gly Phe Leu Ser Ala Ser Arg Arg Cys Pro Arg Gly Ser
 20 25 30
 40 Arg Arg Leu Leu Thr Gly Arg Gly Cys Leu Cys Val Leu Leu Ser Val
 35 40 45
 Arg Gly Thr Ala Arg Pro Arg Gly Pro Glu Gln Asn Ala Ala Arg Ala
 50 55 60
 Glu Ser Gly Gly Arg Arg Ser Arg Gln Gly Ala Gly Gly Arg Arg Pro
 65 70 75 80
 45 Arg Pro Glu Ala Glu Ala Asp Arg Glu Pro Ala Met Ser Val Val Gly
 85 90 95
 Leu Asp Val Gly Ser Gln Ser Cys Tyr Ile Ala Val Ala Arg Ala Gly
 100 105 110
 50 Gly Ile Glu Thr Ile Ala Asn Glu Phe Ser Asp Arg Cys Thr Pro Ser
 115 120 125
 Val Ile Ser Phe Gly Ser Lys Asn Arg Thr Ile Gly Val Ala Ala Lys
 130 135 140
 Asn Gln Gln Ile Thr His Ala Asn Asn Thr Val Ser Asn Phe Lys Arg
 145 150 155 160
 55 Phe His Gly Arg Ala Phe Asn Asp Pro Phe Ile Gln Lys Glu Lys Gly
 165 170 175
 Lys Leu Glu Leu Arg Phe Gly Ser Ile Glu Lys Trp Xaa Ser Trp Asn
 180 185 190
 60 Lys Xaa Asn Val His Gly
 195

<210> 667

<211> 100
 <212> PRT
 <213> Homo sapiens

5

<400> 667

Thr	Ser	Thr	Pro	Thr	His	Met	Leu	Asn	Gly	Glu	Gln	Asn	Ala	Arg	Lys
1				5					10					15	
Leu	Pro	Trp	Gln	Glu	Gln	Met	Leu	Lys	Asp	Phe	Asn	His	Ser	Pro	Leu
			20					25					30		
10	Glu	Gln	Xaa	Val	Gln	Phe	Phe	Phe	Ser	Lys	Arg	Gln	Lys	Ser	Val
			35					40					45		
Ser	Ser	Xaa	Met	Gln	Met	Xaa	Arg	Leu	His	Arg	Lys	Leu	Ser	Met	Asn
			50				55				60				
Ser	Gln	Phe	His	Arg	Asn	Xaa	Lys	Val	Thr	Lys	Ala	Ile	Phe	Pro	Phe
15	65				70					75				80	
Arg	Xaa	Ile	Lys	Thr	Thr	Asp	Leu	Ser	Phe	Phe	Leu	Phe	Pro	Tyr	Asn
				85					90					95	
Xaa	Gln	Lys	Phe												
			100												

20

<210> 668
 <211> 141
 <212> PRT
 <213> Homo sapiens

25

<400> 668

Gly	Arg	Gln	Pro	Glu	Val	Arg	Ser	Asp	Leu	Arg	Arg	Leu	Ser	Pro	Ala
1				5					10					15	
Phe	Ser	Gln	Gly	Phe	Leu	Ser	Ala	Ser	Arg	Arg	Cys	Pro	Arg	Gly	Ser
30			20					25					30		
Arg	Arg	Leu	Thr	Gly	Arg	Gly	Cys	Leu	Cys	Val	Leu	Leu	Ser	Val	
			35				40					45			
Arg	Gly	Thr	Ala	Arg	Pro	Arg	Gly	Pro	Glu	Xaa	Asn	Ala	Ala	Arg	Ala
			50				55				60				
35	Glu	Ser	Gly	Gly	Arg	Arg	Ser	Xaa	Gln	Gly	Ala	Gly	Gly	Arg	Arg
	65				70					75				80	
Arg	Pro	Glu	Ala	Xaa	Ala	Asp	Arg	Glu	Pro	Ala	Met	Ser	Val	Val	Gly
				85				90						95	
Leu	Asp	Val	Gly	Xaa	Gln	Ser	Cys	Tyr	Ile	Ala	Val	Ala	Arg	Ala	Gly
40				100				105					110		
Gly	Ile	Glu	Thr	Ile	Ala	Xaa	Glu	Phe	Xaa	Asp	Arg	Xaa	Thr	Pro	Xaa
			115				120					125			
Val	Ile	Ser	Phe	Xaa	Ser	Lys	Asn	Ile	Asn	Lys	Ser	Glu			
			130				135					140			

45

<210> 669
 <211> 116
 <212> PRT
 <213> Homo sapiens

50

<400> 669

Gln	Leu	Xaa	Glu	Pro	Thr	Ser	Asn	Pro	Thr	Thr	Asp	Met	Ala	Gly	Ser
1				5					10					15	
Arg	Ser	Xaa	Ser	Ala	Ser	Gly	Leu	Gly	Leu	Arg	Pro	Pro	Ala	Pro	Cys
55				20				25					30		
Xaa	Leu	Leu	Leu	Pro	Pro	Leu	Ser	Ala	Leu	Ala	Ala	Xaa	Cys	Ser	Gly
			35				40					45			
Pro	Arg	Gly	Leu	Ala	Val	Pro	Leu	Thr	Leu	Arg	Arg	Thr	His	Arg	Gln
			50				55				60				
60	Pro	Arg	Pro	Val	Arg	Ser	Leu	Leu	Leu	Pro	Arg	Gly	Gln	Arg	Arg
	65				70					75				80	
Ala	Asp	Lys	Lys	Pro	Trp	Glu	Lys	Ala	Gly	Leu	Ser	Leu	Arg	Arg	Ser
				85					90					95	

Leu Arg Thr Ser Gly Cys Leu Pro His Ser Ala Ala Ala Arg Thr Pro
 100 105 110
 Ala Pro Ala Leu
 115

5

<210> 670
 <211> 107
 <212> PRT
 <213> Homo sapiens

10

<400> 670
 Tyr Asp Xaa Arg Gly Xaa Pro Val Xaa Glu Leu Xaa Gly Asp Gly Leu
 1 5 10 15
 Asp Ala Pro Gly Pro Gly Tyr Arg Asp Val Ala Ala Leu Xaa Ala His
 15 20 25 30
 Val Gln Pro His His Arg His Gly Arg Leu Ala Val Arg Xaa Arg Leu
 35 40 45
 Gly Ser Arg Ser Ala Ser Ser Gly Pro Leu Xaa Ala Ser Pro Ala Ala
 50 55 60
 20 Ala Phe Cys Pro Gly Arg Val Xaa Leu Arg Pro Ala Gly Ser Gly Arg
 65 70 75 80
 Ser Ser Asp Thr Gln Lys Asp Thr Gln Thr Ala Ala Ala Cys Gln Glu
 85 90 95
 Pro Pro Thr Pro Pro Gly Thr Ala Ala Ala Gly
 25 100 105

<210> 671
 <211> 139
 <212> PRT
 <213> Homo sapiens

30

<400> 671
 Gly Asn Val Cys Lys Trp Gly Pro Val His Val Ser Val Trp Cys Ala
 1 5 10 15
 35 Cys Gly Asn Val Cys Lys Trp Ala Pro Val Arg Val Cys Gly Val Cys
 20 25 30
 Val Gly Met Cys Ala Ser Gly Arg Leu Cys Glu Cys Val Val Arg Val
 35 40 45
 40 Trp Glu Cys Val Gln Val Gly Ala Cys Pro Cys Glu Cys Val Val Arg
 50 55 60
 Val Leu Glu Cys Val Gln Val Asp Ala Cys Ala Cys Glu Cys Val Val
 65 70 75 80
 Arg Val Gly Met Cys Ala Ser Gly His Leu Cys Glu Cys Val Val Arg
 85 90 95
 45 Val Trp Glu Cys Val Gln Val Gly Thr Cys Pro Trp Glu Cys Val Val
 100 105 110
 Arg Val Trp Glu Cys Val Gln Val Gly Ala Cys Ala Cys Glu Cys Glu
 115 120 125
 50 Asp Thr Ser Cys Ser Gly Val Thr Asn Pro Ile
 130 135

<210> 672
 <211> 139
 <212> PRT
 <213> Homo sapiens

55

<400> 672
 Val Cys Gly Val His Val Gly Met Cys Ala Ser Gly Arg Leu Cys Glu
 1 5 10 15
 60 Cys Val Val Cys Val Trp Glu Cys Val Gln Val Gly Ala Cys Ala Ser
 20 25 30
 Val Trp Cys Val Cys Gly Asn Val Cys Lys Trp Ala Pro Ala His Val
 35 40 45

271

Ser Val Trp Cys Val Cys Trp Asn Val Cys Lys Trp Thr Pro Ala His
 50 55 60
 Val Ser Val Trp Cys Val Trp Glu Cys Val Gln Val Gly Thr Cys Ala
 65 70 75 80
 5 Ser Val Trp Cys Ala Cys Gly Asn Val Cys Lys Trp Ala Pro Ala His
 85 90 95
 Gly Ser Val Trp Cys Ala Cys Gly Asn Val Cys Lys Trp Glu Pro Ala
 100 105 110
 His Val Ser Val Arg Thr Pro Arg Ala Gln Val Ser Pro Thr Pro Phe
 115 120 125
 10 Lys Lys Glu Ile Thr Met Met Thr Thr Ser Leu
 130 135

15 <210> 673
 <211> 134
 <212> PRT
 <213> Homo sapiens

20 <400> 673
 His Leu Ser Thr Arg Cys Pro His Thr His Met Arg Arg Leu Pro Leu
 1 5 10 15
 Ala His Ile Pro Thr Arg Ala Pro His Thr Pro Met Gly Arg Cys Pro
 20 25 30
 25 Leu Ala His Ile Pro Thr Arg Ala Pro His Thr Arg Thr Gly Ala His
 35 40 45
 Leu His Thr Phe Pro His Ala Pro His Thr His Met Arg Arg Arg Pro
 50 55 60
 Leu Ala His Ile Pro Thr His Ala Pro His Thr His Met Gly Arg Arg
 65 70 75 80
 30 Pro Leu Ala His Ile Pro Thr His Ala Pro His Thr Arg Thr Gly Ala
 85 90 95
 His Leu His Thr Phe Pro His Thr His His Thr Leu Ala Gln Ala Pro
 100 105 110
 Thr Cys Thr His Ser His Met His Thr Thr His Ser His Ala Gln Ala
 115 120 125
 35 Pro Thr Cys Thr His Ser
 130

40 <210> 674
 <211> 132
 <212> PRT
 <213> Homo sapiens

45 <400> 674
 Ala Arg Gly Val Leu Thr Leu Thr Cys Ala Gly Ser His Leu His Thr
 1 5 10 15
 Phe Pro His Ala His His Thr Leu Pro Trp Ala Gly Ala His Leu His
 20 25 30
 50 Thr Phe Pro His Ala His His Thr Leu Ala Gln Val Pro Thr Cys Thr
 35 40 45
 His Ser His Thr His His Thr Leu Thr Cys Ala Gly Val His Leu His
 50 55 60
 Thr Phe Gln His Thr His His Thr Leu Thr Trp Ala Gly Ala His Leu
 65 70 75 80
 55 His Thr Phe Pro His Thr His His Thr Leu Ala Gln Ala Pro Thr Cys
 85 90 95
 Thr His Ser His Thr His Thr Thr His Ser His Arg Arg Pro Leu Ala
 100 105 110
 His Ile Pro Thr Cys Thr Pro His Thr His Met His Arg Pro Pro Leu
 115 120 125
 60 Ala His Ile Pro
 130

<210> 675
 <211> 138
 <212> PRT
 <213> Homo sapiens

5

<400> 675

Met Gly Leu Val Thr Pro Glu His Glu Val Ser Ser His Ser His Ala
 1 5 10 15
 Gln Ala Pro Thr Cys Thr His Ser His Thr Arg Thr Thr His Ser His
 10 20 25 30
 Gly Gln Val Pro Thr Cys Thr His Ser His Thr Arg Thr Thr His Ser
 35 40 45
 His Arg Cys Pro Leu Ala His Ile Pro Thr Arg Thr Thr His Ser His
 50 55 60
 15 Ala Gln Ala Ser Thr Cys Thr His Ser Asn Thr Arg Thr Thr His Ser
 65 70 75 80
 His Gly Gln Ala Pro Thr Cys Thr His Ser His Thr Arg Thr Thr His
 85 90 95
 20 Ser His Arg Arg Pro Leu Ala His Ile Pro Thr His Thr Pro His Thr
 100 105 110
 Arg Thr Gly Ala His Leu His Thr Phe Pro His Ala His His Thr Leu
 115 120 125
 Thr Cys Thr Gly Pro His Leu His Thr Phe
 130 135

25

<210> 676
 <211> 96
 <212> PRT
 <213> Homo sapiens

30

<400> 676

Met Glu Ser Lys Met Gln Glu Asn Tyr Leu Gly Arg Asn Lys Cys Leu
 1 5 10 15
 Lys Ile Leu Ile Thr Ala Leu Leu Asn Lys Gln Tyr Lys Phe Phe Phe
 15 20 25 30
 Ser Lys Arg Gln Lys Ser Val Ser Ser Ser Val Met Gln Met Xaa Arg
 35 40 45
 Leu His Arg Lys Leu Ser Met Asn Ser Gln Phe His Arg Asn Leu Lys
 50 55 60
 40 Val Thr Lys Ala Ile Phe Pro Phe Arg Ile Ile Lys Thr Thr Xaa Leu
 65 70 75 80
 Lys Leu Phe Phe Phe Phe His Ile Ile His Lys Ile Ser Lys Tyr Pro
 85 90 95

45

<210> 677
 <211> 178
 <212> PRT
 <213> Homo sapiens

50

<400> 677

Glu Asp Gln Ala Lys Gln Ala Tyr Val Asp Lys Leu Glu Glu Leu Met
 1 5 10 15
 Lys Ile Gly Thr Pro Val Lys Val Arg Phe Gln Glu Ala Glu Glu Arg
 20 25 30
 55 Pro Lys Met Phe Glu Glu Leu Gly Gln Arg Leu Gln His Tyr Ala Lys
 35 40 45
 Ile Ala Ala Asp Phe Arg Asn Lys Asp Glu Lys Tyr Asn His Ile Asp
 50 55 60
 Glu Ser Glu Met Lys Lys Val Glu Lys Ser Val Asn Glu Val Met Glu
 60 65 70 75 80
 Trp Met Asn Asn Val Met Asn Ala Gln Ala Lys Lys Ser Leu Asp Gln
 85 90 95
 Asp Pro Val Val Arg Ala Gln Glu Ile Lys Thr Lys Ile Lys Glu Leu

100 105 110
 Asn Asn Thr Cys Glu Pro Val Val Thr Gln Pro Lys Pro Lys Ile Glu
 115 120 125
 Ser Pro Lys Leu Glu Arg Thr Pro Asn Gly Pro Asn Ile Asp Lys Lys
 5 130 135 140
 Glu Glu Asp Leu Glu Asp Lys Asn Asn Phe Gly Ala Glu Pro Pro His
 145 150 155 160
 Gln Asn Gly Glu Cys Tyr Pro Asn Glu Lys Asn Ser Val Asn Met Asp
 165 170 175
 10 Leu Asp

<210> 678
 <211> 215
 15 <212> PRT
 <213> Homo sapiens

<400> 678
 Glu Asn Glu Met Ser Ser Glu Ala Asp Met Glu Cys Leu Asn Gln Arg
 20 1 5 10 15
 Pro Pro Glu Asn Pro Asp Thr Asp Lys Asn Val Gln Gln Asp Asn Ser
 20 25 30
 Glu Ala Gly Thr Gln Pro Gln Val Gln Thr Asp Ala Gln Gln Thr Ser
 35 40 45
 25 Gln Ser Pro Pro Ser Pro Glu Leu Thr Ser Glu Glu Asn Lys Ile Pro
 50 55 60
 Asp Ala Asp Lys Ala Asn Glu Lys Lys Val Asp Gln Pro Pro Glu Ala
 65 70 75 80
 Lys Lys Pro Lys Ile Lys Val Val Asn Val Glu Leu Pro Ile Glu Ala
 30 85 90 95
 Asn Leu Val Trp Gln Leu Gly Lys Asp Leu Leu Asn Met Tyr Ile Glu
 100 105 110
 Thr Glu Gly Lys Met Ile Met Gln Asp Lys Leu Glu Lys Glu Arg Asn
 115 120 125
 35 Asp Ala Lys Asn Ala Val Glu Glu Tyr Val Tyr Glu Phe Arg Asp Lys
 130 135 140
 Leu Cys Gly Pro Tyr Glu Lys Phe Ile Cys Glu Gln Asp His Gln Asn
 145 150 155 160
 Phe Leu Arg Leu Leu Thr Glu Thr Glu Asp Trp Leu Tyr Glu Glu Gly
 40 165 170 175
 Glu Asp Gln Ala Lys Gln Ala Tyr Val Asp Lys Leu Glu Glu Leu Met
 180 185 190
 Lys Ile Gly Thr Pro Val Lys Val Arg Phe Gln Glu Ala Glu Arg Thr
 195 200 205
 45 Ala Gln Lys Cys Leu Lys Asn
 210 215

<210> 679
 <211> 233
 50 <212> PRT
 <213> Homo sapiens

<400> 679
 Ser Asp Pro Gln Gly Val Pro Tyr Pro Glu Ala Lys Ile Gly Arg Phe
 55 1 5 10 15
 Val Val Gln Asn Val Ser Ala Gln Lys Asp Gly Glu Lys Ser Arg Val
 20 25 30
 Lys Val Lys Val Arg Val Asn Thr His Gly Ile Phe Thr Ile Ser Thr
 35 40 45
 60 Ala Ser Met Val Glu Lys Val Pro Thr Glu Glu Asn Glu Met Ser Ser
 50 55 60
 Glu Ala Asp Met Glu Cys Leu Asn Gln Arg Pro Pro Glu Asn Pro Asp
 65 70 75 80

Thr Asp Lys Asn Val Gln Gln Asp Asn Ser Glu Ala Gly Thr Gln Pro
 85 90 95
 Gln Val Gln Thr Asp Ala Gln Gln Thr Ser Gln Ser Pro Pro Ser Pro
 100 105 110
 5 Glu Leu Thr Ser Glu Glu Asn Lys Ile Pro Asp Ala Asp Lys Ala Asn
 115 120 125
 Glu Lys Lys Val Asp Gln Pro Pro Glu Ala Lys Lys Pro Lys Ile Lys
 130 135 140
 Val Val Asn Val Glu Leu Pro Ile Glu Ala Asn Leu Val Trp Gln Leu
 145 150 155 160
 10 Gly Lys Asp Leu Leu Asn Met Tyr Ile Glu Thr Glu Gly Lys Met Ile
 165 170 175
 Met Gln Asp Lys Leu Glu Lys Glu Arg Asn Asp Ala Lys Asn Ala Val
 180 185 190
 15 Glu Glu Tyr Val Tyr Glu Phe Arg Asp Lys Leu Cys Gly Pro Tyr Glu
 195 200 205
 Lys Phe Ile Cys Glu Gln Asp His Gln Lys Phe Phe Glu Asp Ser Ser
 210 215 220
 Gln Lys Thr Gly Arg Thr Gly Leu Phe
 20 225 230

<210> 680

<211> 471

<212> PRT

25 <213> Homo sapiens

<400> 680

Leu Asp Met Ala Pro Glu Ile Asn Leu Pro Gly Pro Met Ser Leu Ile
 1 5 10 15
 30 Asp Asn Thr Lys Gly Gln Leu Val Val Asn Pro Glu Ala Leu Lys Ile
 20 25 30
 Leu Ser Ala Ile Thr Gln Pro Val Val Val Ala Ile Val Gly Leu
 35 40 45
 Tyr Arg Thr Gly Lys Ser Tyr Leu Met Asn Lys Leu Ala Gly Lys Lys
 50 55 60
 Asn Gly Phe Ser Leu Gly Ser Thr Val Lys Ser His Thr Lys Gly Ile
 65 70 75 80
 Trp Met Trp Xaa Val Pro His Pro Lys Lys Pro Glu His Thr Leu Val
 85 90 95
 40 Leu Leu Asp Thr Glu Gly Leu Gly Asp Ile Glu Lys Gly Asp Asn Glu
 100 105 110
 Asn Asp Ser Trp Ile Phe Ala Leu Ala Ile Leu Leu Ser Ser Thr Phe
 115 120 125
 Val Tyr Asn Ser Met Gly Thr Ile Asn Gln Gln Ala Met Asp Gln Leu
 130 135 140
 45 His Tyr Val Thr Glu Leu Thr Asp Arg Ile Lys Ala Asn Ser Ser Pro
 145 150 155 160
 Gly Asn Asn Ser Val Asp Asp Ser Ala Asp Phe Val Ser Phe Phe Pro
 165 170 175
 50 Ala Phe Val Trp Thr Leu Arg Asp Phe Thr Leu Glu Leu Glu Val Asp
 180 185 190
 Gly Glu Pro Ile Thr Ala Asp Asp Tyr Leu Glu Leu Ser Leu Lys Leu
 195 200 205
 Arg Lys Gly Thr Asp Lys Lys Ser Lys Ser Phe Asn Asp Pro Arg Leu
 210 215 220
 55 Cys Ile Arg Lys Phe Phe Pro Lys Arg Lys Cys Phe Val Phe Asp Trp
 225 230 235 240
 Pro Ala Pro Lys Lys Tyr Leu Ala His Leu Glu Gln Leu Lys Glu Glu
 245 250 255
 60 Glu Leu Asn Pro Asp Phe Ile Glu Gln Val Ala Glu Phe Cys Ser Tyr
 260 265 270
 Ile Leu Ser His Ser Asn Val Lys Thr Leu Ser Gly Gly Ile Ala Val
 275 280 285

Asn Gly Pro Arg Leu Glu Ser Leu Val Leu Thr Tyr Val Asn Ala Ile
 290 295 300
 Ser Ser Gly Asp Leu Pro Cys Met Glu Asn Ala Val Leu Ala Leu Ala
 305 310 315 320
 5 Gln Ile Glu Asn Ser Ala Ala Val Glu Lys Ala Ile Ala His Tyr Glu
 325 330 335
 Gln Gln Met Gly Gln Lys Val Gln Leu Pro Thr Glu Thr Leu Gln Glu
 340 345 350
 Leu Leu Asp Leu His Arg Asp Ser Glu Arg Glu Ala Ile Glu Val Phe
 355 360 365
 10 Met Lys Asn Ser Phe Lys Asp Val Asp Gln Met Phe Gln Arg Lys Leu
 370 375 380
 Gly Ala Gln Leu Glu Ala Arg Arg Asp Asp Phe Cys Lys Gln Asn Ser
 385 390 395 400
 15 Lys Ala Ser Ser Asp Cys Cys Met Ala Leu Leu Gln Asp Ile Phe Gly
 405 410 415
 Pro Leu Glu Glu Asp Val Lys Gln Gly Thr Phe Ser Lys Pro Gly Gly
 420 425 430
 Tyr Arg Leu Phe Thr Gln Lys Leu Gln Glu Leu Lys Asn Lys Ser Thr
 435 440 445
 20 Arg Ala Lys Glu Gly Asp Thr Gly Gln Arg Gly Ala Glu Lys Ile Phe
 450 455 460
 Gly Val Gln Gly Gly Cys Gly
 465 470
 25
 <210> 681
 <211> 198
 <212> PRT
 <213> Homo sapiens
 30
 <400> 681
 Leu Asp Met Ala Pro Glu Ile Asn Leu Pro Gly Pro Met Ser Leu Ile
 1 5 10 15
 Asp Asn Thr Lys Gly Gln Leu Val Val Asn Pro Glu Ala Leu Lys Ile
 20 25 30
 35 Leu Ser Ala Ile Thr Gln Pro Val Val Val Val Ala Ile Val Gly Leu
 35 40 45
 Tyr Arg Thr Gly Lys Ser Tyr Leu Met Asn Lys Leu Ala Gly Lys Lys
 50 55 60
 40 Asn Gly Phe Ser Leu Gly Ser Thr Val Lys Ser His Thr Lys Gly Ile
 65 70 75 80
 Trp Met Trp Xaa Val Pro His Pro Lys Lys Pro Glu His Thr Leu Val
 85 90 95
 Leu Leu Asp Thr Glu Gly Leu Gly Asp Ile Glu Lys Gly Asp Asn Glu
 100 105 110
 45 Asn Asp Ser Trp Ile Phe Ala Leu Ala Ile Leu Leu Ser Ser Thr Phe
 115 120 125
 Val Tyr Asn Ser Met Gly Thr Ile Asn Gln Gln Ala Met Asp Gln Leu
 130 135 140
 50 His Tyr Val Thr Glu Leu Thr Asp Arg Ile Lys Ala Asn Xaa Ser Pro
 145 150 155 160
 Gly Asn Asn Ser Val Asp Asp Ser Xaa Asp Phe Val Ser Phe Phe Pro
 165 170 175
 Ala Phe Val Trp Thr Leu Lys Xaa Phe Thr Leu Glu Leu Gly Ser Arg
 180 185 190
 55 Trp Arg Thr His His Cys
 195
 60
 <210> 682
 <211> 147
 <212> PRT
 <213> Homo sapiens

<400> 682
 Ser Pro Gly Ala Lys Gly Arg Gly Tyr Lys Ala Lys Glu Val Xaa Lys
 1 5 10 15
 Lys Tyr Leu Glu Ser Lys Xaa Asp Val Ala Asp Ala Leu Leu Gln Thr
 20 25 30
 Asp Gln Ser Leu Ser Glu Lys Glu Lys Ala Ile Glu Val Glu Arg Ile
 35 40 45
 Lys Ala Glu Ser Ala Glu Ala Ala Lys Lys Met Leu Glu Glu Ile Xaa
 50 55 60
 Lys Lys Asn Glu Glu Met Met Glu Gln Lys Glu Lys Ser Tyr Gln Glu
 65 70 75 80
 His Val Lys Gln Leu Thr Glu Lys Met Glu Arg Asp Arg Ala Gln Leu
 85 90 95
 Met Ala Glu Gln Glu Lys Thr Leu Ala Leu Lys Leu Gln Glu Gln Glu
 100 105 110
 Arg Leu Leu Lys Glu Gly Phe Glu Asn Glu Ser Lys Arg Leu Gln Lys
 115 120 125
 Asp Ile Trp Asp Ile Gln Met Arg Ser Lys Ser Leu Glu Pro Ile Cys
 130 135 140
 Asn Ile Leu
 145

<210> 683
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 683
 Glu Arg Gly Ser Ser Leu Ala Leu Pro Leu Thr Gly Pro Cys Pro Ser
 1 5 10 15
 Pro Ser Ser Gln Ser Ile Val Ser His Val Pro Asp Asn Ser Ser Leu
 20 25 30
 Ser Val Pro Ser Ser Pro His Ser Ser Xaa Val Phe Pro Pro Thr Phe
 35 40 45
 Ser Leu Gln Leu Leu Gln Ile Gln Pro Leu Tyr Val Pro Leu Gln Ser
 50 55 60
 Leu Phe Pro Phe Leu Arg Val Thr Asp Gln Ser Val Glu Val His Gln
 65 70 75 80
 Pro His Pro Xaa Trp Thr Pro Asn Ile Phe Ser Xaa Pro Leu Trp Pro
 85 90 95
 Cys Ile Pro Phe Leu Trp His Leu Gly
 100 105

<210> 684
 <211> 274
 <212> PRT
 <213> Homo sapiens

<400> 684
 Ile Leu Leu Ser Ser Thr Phe Val Tyr Asn Ser Met Gly Thr Ile Asn
 1 5 10 15
 Gln Gln Ala Met Asp Gln Leu His Tyr Val Thr Glu Leu Thr Asp Arg
 20 25 30
 Ile Lys Ala Asn Ser Ser Pro Gly Asn Asn Ser Val Asp Asp Ser Ala
 35 40 45
 Asp Phe Val Ser Phe Phe Pro Ala Phe Val Trp Thr Leu Arg Asp Phe
 50 55 60
 Thr Leu Glu Leu Glu Val Asp Gly Glu Pro Ile Thr Ala Asp Asp Tyr
 65 70 75 80
 Leu Glu Leu Ser Leu Lys Leu Arg Lys Gly Thr Asp Lys Lys Ser Lys
 85 90 95
 Ser Phe Asn Asp Pro Arg Leu Cys Ile Arg Lys Phe Phe Pro Lys Arg
 100 105 110
 247

Lys Cys Phe Val Phe Asp Trp Pro Ala Pro Lys Lys Tyr Leu Ala His
 115 120 125
 Leu Glu Gln Leu Lys Glu Glu Glu Leu Asn Pro Asp Phe Ile Glu Gln
 130 135 140
 5 Val Ala Glu Phe Cys Ser Tyr Ile Leu Ser His Ser Asn Val Lys Thr
 145 150 155 160
 Leu Ser Gly Gly Ile Ala Val Asn Gly Pro Arg Leu Glu Ser Leu Val
 165 170 175
 Leu Thr Tyr Val Asn Ala Ile Gly Ser Gly Asp Leu Pro Cys Met Glu
 180 185 190
 10 Asn Ala Val Leu Ala Leu Ala Gln Ile Glu Glu Leu Ser Pro Gln Xaa
 195 200 205
 Lys Arg Leu Leu Xaa Thr Tyr Glu Gln Gln Asp Gly Ala Arg Arg Gly
 210 215 220
 15 Ser Cys Pro Pro Glu Thr Leu Pro Gly Ala Xaa Gly Thr Cys Xaa Xaa
 225 230 235 240
 Thr Val Arg Lys Xaa Ala Ile Glu Val Phe Ile Glu Xaa Thr Phe Phe
 245 250 255
 Lys Asp Val Gly Pro Asn Gly Ser Lys Xaa Lys Leu Gly Gly Pro Ile
 260 265 270
 20 Trp Glu

25 <210> 685
 <211> 120
 <212> PRT
 <213> Homo sapiens

<400> 685
 30 Cys Thr Xaa Thr Ala Asp Gln Xaa Leu Ser Glu Lys Glu Lys Ala Ile
 1 5 10 15
 Glu Val Glu Arg Ile Lys Val Xaa Ser Ala Glu Ala Ala Lys Lys Met
 20 25 30
 Leu Glu Glu Ile Gln Lys Lys Asn Glu Glu Met Met Asp Gln Lys Glu
 35 35 40 45
 Lys Xaa Tyr Gln Glu His Val Xaa Gln Leu Xaa Xaa Xaa Met Xaa Arg
 50 55 60
 Xaa Arg Ala Gln Leu Met Ala Glu Gln Xaa Lys Pro Leu Xaa Xaa Lys
 65 70 75 80
 40 Leu Gln Glu Gln Glu Xaa Leu Xaa Lys Glu Gly Xaa Glu Asn Glu Ser
 85 90 95
 Lys Arg Xaa Gln Lys Asp Ile Trp Asp Ile Gln Met Arg Ser Lys Ser
 100 105 110
 Leu Glu Pro Ile Cys Asn Ile Leu
 115 120
 45

50 <210> 686
 <211> 205
 <212> PRT
 <213> Homo sapiens

<400> 686
 Pro Met Ser Leu Ile Asp Asn Thr Lys Gly Gln Leu Val Val Asn Pro
 1 5 10 15
 55 Glu Ala Leu Lys Ile Leu Ser Ala Ile Thr Gln Pro Val Val Val
 20 25 30
 Ala Ile Val Gly Leu Tyr Arg Thr Gly Lys Ser Tyr Leu Met Asn Lys
 35 40 45
 Leu Ala Gly Lys Lys Asn Gly Phe Ser Leu Gly Ser Thr Val Lys Ser
 50 55 60
 His Thr Lys Gly Ile Trp Met Trp Cys Val Pro His Pro Lys Lys Pro
 65 70 75 80
 Glu His Thr Leu Val Leu Asp Thr Glu Gly Leu Gly Asp Ile Glu
 247

85 90 95
 Lys Gly Asp Asn Glu Asn Asp Ser Trp Ile Phe Ala Leu Ala Ile Leu
 100 105 110
 5 Leu Ser Ser Thr Phe Val Tyr Asn Ser Met Gly Thr Ile Asn Gln Gln
 115 120 125
 Ala Met Asp Gln Leu His Tyr Val Thr Glu Leu Thr Asp Arg Ile Lys
 130 135 140
 Ala Asn Ser Ser Pro Gly Asn Asn Ser Val Asp Asp Ser Ala Asp Phe
 145 150 155 160
 10 Val Ser Phe Phe Pro Ala Phe Val Trp Thr Leu Arg Asp Phe Thr Leu
 165 170 175
 Glu Leu Glu Val Asp Gly Glu Pro Ile Thr Ala Asp Asp Tyr Leu Glu
 180 185 190
 15 Leu Ser Leu Lys Leu Arg Lys Gly Thr Asp Lys Glu Lys
 195 200 205
 <210> 687
 <211> 111
 <212> PRT
 20 <213> Homo sapiens
 <400> 687
 Lys Arg Leu Ser Thr Gly Thr Ile Phe Leu Thr Gln Glu Val Pro Val
 1 5 10 15
 25 Xaa Xaa Ser Lys Cys Arg Ser Xaa Arg Ile Ser Xaa Pro Arg Val Pro
 20 25 30
 Lys Glu Gly Asp Thr Gly Asn Leu Pro Ala Lys Glu Val Xaa Lys Asn
 35 40 45
 30 Ile Trp Ser Pro Arg Xaa Met Gly Xaa Cys Thr Xaa Thr Asp Cys Gln
 50 55 60
 Ser Leu Phe Lys Lys Glu Lys Ala Ile Glu Val Asp Gly Ile Lys Ala
 65 70 75 80
 Glu Phe Ala Glu Ala Ala Lys Lys Met Leu Glu Glu Xaa Gln Lys Lys
 85 90 95
 35 Asn Glu Glu Met Met Ala Arg Lys Arg Arg Val Ile Arg Asn Met
 100 105 110
 <210> 688
 <211> 115
 40 <212> PRT
 <213> Homo sapiens
 <400> 688
 Lys Val Thr Asp Ser Leu Xaa Lys Cys Ile Xaa Pro Xaa Ser Leu Asp
 1 5 10 15
 Ser Lys Tyr Phe Phe Xaa Pro Leu Trp Pro Gly Gly Tyr Leu Tyr Pro
 20 25 30
 Leu Pro Trp Ala Pro Trp Xaa Asp Leu Phe Xaa Ser Ser Cys Thr Leu
 35 40 45
 50 Xaa Lys Xaa Pro Glu Pro Pro Gly Leu Lys Lys Trp Ser Leu Leu Thr
 50 55 60
 Ile Phe Phe Lys Arg Ala Gln Xaa Xaa Leu Glu Val Lys Xaa Cys His
 65 70 75 80
 Lys Ser Asp Asp Ala Phe Gly Ile Leu Leu Thr Lys Xaa Ile Xaa Pro
 85 90 95
 55 Leu Val Xaa Thr Gly Ala Leu Asn Ser Xaa Gly Gln Xaa Gly Pro His
 100 105 110
 Pro Trp Lys
 115
 60 <210> 689
 <211> 133
 <212> PRT

<213> Homo sapiens

<400> 689

5 Glu Arg Gly Ser Ser Leu Ala Leu Pro Leu Thr Gly Pro Cys Pro Ser
 1 5 10 15
 Pro Ser Ser Gln Ser Ile Val Ser His Val Pro Asp Asn Ser Ser Leu
 20 25 30
 Ser Gly His His Leu Leu Ile Leu Leu Xaa Phe Leu Gln His Phe
 35 40 45
 10 Leu Cys Ser Phe Cys Arg Phe Ser Leu Tyr Thr Val Pro Leu Gln Ser
 50 55 60
 Leu Phe Pro Phe Leu Arg Val Thr Asp Gln Val Cys Arg Ser Ala Ser
 65 70 75 80
 Thr Thr Ser Ser Leu Asp Ser Lys Tyr Phe Phe Ser Thr Ser Leu Ala
 15 85 90 95
 Xaa Ile Pro Xaa Leu Gly Pro Xaa Xaa Leu Ile Leu Gln Leu Leu Gln
 100 105 110
 Leu Leu Ser Lys Lys Thr Xaa Thr Xaa Trp Val Lys Lys Arg Xaa Leu
 115 120 125
 20 Leu Asp Ile Phe Phe
 130

<210> 690

<211> 112

25 <212> PRT

<213> Homo sapiens

<400> 690

30 Leu Ala Gly Gly Phe Pro Glu Glu Thr Ser Xaa Pro Gly Xaa Lys Lys
 1 5 10 15
 Leu Thr Pro Xaa Lys Val Xaa Pro Leu Xaa Xaa Gln Trp Pro Lys Gly
 20 25 30
 Xaa Cys Pro Gly Thr Pro Xaa Ser Cys Gly Xaa Pro Gln Xaa Ser Lys
 35 40 45
 35 Lys Gly Xaa Xaa Ser Phe His Xaa Asn Xaa Phe Lys Xaa Gly Pro Lys
 50 55 60
 Cys Ser Lys Xaa Ile Arg Ala Gln Trp Lys Gln Xaa Xaa Met Xaa Phe
 65 70 75 80
 Val Thr Glu Phe Gln Ser Phe Ile Arg Leu Trp Gln Ala Leu Leu Gln
 40 85 90 95
 Xaa Ile Phe Gly Pro Phe Arg Arg Arg Cys Gln Ala Xaa Thr Phe Phe
 100 105 110

<210> 691

45 <211> 93

<212> PRT

<213> Homo sapiens

<400> 691

50 Ser Leu Pro Gln Ser Asp Glu Ala Leu Glu Phe Cys Tyr Lys Xaa His
 1 5 10 15
 Xaa Xaa Leu Leu Pro Leu Gly Pro Asn Xaa Phe Gly Thr Phe Gly Pro
 20 25 30
 Xaa Leu Glu Xaa Ile Xaa Met Lys Thr Xaa Xaa Ala Phe Phe Thr Xaa
 35 40 45
 55 Leu Gly Xaa Ala Thr Thr Xaa Gly Gly Ser Arg Ala Xaa Ala Leu Trp
 50 55 60
 Pro Leu Xaa Xaa Lys Gly Xaa Asn Phe Xaa Gly Gly Glu Phe Phe Xaa
 65 70 75 80
 60 Ala Arg Xaa Thr Gly Phe Leu Arg Glu Thr Pro Cys Gln
 85 90

<210> 692

<211> 194
 <212> PRT
 <213> Homo sapiens

5 <400> 692
 Lys Lys Tyr Leu Ala His Leu Glu Gln Leu Lys Glu Glu Glu Leu Asn
 1 5 10 15
 Pro Asp Phe Ile Glu Gln Val Ala Glu Phe Cys Ser Tyr Ile Leu Ser
 20 25 30
 10 His Ser Asn Val Lys Thr Leu Ser Gly Leu Glu Ser Leu Val Leu Thr
 35 40 45
 Tyr Val Asn Ala Ile Ser Ser Gly Asp Leu Pro Cys Met Glu Asn Ala
 50 55 60
 15 Val Leu Ala Leu Ala Gln Ile Glu Asn Ser Ala Ala Val Glu Lys Ala
 65 70 75 80
 Ile Ala His Tyr Glu Gln Gln Met Gly Gln Lys Val Gln Leu Pro Thr
 85 90 95
 Glu Thr Leu Gln Glu Leu Leu Asp Leu His Arg Asp Ser Glu Arg Glu
 100 105 110
 20 Ala Ile Glu Val Phe Met Lys Asn Ser Phe Lys Asp Val Asp Gln Met
 115 120 125
 Phe Gln Arg Lys Leu Gly Ala Gln Leu Glu Ala Arg Arg Asp Asp Phe
 130 135 140
 25 Cys Lys Gln Asn Ser Lys Ala Ser Ser Asp Cys Cys Met Ala Leu Leu
 145 150 155 160
 Gln Asp Ile Phe Gly Pro Leu Glu Glu Asp Val Lys Gln Gly Thr Phe
 165 170 175
 Ser Lys Pro Gly Gly Tyr Arg Leu Phe Thr Gln Lys Leu Gln Gly Ala
 180 185 190
 30 Glu Glu

<210> 693
 <211> 130
 <212> PRT
 <213> Homo sapiens

35 <400> 693
 Pro Pro Gly Asn Xaa Pro Glu Val Val Ala Leu Xaa Arg Ala Ser Lys
 40 5 10 15
 Lys Gly Xaa Xaa Ser Xaa Asn Lys Asp Phe Phe Lys Xaa Gly Pro Lys
 20 25 30
 Cys Ser Arg Glu Ile Arg Gly Pro Val Glu Ala Xaa Arg Asn Xaa Phe
 35 40 45
 45 Cys Ser Gln Ile Pro Lys Leu Ile Arg Leu Trp Xaa Gly Phe Thr Ser
 50 55 60
 Arg Ile Tyr Trp Ala Xaa Xaa Lys Lys Met Ser Ser Arg Glu His Phe
 65 70 75 80
 50 Leu Asn Pro Glu Gly Ser Gly Phe Phe Thr Gln Lys Leu Gln Glu Leu
 85 90 95
 Lys Asn Lys Ser Thr Arg Ala Lys Lys Gly Ile Gln Ala Lys Glu Val
 100 105 110
 Leu Lys Lys Tyr Leu Glu Ser Lys Glu Asp Val Ala Asp Ala Leu Leu
 115 120 125
 55 Gln Thr
 130

60 <210> 694
 <211> 89
 <212> PRT
 <213> Homo sapiens

<400> 694

Val Lys Lys Pro Glu Pro Ser Gly Leu Arg Lys Cys Ser Leu Leu Asp
 1 5 10 15
 Ile Phe Xaa Xaa Xaa Ala Gln Tyr Ile Leu Glu Val Lys Xaa Cys His
 20 25 30
 5 Asn Leu Met Ser Phe Gly Ile Trp Leu Gln Lys Xaa Phe Xaa Leu Ala
 35 40 45
 Ser Thr Gly Pro Leu Ile Ser Leu Glu His Leu Gly Pro Xaa Leu Lys
 50 55 60
 Lys Ser Leu Leu Xaa Leu Xaa Xaa Pro Phe Leu Leu Ala Leu Xaa Arg
 10 65 70 75 80
 Ala Thr Thr Ser Gly Xaa Phe Pro Gly
 85

15 <210> 695
 <211> 203
 <212> PRT
 <213> Homo sapiens

<400> 695
 20 Pro Lys Lys Tyr Leu Ala His Leu Glu Gln Leu Lys Glu Glu Glu Leu
 1 5 10 15
 Asn Pro Asp Phe Ile Glu Gln Val Ala Glu Phe Cys Ser Tyr Ile Leu
 20 25 30
 25 Ser His Ser Asn Val Lys Thr Leu Ser Gly Gly Ile Pro Val Asn Gly
 35 40 45
 Pro Arg Leu Glu Ser Leu Val Leu Thr Tyr Val Asn Ala Ile Ser Ser
 50 55 60
 Gly Asp Leu Pro Cys Met Glu Asn Ala Val Leu Ala Leu Ala Gln Ile
 65 70 75 80
 30 Glu Asn Ser Ala Ala Val Glu Lys Ala Ile Ala His Tyr Glu Gln Gln
 85 90 95
 Met Gly Gln Lys Val Gln Leu Pro Thr Glu Thr Leu Gln Glu Leu Leu
 100 105 110
 Asp Leu His Arg Asp Ser Glu Arg Glu Ala Ile Glu Val Phe Met Lys
 115 120 125
 35 Asn Ser Phe Lys Asp Val Asp Gln Met Phe Gln Arg Lys Leu Gly Ala
 130 135 140
 Gln Leu Glu Ala Arg Arg Asp Asp Phe Cys Lys Gln Asn Ser Lys Ala
 145 150 155 160
 40 Ser Ser Asp Cys Cys Met Ala Leu Leu Gln Asp Ile Phe Gly Pro Leu
 165 170 175
 Glu Glu Asp Val Lys Gln Gly Thr Phe Ser Lys Pro Gly Gly Tyr Arg
 180 185 190
 Leu Phe Thr Gln Lys Leu Ala Gly Ala Glu Glu
 195 200
 45

<210> 696
 <211> 159
 <212> PRT
 50 <213> Homo sapiens

<400> 696
 Gly Thr Ile Asn Gln Gln Ala Met Asp Gln Leu His Tyr Val Thr Glu
 1 5 10 15
 55 Leu Thr Asp Arg Ile Lys Ala Asn Ser Ser Pro Gly Asn Asn Ser Val
 20 25 30
 Asp Asp Ser Ala Asp Phe Val Ser Phe Phe Pro Ala Phe Val Trp Thr
 35 40 45
 Leu Arg Asp Phe Thr Leu Glu Leu Glu Val Asp Gly Glu Pro Ile Thr
 50 55 60
 60 Ala Asp Asp Tyr Leu Glu Leu Ser Leu Lys Leu Arg Lys Gly Thr Asp
 65 70 75 80
 Xaa Lys Ser Lys Ser Phe Asn Asp Pro Arg Leu Cys Ile Arg Lys Phe

85 90 95
 Phe Pro Lys Arg Lys Cys Phe Val Phe Asp Trp Pro Ala Pro Lys Lys
 100 105 110
 5 Tyr Leu Ala His Leu Glu Gln Leu Lys Glu Glu Glu Leu Asn Pro Asp
 115 120 125
 Phe Ile Glu Gln Xaa Ala Glu Phe Cys Ser Tyr Ile Leu Xaa Xaa Ser
 130 135 140
 Asn Val Lys Thr Leu Ser Gly Xaa Ile Pro Ala Met Gly Leu Val
 145 150 155
 10
 <210> 697
 <211> 194
 <212> PRT
 <213> Homo sapiens
 15
 <400> 697
 Tyr Gly Gln Gly Ile Asn Pro Ile Ser Arg Leu Ala Gln Ile Gln Gln
 1 5 10 15
 20 Ala Lys Lys Glu Lys Glu Pro Glu Tyr Thr Leu Leu Thr Glu Arg Gly
 20 25 30
 Leu Pro Arg Arg Arg Glu Phe Val Met Gln Val Lys Val Gly Asn His
 35 40 45
 Thr Ala Glu Gly Thr Gly Thr Asn Lys Lys Val Ala Lys Arg Asn Ala
 50 55 60
 25 Ala Glu Asn Met Leu Glu Ile Leu Gly Phe Lys Val Pro Gln Ala Gln
 65 70 75 80
 Pro Thr Lys Pro Ala Leu Lys Ser Glu Glu Lys Thr Pro Ile Lys Lys
 85 90 95
 30 Pro Gly Asp Gly Arg Lys Val Thr Phe Phe Glu Pro Gly Ser Gly Asp
 100 105 110
 Glu Asn Gly Thr Ser Asn Lys Glu Asp Glu Phe Arg Met Pro Tyr Leu
 115 120 125
 Ser His Gln Gln Leu Pro Ala Gly Ile Leu Pro Met Val Pro Glu Val
 130 135 140
 35 Ala Gln Ala Val Gly Val Ser Gln Gly His His Thr Lys Asp Phe Thr
 145 150 155 160
 Arg Ala Ala Pro Asn Pro Ala Lys Ala Thr Val Thr Ala Met Ile Ala
 165 170 175
 40 Arg Glu Leu Leu Tyr Gly Gly Thr Ser Pro Thr Ala Glu Thr Ile Leu
 180 185 190
 Lys Glu
 45
 <210> 698
 <211> 92
 <212> PRT
 <213> Homo sapiens
 50
 <400> 698
 Gln Tyr Arg Ala Leu Trp Lys Ile Thr Leu Gln Val Tyr Met Asp Tyr
 1 5 10 15
 Met Glu Ile Ile Ser Cys Ser Val Val Lys Ala Lys Ser Ser Arg Ala
 20 25 30
 55 Ile Cys Ile Asp Thr Gln Cys Phe Leu Ile Ile Phe Lys Thr Glu Ile
 35 40 45
 Lys Val His Leu Ser Pro Val Cys Ile Asn Lys Asn Lys Asn Glu Ile
 50 55 60
 Lys Met Glu Pro Asn Asp His Leu Lys Phe Lys Ile Pro Lys Leu Ser
 65 70 75 80
 60 Asn Leu Tyr Asn Cys Gly Arg Leu Ile Gln Gly Phe
 85 90
 <210> 699

<211> 395
 <212> PRT
 <213> Homo sapiens

5 <400> 699
 His Lys Ser Asp Leu Pro Ala Phe Ser Ala Glu Val Glu Glu Glu Ser
 1 5 10 15
 Glu Ala Gly Lys Glu Ser Glu Glu Thr Glu Thr Lys Gln Thr Leu Lys
 20 25 30
 10 Glu Phe Arg Cys Gln Val Ser Asp Cys Ser Arg Ile Phe Gln Ala Ile
 35 40 45
 Thr Gly Leu Ile Gln His Tyr Met Lys Leu His Glu Met Thr Pro Glu
 50 55 60
 Glu Ile Glu Ser Met Thr Ala Ser Val Asp Val Gly Lys Phe Pro Cys
 15 65 70 75 80
 Asp Gln Leu Glu Cys Lys Ser Ser Phe Thr Thr Tyr Leu Asn Tyr Val
 85 90 95
 Val His Leu Glu Ala Asp His Gly Ile Gly Leu Arg Ala Ser Lys Thr
 100 105 110
 20 Glu Glu Asp Gly Val Tyr Lys Cys Asp Cys Glu Gly Cys Asp Arg Ile
 115 120 125
 Tyr Ala Thr Arg Ser Asn Leu Arg His Ile Phe Asn Lys His Asn
 130 135 140
 Asp Lys His Lys Ala His Leu Ile Arg Pro Arg Arg Leu Thr Pro Gly
 25 145 150 155 160
 Gln Glu Asn Met Ser Ser Lys Ala Asn Gln Glu Lys Ser Lys Ser Lys
 165 170 175
 His Arg Gly Thr Lys His Ser Arg Cys Gly Lys Glu Gly Ile Lys Met
 180 185 190
 30 Pro Lys Thr Lys Arg Lys Lys Lys Asn Asn Leu Glu Asn Lys Asn Ala
 195 200 205
 Lys Ile Val Gln Ile Glu Glu Asn Lys Pro Tyr Ser Leu Lys Arg Gly
 210 215 220
 Lys His Val Tyr Ser Ile Lys Ala Arg Asn Asp Ala Leu Ser Glu Cys
 35 225 230 235 240
 Thr Ser Arg Phe Val Thr Gln Tyr Pro Cys Met Ile Lys Gly Cys Thr
 245 250 255
 Ser Val Val Thr Ser Glu Ser Asn Ile Ile Arg His Tyr Lys Cys His
 260 265 270
 40 Lys Leu Ser Lys Ala Phe Thr Ser Gln His Arg Asn Leu Leu Ile Val
 275 280 285
 Phe Lys Arg Cys Cys Asn Ser Gln Val Lys Glu Thr Ser Glu Gln Glu
 290 295 300
 Gly Ala Lys Asn Asp Val Lys Asp Ser Asp Thr Cys Val Ser Glu Ser
 45 305 310 315 320
 Asn Asp Asn Ser Arg Thr Thr Ala Thr Val Ser Gln Lys Glu Val Glu
 325 330 335
 Lys Asn Glu Lys Asp Glu Met Asp Glu Leu Thr Glu Leu Phe Ile Thr
 340 345 350
 50 Lys Leu Ile Asn Glu Asp Ser Thr Ser Val Glu Thr Gln Ala Asn Thr
 355 360 365
 Ser Ser Asn Val Ser Asn Asp Phe Gln Gly Arg Tyr Leu Cys Gln Ser
 370 375 380
 Glu Arg Gln Lys Ala Ser Asn Leu Lys Lys Ser
 55 385 390 395

<210> 700
 <211> 209
 <212> PRT

60 <213> Homo sapiens

<400> 700

Lys Glu Gly Ile Lys Met Pro Lys Thr Lys Arg Lys Lys Lys Asn Asn

1 5 10 15
 Leu Glu Asn Lys Asn Ala Lys Ile Val Gln Ile Glu Glu Asn Lys Pro
 20 25 30
 Tyr Ser Leu Lys Arg Gly Lys His Val Tyr Ser Ile Lys Ala Arg Asn
 35 40 45
 Asp Ala Leu Ser Glu Cys Thr Ser Arg Phe Val Thr Gln Tyr Pro Cys
 50 55 60
 Met Ile Lys Gly Cys Thr Ser Val Val Thr Ser Glu Ser Asn Ile Ile
 65 70 75 80
 10 Arg His Tyr Lys Cys His Lys Leu Ser Lys Ala Phe Thr Ser Gln His
 85 90 95
 Arg Asn Leu Leu Ile Val Phe Lys Arg Cys Cys Asn Ser Gln Val Lys
 100 105 110
 Glu Thr Ser Glu Gln Glu Gly Ala Lys Asn Asp Val Lys Asp Ser Asp
 115 120 125
 15 Thr Cys Val Ser Glu Ser Asn Asp Asn Ser Arg Thr Thr Ala Thr Val
 130 135 140
 Ser Gln Lys Glu Val Glu Lys Asn Glu Lys Asp Glu Met Asp Glu Leu
 145 150 155 160
 20 Thr Glu Leu Phe Ile Thr Lys Leu Ile Asn Glu Asp Ser Thr Ser Val
 165 170 175
 Glu Thr Gln Ala Asn Thr Ser Ser Asn Val Ser Asn Asp Phe Gln Gly
 180 185 190
 25 Arg Tyr Leu Cys Gln Ser Glu Arg Gln Lys Ala Ser Asn Leu Lys Lys
 195 200 205
 Ser

30 <210> 701
 <211> 139
 <212> PRT
 <213> Homo sapiens

<400> 701
 35 Phe Phe Xaa Phe Val Pro Xaa Ser Xaa Asn Gln Tyr Phe Phe Phe Glu
 1 5 10 15
 Phe Glu Arg Xaa Pro Phe Phe Cys Phe Pro Val Phe Gly Arg Val Phe
 20 25 30
 40 Gly Arg Ile Phe Phe Trp Val Xaa Leu Gln Thr Xaa Gln Lys Phe Gln
 35 40 45
 Lys Arg Xaa Phe Asn Ser His Trp Leu Lys Arg Ala Pro Val Lys Glu
 50 55 60
 Ala Glu Cys Ser Ser Met Val Glu Cys Gln Gln Gln Phe Xaa Phe Leu
 65 70 75 80
 45 Xaa Gly Thr Leu Leu Asn Ser Ala Ala Asp Ala Gly Ser Ala Phe Ser
 85 90 95
 Thr Phe Leu Phe Leu Phe Cys Glu Thr Phe Phe Ser Xaa Ile Asn Ser
 100 105 110
 Ser Ser Asn Tyr Trp Leu Phe Val Phe Arg Thr Gly Arg Gly Ile Phe
 115 120 125
 50 Pro Glu Asn His Tyr Leu His Leu Lys Lys Tyr
 130 135

55 <210> 702
 <211> 135
 <212> PRT
 <213> Homo sapiens

<400> 702
 60 Phe Ser Xaa Leu Ser Gln Xaa Xaa Leu Thr Asn Ile Phe Phe Leu Asn
 1 5 10 15
 Leu Lys Gly Xaa Pro Phe Phe Val Ser Gln Tyr Ser Glu Gly Phe Leu
 20 25 30

Ala Gly Phe Phe Phe Gly Phe Xaa Cys Arg Leu Xaa Lys Asn Phe Lys
 35 40 45
 Lys Xaa Thr Ser Ile Pro Ile Gly Leu Lys Glu Leu Gln Ser Lys Lys
 50 55 60
 5 Gln Asn Ala Pro Gln Trp Leu Asn Ala Asn Ser Ser Xaa Phe Phe Xaa
 65 70 75 80
 Thr Ala Arg Tyr Leu Thr Gln Leu Leu Met Leu Val Gln Leu Phe Gln
 85 90 95
 10 Leu Ser Phe Phe Tyr Phe Val Arg His Phe Phe Xaa Leu Leu Thr Leu
 100 105 110
 Leu Gln Ile Thr Gly Phe Leu Ser Phe Gly Leu Ala Glu Val Ser Ser
 115 120 125
 Leu Lys Ile Ile Thr Tyr Ile
 130 135
 15
 <210> 703
 <211> 135
 <212> PRT
 <213> Homo sapiens
 20
 <400> 703
 Phe Pro Leu Val Thr Ala Val Leu Ser Ile Phe Phe Leu Glu Phe Glu
 1 5 10 15
 25 Trp Asp Pro Phe Leu Phe Pro Val Phe Gly Trp Xaa Leu Gln Tyr Phe
 20 25 30
 Ser Ser Ala Ser Leu Gln Thr Pro Gln Glu Thr Ser Glu Met Ile Phe
 35 40 45
 Lys Ser His Trp Leu Lys Lys Ser Xaa Ser Gln Lys Asp Ala Arg Xaa
 50 55 60
 30 Ser Ser Met Gly Xaa Met Ala Pro Ala Val Ser Xaa Ser Leu Pro Xaa
 65 70 75 80
 Xaa Leu Asn Ser Ala Xaa Gly Cys Trp Val Asn Leu Phe Gln Leu Phe
 85 90 95
 35 Leu Phe Leu Phe Xaa Glu Xaa Xaa Phe Ser Leu Leu Thr Leu Phe Lys
 100 105 110
 Tyr Leu Ala Phe Trp Leu Ser Asp Trp Ala Xaa Gly Phe Xaa Pro Glu
 115 120 125
 Asn His Ser Leu His Leu Lys
 130 135
 40
 <210> 704
 <211> 123
 <212> PRT
 <213> Homo sapiens
 45
 <400> 704
 Gly Val Cys Ser Glu Ala Glu Glu Lys Tyr Cys Lys Xaa His Pro Asn
 1 5 10 15
 50 Thr Gly Asn Lys Lys Gly Ser His Ser Asn Ser Arg Lys Asn Ile Asp
 20 25 30
 Lys Thr Ala Val Thr Ser Gly Asn His Val Cys Pro Cys Lys Glu Ser
 35 40 45
 Glu Thr Phe Val Gln Phe Ala Asn Pro Ser Gln Leu Gln Cys Ser Asp
 50 55 60
 55 Asn Val Lys Ile Val Leu Asp Lys Asn Leu Lys Asp Cys Thr Glu Leu
 65 70 75 80
 Val Leu Lys Gln Leu Gln Glu Met Lys Pro Thr Val Ser Leu Lys Lys
 85 90 95
 60 Leu Glu Val His Ser Asn Asp Pro Asp Met Ser Val Met Lys Asp Ile
 100 105 110
 Ser Ile Gly Lys Ala Thr Gly Arg Gly Gln Tyr
 115 120

<210> 705
 <211> 242
 <212> PRT
 <213> Homo sapiens

5

<400> 705
 His Glu Met Thr Pro Glu Glu Ile Glu Ser Met Thr Ala Ser Val Asp
 1 5 10 15
 Val Gly Lys Phe Pro Cys Asp Gln Leu Glu Cys Lys Ser Ser Phe Thr
 10 20 25 30
 Thr Tyr Leu Asn Tyr Val Val His Leu Glu Ala Asp His Gly Ile Gly
 35 40 45
 Leu Arg Ala Ser Lys Thr Glu Glu Asp Gly Val Tyr Lys Cys Asp Cys
 50 55 60
 Glu Gly Cys Asp Arg Ile Tyr Ala Thr Arg Ser Asn Leu Leu Arg His
 15 65 70 75 80
 Ile Phe Asn Lys His Asn Asp Lys His Lys Ala His Leu Ile Arg Pro
 85 90 95
 Arg Arg Leu Thr Pro Gly Gln Glu Asn Met Ser Ser Lys Ala Asn Gln
 100 105 110
 Glu Lys Ser Lys Ser Lys His Arg Gly Thr Lys His Ser Arg Cys Gly
 115 120 125
 Lys Glu Gly Ile Lys Met Pro Lys Thr Lys Arg Lys Lys Lys Asn Asn
 130 135 140
 Leu Glu Asn Lys Asn Ala Lys Ile Val Gln Ile Glu Glu Asn Lys Pro
 145 150 155 160
 Tyr Ser Leu Lys Arg Gly Lys His Val Tyr Ser Ile Lys Ala Xaa Asn
 165 170 175
 Asp Ala Leu Ser Glu Cys Thr Ser Arg Phe Val Thr Gln Tyr Pro Cys
 180 185 190
 Met Ile Lys Gly Cys Thr Ser Val Thr Ser Glu Ser Asn Ile Ile
 195 200 205
 Arg His Tyr Lys Xaa His Lys Leu Ser Lys Ala Leu His His Thr Pro
 210 215 220
 Glu Xaa Xaa Leu Leu Phe Ser Asn Xaa Val Cys Thr Pro Ser Lys Gly
 225 230 235 240
 Asn Val

40 <210> 706
 <211> 200
 <212> PRT
 <213> Homo sapiens

45 <400> 706
 His Lys Ser Asp Leu Pro Ala Phe Ser Ala Glu Val Glu Glu Glu Ser
 1 5 10 15
 Glu Ala Gly Xaa Glu Ser Xaa Glu Thr Glu Thr Lys Gln Thr Leu Lys
 20 25 30
 Glu Phe Arg Cys Xaa Xaa Ser Asp Cys Ser Arg Ile Phe Gln Ala Ile
 35 40 45
 Thr Gly Leu Ile Gln His Tyr Met Lys Leu His Glu Met Thr Pro Glu
 50 55 60
 Glu Ile Glu Ser Met Thr Ala Ser Val Asp Val Gly Lys Phe Pro Cys
 55 65 70 75 80
 Asp Xaa Leu Glu Cys Lys Ser Ser Phe Thr Thr Tyr Leu Asn Tyr Val
 85 90 95
 Val His Leu Glu Ala Asp His Gly Ile Gly Leu Arg Ala Ser Lys Thr
 100 105 110
 Glu Glu Asp Gly Val Tyr Lys Cys Asp Cys Glu Gly Cys Asp Arg Ile
 115 120 125
 Tyr Ala Thr Arg Thr Asn Leu Leu Arg Xaa Ile Phe Asn Lys His Asn
 130 135 140

Asp Lys His Lys Ala His Leu Ile Arg Pro Arg Arg Leu Thr Pro Gly
 145 150 155 160
 Gln Glu Asn Met Xaa Ser Lys Ala Asn Gln Glu Lys Ser Lys Ser Lys
 165 170 175
 5 His Arg Gly Thr Lys His Xaa Lys Cys Gly Lys Glu Gly Ile Lys Met
 180 185 190
 Pro Arg Pro Thr Lys Glu Xaa Lys
 195 200

10 <210> 707
 <211> 103
 <212> PRT
 <213> Homo sapiens

15 <400> 707
 Xaa Ser Tyr Arg Asn Xaa Gly Leu Gln Ile Leu Leu Gly His Ser Asp
 1 5 10 15
 Arg Ala Ser Phe Xaa Ser Leu Asn Arg Ile Xaa Met Leu Pro Thr Phe
 20 25 30
 20 Gln Lys Ile Arg Leu Ile Xaa Phe Gln Phe Ala Gln Ser Leu His Ser
 35 40 45
 Cys Phe Leu Asn Tyr Xaa Phe Ser Phe Val Gly Arg Gly Ile Phe Ile
 50 55 60
 Pro Ser Phe Pro His Xaa Leu Cys Leu Val Pro Arg Cys Leu Asp Phe
 25 65 70 75 80
 Asp Phe Ser Trp Phe Ala Leu Leu Xaa Ile Phe Ser Trp Pro Gly Val
 85 90 95
 Asn Leu Leu Gly Arg Ile Lys
 100

30 <210> 708
 <211> 135
 <212> PRT
 <213> Homo sapiens

35 <400> 708
 Met Gly Ser Phe Phe Val Ser Ser Ile Arg Met Val Phe Ala Val Phe
 1 5 10 15
 Phe Phe Cys Phe Thr Xaa Asp Xaa Ser Arg Asn Phe Arg Asn Asp Leu
 40 20 25 30
 Gln Ile Pro Leu Gly Leu Lys Xaa Leu Gln Ser Lys Arg Cys Xaa Asp
 35 40 45
 Ala Pro His Xaa Leu Asn Gly Asn Ser Lys Phe Xaa Xaa Leu Tyr Xaa
 50 55 60
 45 Arg Tyr Leu Thr Xaa Leu Xaa Met Leu Xaa Gln Leu Phe Gln Leu Ser
 65 70 75 80
 Phe Phe Ile Xaa Xaa Asp Xaa Phe Xaa Phe Tyr Leu Ser Ser Asn Thr
 85 90 95
 Cys Phe Trp Leu Ser Asp Gly Arg Gly Phe Phe Arg Lys His Phe Phe
 50 100 105 110
 Xaa Leu Xaa Lys Phe Asn Leu Gly Xaa Ser Xaa Gly Leu Ser Xaa Leu
 115 120 125
 Leu Ile Trp Lys Lys Gln Ser
 130 135

55 <210> 709
 <211> 67
 <212> PRT
 <213> Homo sapiens

60 <400> 709
 Ser Ser Lys Pro Ile Gly Leu Lys Glu Leu Gln Ser Lys Asp Ala Xaa
 1 5 10 15

Cys Ser Ser Met Gly Glu Trp His Ser Ser Phe Phe Phe Phe Thr Xaa
 20 25 30
 Arg Tyr Leu Thr Xaa Leu Leu Met Ala Gly Ser Thr Phe Ser Thr Phe
 35 40 45
 5 Leu Phe Tyr Leu Gly Arg His Phe Phe Leu Ile Thr Leu Ser Lys Thr
 50 55 60
 Ala Phe Gly
 65

 10 <210> 710
 <211> 131
 <212> PRT
 <213> Homo sapiens

 15 <400> 710
 Arg Ser Phe Leu Lys Phe Leu Glu Xaa Ser Ala Val Lys Gln Lys Lys
 1 5 10 15
 Asn Xaa Xaa Lys Xaa His Pro Asn Thr Gly Asn Lys Lys Gly Ser His
 20 25 30
 20 Ser Asn Ser Arg Lys Asn Ile Asp Lys Thr Ala Val Thr Ser Gly Asn
 35 40 45
 His Val Cys Pro Cys Lys Glu Ser Glu Thr Phe Val Gln Phe Ala Asn
 50 55 60
 Pro Ser Gln Leu Gln Cys Ser Asp Asn Val Lys Ile Val Leu Xaa Lys
 25 65 70 75 80
 Asn Leu Lys Asp Cys Xaa Glu Leu Val Leu Lys Gln Leu Gln Glu Met
 85 90 95
 Lys Pro Xaa Val Ser Leu Lys Lys Leu Glu Val His Ser Asn Asp Pro
 100 105 110
 30 Asp Met Ser Val Met Lys Asp Ile Ser Ile Gly Lys Ala Thr Gly Arg
 115 120 125
 Gly Gln Tyr
 130

 35 <210> 711
 <211> 528
 <212> PRT
 <213> Homo sapiens

 40 <400> 711
 Lys Asn Arg Ser Ile Gly Ala Ala Ala Lys Ser Gln Val Ile Ser Asn
 1 5 10 15
 Ala Lys Asn Thr Val Gln Gly Phe Lys Arg Phe His Gly Arg Ala Phe
 20 25 30
 45 Ser Asp Pro Phe Val Glu Ala Glu Lys Ser Asn Leu Ala Tyr Asp Ile
 35 40 45
 Val Gln Leu Pro Thr Gly Leu Thr Gly Ile Lys Val Thr Tyr Met Glu
 50 55 60
 Glu Glu Arg Asn Phe Thr Thr Glu Gln Val Thr Ala Met Leu Leu Ser
 50 65 70 75 80
 Lys Leu Lys Glu Thr Ala Glu Ser Val Leu Lys Lys Pro Val Val Asp
 85 90 95
 Cys Val Val Ser Val Pro Cys Phe Tyr Thr Asp Ala Glu Arg Arg Ser
 100 105 110
 55 Val Met Asp Ala Thr Gln Ile Ala Gly Leu Asn Cys Leu Arg Leu Met
 115 120 125
 Asn Glu Thr Thr Ala Val Ala Leu Ala Tyr Gly Ile Tyr Lys Gln Asp
 130 135 140
 Leu Pro Ala Leu Glu Glu Lys Pro Arg Asn Val Val Phe Val Asp Met
 60 145 150 155 160
 Gly His Ser Ala Tyr Gln Val Ser Val Cys Ala Phe Asn Arg Gly Lys
 165 170 175
 Leu Lys Val Leu Ala Thr Ala Phe Asp Thr Thr Leu Gly Gly Arg Lys

180 185 190
 Phe Asp Glu Val Leu Val Asn His Phe Cys Glu Glu Phe Gly Lys Lys
 195 200 205
 5 Tyr Lys Leu Asp Ile Lys Ser Lys Ile Arg Ala Leu Leu Arg Leu Ser
 210 215 220
 Gln Glu Cys Glu Lys Leu Lys Lys Leu Met Ser Ala Asn Ala Ser Asp
 225 230 235 240
 Leu Pro Leu Ser Ile Glu Cys Phe Met Asn Asp Val Asp Val Ser Gly
 245 250 255
 10 Thr Met Asn Arg Gly Lys Phe Leu Glu Met Cys Asn Asp Leu Leu Ala
 260 265 270
 Arg Val Glu Pro Pro Leu Arg Ser Val Leu Glu Gln Thr Lys Leu Lys
 275 280 285
 15 Lys Glu Asp Ile Tyr Ala Val Glu Ile Val Gly Gly Ala Thr Arg Ile
 290 295 300
 Pro Ala Val Lys Glu Lys Ile Ser Lys Phe Phe Gly Lys Glu Leu Ser
 305 310 315 320
 Thr Thr Leu Asn Ala Asp Glu Ala Val Thr Arg Gly Cys Ala Leu Gln
 325 330 335
 20 Cys Ala Ile Leu Ser Pro Ala Phe Lys Val Arg Glu Phe Ser Ile Thr
 340 345 350
 Asp Val Val Pro Tyr Pro Ile Ser Leu Arg Trp Asn Ser Pro Xaa Glu
 355 360 365
 25 Glu Gly Ser Ser Asp Cys Glu Val Phe Ser Lys Asn His Ala Ala Pro
 370 375 380
 Phe Ser Lys Val Leu Thr Phe Tyr Arg Lys Glu Pro Phe Thr Leu Glu
 385 390 395 400
 Ala Tyr Tyr Ser Ser Pro Gln Asp Leu Pro Tyr Pro Asp Pro Ala Ile
 405 410 415
 30 Ala Gln Phe Ser Val Gln Lys Val Thr Pro Gln Ser Asp Gly Ser Ser
 420 425 430
 Ser Lys Val Lys Val Lys Val Arg Val Asn Val His Gly Ile Phe Ser
 435 440 445
 35 Val Ser Ser Ala Ser Leu Val Glu Val His Lys Ser Glu Glu Asn Glu
 450 455 460
 Glu Pro Met Glu Thr Asp Gln Asn Ala Lys Glu Glu Glu Lys Met Gln
 465 470 475 480
 Val Asp Gln Glu Glu Pro His Val Glu Glu Gln Gln Gln Thr Pro
 485 490 495
 40 Ala Glu Asn Lys Ala Glu Ser Glu Glu Met Glu Thr Ser Gln Ala Gly
 500 505 510
 Ser Lys Asp Lys Lys Met Asp Gln Pro Pro Lys Pro Arg Arg Gln Lys
 515 520 525
 45 <210> 712
 <211> 156
 <212> PRT
 <213> Homo sapiens
 50 <400> 712
 Asp Cys Glu Val Phe Ser Lys Asn His Ala Ala Pro Phe Ser Lys Val
 1 5 10 15
 Leu Thr Phe Tyr Arg Lys Glu Pro Phe Thr Leu Glu Ala Tyr Tyr Ser
 20 25 30
 55 Ser Pro Gln Asp Leu Pro Tyr Pro Asp Pro Ala Ile Ala Gln Phe Ser
 35 40 45
 Val Gln Lys Val Thr Pro Gln Ser Asp Gly Ser Ser Ser Lys Val Lys
 50 55 60
 Val Lys Val Arg Val Asn Val His Gly Ile Phe Ser Val Ser Ser Ala
 65 70 75 80
 Ser Leu Val Glu Val His Lys Ser Glu Glu Asn Glu Glu Pro Met Glu
 85 90 95
 60 Thr Asp Gln Asn Ala Lys Glu Glu Glu Lys Met Gln Val Asp Gln Glu
 260

100 105 110
 Glu Pr His Val Glu Glu Gln Gln Gln Gln Thr Pro Ala Glu Asn Lys
 115 120 125
 Ala Glu Ser Glu Glu Met Glu Thr Ser Gln Ala Gly Ser Lys Asp Lys
 130 135 140
 Lys Met Asp Gln Pro Pro Lys Pro Arg Arg Gln Lys
 145 150 155

 <210> 713
 <211> 166
 <212> PRT
 <213> Homo sapiens

 <400> 713
 15 Val Asn Leu Leu Arg Tyr Val Ser Arg Asn Leu Lys Asn Asp Gln Lys
 1 5 10 15
 Leu Phe Glu Glu Leu Gly Lys Gln Ile His Gln Tyr Met Lys Ile Ile
 20 25 30
 Ser Ser Phe Lys Asn Lys Glu Asp Gln Tyr Asp His Leu Asp Ala Ala
 35 40 45
 Asp Met Thr Lys Val Glu Lys Ser Thr Asn Glu Ala Met Glu Trp Met
 50 55 60
 Asn Asn Lys Leu Asn Leu Gln Asn Lys Gln Ser Leu Thr Met Asp Pro
 65 70 75 80
 25 Val Val Lys Ser Lys Glu Ile Glu Ala Lys Ile Lys Glu Leu Thr Ser
 85 90 95
 Thr Cys Ser Pro Ile Ile Ser Lys Pro Lys Pro Lys Val Glu Pro Pro
 100 105 110
 Lys Glu Gly Xaa Lys Met Xaa Xaa Arg Xaa Ala Xaa Trp Met Asp Lys
 115 120 125
 30 Glu Thr Thr Gln Ala Pro Arg Xaa Xaa Ser Arg Val Gln Thr Gln Leu
 130 135 140
 Cys Leu Arg Ile Gln Thr Arg Ser Phe Leu Lys Trp Thr Leu Ile Asp
 145 150 155 160
 35 Ser Asn Thr Cys Phe Tyr
 165

 <210> 714
 <211> 219
 <212> PRT
 <213> Homo sapiens

 <400> 714
 45 Val Val Ser Val Pro Cys Phe Tyr Thr Asp Ala Glu Arg Arg Ser Val
 1 5 10 15
 Met Asp Ala Thr Gln Ile Ala Gly Leu Asn Cys Leu Arg Leu Met Asn
 20 25 30
 Glu Thr Thr Ala Val Ala Leu Ala Tyr Gly Ile Tyr Lys Gln Asp Leu
 35 40 45
 50 Pro Ala Leu Glu Glu Lys Pro Arg Asn Val Val Phe Val Asp Met Gly
 50 55 60
 His Ser Ala Tyr Gln Val Ser Val Cys Ala Phe Asn Arg Gly Lys Leu
 65 70 75 80
 Lys Val Leu Ala Thr Ala Phe Asp Thr Thr Leu Gly Gly Arg Lys Phe
 85 90 95
 55 Asp Glu Val Leu Val Asn His Phe Cys Glu Glu Phe Gly Lys Lys Tyr
 100 105 110
 Lys Leu Asp Ile Lys Ser Lys Ile Arg Ala Leu Leu Arg Leu Ser Gln
 115 120 125
 60 Glu Cys Glu Lys Leu Lys Lys Leu Met Ser Ala Asn Ala Ser Asp Leu
 130 135 140
 Pro Leu Ser Ile Glu Cys Phe Met Asn Asp Val Asp Val Ser Gly Thr
 145 150 155 160

Met Asn Arg Gly Lys Phe Leu Glu Met Cys Asn Asp Leu Leu Ala Arg
 165 170 175
 Val Glu Pro Pro Leu Arg Ser Val Leu Glu Gln Thr Lys Leu Lys Lys
 180 185 190
 5 Glu Asp Ile Tyr Ala Val Glu Ile Val Gly Gly Ala Thr Arg Ile Pro
 195 200 205
 Ala Val Lys Glu Lys Ile Ser Gln Ile Phe Arg
 210 215

10 <210> 715
 <211> 184
 <212> PRT
 <213> Homo sapiens

15 <400> 715
 Lys Asn Arg Ser Ile Gly Ala Ala Ala Lys Ser Gln Val Ile Ser Asn
 1 5 10 15
 Ala Lys Asn Thr Val Gln Gly Phe Lys Arg Phe His Gly Arg Ala Phe
 20 25 30
 20 Ser Asp Pro Phe Val Glu Ala Glu Lys Ser Asn Leu Ala Tyr Asp Ile
 35 40 45
 Val Gln Leu Pro Thr Gly Leu Thr Gly Ile Lys Val Thr Tyr Met Glu
 50 55 60
 Glu Glu Arg Asn Phe Thr Thr Glu Gln Val Thr Ala Met Leu Leu Ser
 25 65 70 75 80
 Lys Leu Lys Glu Thr Ala Glu Ser Val Leu Lys Lys Pro Val Val Asp
 85 90 95
 Cys Val Val Ser Val Pro Cys Phe Tyr Thr Asp Ala Glu Arg Arg Ser
 100 105 110
 30 Val Met Asp Ala Thr Gln Ile Ala Gly Leu Asn Cys Leu Arg Leu Met
 115 120 125
 Asn Glu Thr Thr Ala Val Ala Leu Ala Tyr Gly Ile Tyr Lys Gln Asp
 130 135 140
 Leu Pro Ala Leu Glu Glu Lys Pro Arg Asn Val Val Phe Val Asp Met
 35 145 150 155 160
 Gly His Ser Ala Tyr Gln Val Ser Val Cys Ala Phe Asn Arg Gly Lys
 165 170 175
 Leu Lys Val Ser Gly His Cys Ile
 180

40 <210> 716
 <211> 247
 <212> PRT
 <213> Homo sapiens

45 <400> 716
 Phe His Gly Arg Ala Phe Ser Asp Pro Phe Val Glu Ala Glu Lys Ser
 1 5 10 15
 Asn Leu Ala Tyr Asp Ile Val Gln Leu Pro Thr Gly Leu Thr Gly Ile
 20 25 30
 50 Lys Val Thr Tyr Met Glu Glu Glu Arg Asn Phe Thr Thr Glu Gln Val
 35 40 45
 Thr Ala Met Leu Leu Ser Lys Leu Lys Glu Thr Ala Glu Ser Val Leu
 50 55 60
 55 Lys Lys Pro Val Val Asp Cys Val Val Ser Val Pro Cys Phe Tyr Thr
 65 70 75 80
 Asp Ala Glu Arg Arg Ser Val Met Asp Ala Thr Gln Ile Ala Gly Phe
 85 90 95
 Asn Cys Leu Arg Leu Met Asn Glu Thr Thr Ala Val Ala Leu Ala Tyr
 100 105 110
 60 Gly Ile Tyr Lys Gln Asp Leu Pro Ala Leu Glu Glu Lys Pro Arg Asn
 115 120 125
 Val Val Phe Val Asp Met Gly His Ser Ala Tyr Gln Val Ser Val Cys
 130

130 135 140
 Ala Phe Asn Arg Gly Lys Leu Lys Val Leu Ala Thr Ala Phe Asp Thr
 145 150 155 160
 5 Thr Leu Gly Gly Arg Lys Phe Asp Glu Val Leu Val Asn His Phe Cys
 165 170 175
 Glu Glu Phe Gly Lys Lys Tyr Lys Leu Asp Ile Lys Ser Lys Ile Arg
 180 185 190
 Ala Leu Leu Arg Leu Ser Gln Glu Cys Glu Lys Leu Lys Lys Ile Asp
 195 200 205
 10 Glu Val Gln Met Leu Gln Ile Ser Leu Leu Ser Ile Glu Trp Phe Met
 210 215 220
 Asn Asp Val Asp Val Ser Trp Asn Tyr Glu Ile Xaa Xaa Asn Phe Xaa
 225 230 235 240
 15 Glu Lys Val Pro Met Ile Ser
 245
 <210> 717
 <211> 176
 <212> PRT
 20 <213> Homo sapiens
 <400> 717
 Leu Arg Leu Ser Gln Glu Cys Glu Lys Leu Lys Lys Leu Met Ser Ala
 1 5 10 15
 25 Asn Ala Ser Asp Leu Pro Leu Ser Ile Glu Cys Phe Met Asn Asp Val
 20 25 30
 Asp Val Ser Gly Thr Met Asn Arg Gly Lys Phe Leu Glu Met Cys Asn
 35 40 45
 Asp Leu Leu Ala Arg Val Glu Pro Pro Leu Arg Ser Val Leu Glu Gln
 50 55 60
 30 Thr Lys Leu Lys Lys Glu Asp Ile Tyr Ala Val Glu Ile Val Gly Gly
 65 70 75 80
 Ala Thr Arg Ile Pro Ala Val Lys Glu Lys Ile Ser Lys Phe Phe Gly
 85 90 95
 35 Lys Glu Leu Ser Thr Thr Leu Asn Ala Asp Glu Ala Val Thr Arg Gly
 100 105 110
 Cys Ala Leu Gln Cys Ala Ile Leu Ser Pro Ala Phe Lys Val Arg Glu
 115 120 125
 Phe Ser Ile Thr Asp Val Val Pro Tyr Pro Ile Ser Leu Arg Trp Asn
 130 135 140
 40 Ser Pro Xaa Glu Glu Gly Ser Ser Asp Cys Glu Val Phe Phe Lys Asn
 145 150 155 160
 His Ala Ala Pro Phe Ser Lys Val Leu Thr Phe Tyr Arg Lys Glu Pro
 165 170 175
 45 <210> 718
 <211> 178
 <212> PRT
 50 <213> Homo sapiens
 <400> 718
 Glu Asp Ala Phe Lys Ile Trp Val Ile Phe Asn Phe Leu Ser Glu Asp
 1 5 10 15
 55 Lys Tyr Pro Leu Ile Ile Val Ser Glu Glu Ile Glu Tyr Leu Leu Lys
 20 25 30
 Lys Leu Thr Glu Ala Met Gly Gly Gly Trp Gln Gln Glu Gln Phe Glu
 35 40 45
 His Tyr Lys Ile Asn Phe Asp Asp Ser Lys Asn Gly Leu Ser Ala Trp
 50 55 60
 60 Glu Leu Ile Glu Leu Ile Gly Asn Gly Gln Phe Ser Lys Gly Met Asp
 65 70 75 80
 Arg Gln Thr Val Ser Met Ala Ile Asn Glu Val Phe Asn Glu Leu Ile
 85 90 95

Leu Asp Val Leu Lys Gln Gly Tyr Met Met Lys Lys Gly His Arg Arg
 100 105 110
 Lys Asn Trp Thr Glu Arg Trp Phe Val Leu Lys Pro Asn Ile Ile Ser
 115 120 125
 5 Tyr Tyr Val Ser Glu Asp Leu Lys Asp Lys Lys Gly Asp Ile Leu Leu
 130 135 140
 Asp Glu Asn Cys Cys Val Glu Ser Leu Pro Asp Lys Asp Gly Lys Lys
 145 150 155 160
 10 Cys Leu Phe Leu Val Lys Cys Phe Asp Lys Thr Phe Glu Ile Ser Ala
 165 170 175
 Phe Arg

15 <210> 719
 <211> 107
 <212> PRT
 <213> Homo sapiens

20 <400> 719
 Phe Val Leu Arg Trp Ser Leu Thr Leu Leu Pro Lys Leu Glu Tyr Asn
 1 5 10 15
 Gly Ile Ile Ser Ala Arg Cys Asn Leu Arg Leu Pro Arg Ser Ser Asp
 20 25 30
 25 Ser Pro Ala Ser Ala Ser Gln Val Ala Gly Ile Thr Gly Ala Arg His
 35 40 45
 Gln Ala Gln Leu Ile Phe Phe Val Phe Leu Val Glu Thr Gly Phe His
 50 55 60
 Gln Val Gly Gln Ala Gly Leu Glu Leu Leu Thr Ser Gly Asp Pro Pro
 65 70 75 80
 30 Ala Ser Ala Ser Gln Ser Ala Gly Ile Thr Gly Val Ser His His Ala
 85 90 95
 Arg Pro Pro Lys Leu Phe Leu Leu Ser Leu Xaa
 100 105

35 <210> 720
 <211> 45
 <212> PRT
 <213> Homo sapiens

40 <400> 720
 Leu Tyr His Asn Ile His Asn Gly Glu Leu Tyr Asp Met Val Ala Glu
 1 5 10 15
 Ile Gly Pro Phe Met Cys Cys Phe Tyr Phe Thr Ser Asn Cys Arg Tyr
 20 25 30
 45 Arg Val Ile Asn Lys Ile His Pro Cys Leu Ser His Pro
 35 40 45

50 <210> 721
 <211> 201
 <212> PRT
 <213> Homo sapiens

55 <400> 721
 Glu Glu Glu Glu Glu Ile Glu Pro Phe Pro Glu Glu Arg Glu Asn Phe
 1 5 10 15
 Leu Gln Gln Leu Tyr Lys Phe Met Glu Asp Arg Gly Thr Pro Ile Asn
 20 25 30
 Lys Arg Pro Val Leu Gly Tyr Arg Asn Leu Asn Leu Phe Lys Leu Phe
 35 40 45
 60 Arg Leu Val His Lys Leu Gly Gly Phe Asp Asn Ile Glu Ser Gly Ala
 50 55 60
 Val Trp Lys Gln Val Tyr Gln Asp Leu Gly Ile Pro Val Leu Asn Ser
 65 70 75 80

264

20 <210> 722
 <211> 205
 <212> PRT
 <213> Homo sapiens

<210> 723
<211> 228
<212> PRT
<213> Homo sapiens

60 <400> 723
 Ile Asn Lys Arg Pro Val Leu Gly Tyr Arg Asn Leu Asn Leu Phe Lys
 1 5 10 15
 Leu Phe Arg Leu Val His Lys Leu Gly Phe Asp Asn Ile Glu Ser
 20 25 30
 Gly Ala Val Trp Lys Gln Val Tyr Gln Asp Leu Gly Ile Pro Val Leu
 35 40 45
 Asn Ser Ala Ala Gly Tyr Asn Val Lys Cys Ala Tyr Lys Lys Tyr Leu

50 55 60
 Tyr Gly Phe Glu Glu Tyr Cys Arg Ser Ala Asn Ile Glu Phe Gln Met
 65 70 75 80
 5 Ala Leu Pro Glu Lys Val Val Asn Lys Gln Cys Lys Glu Cys Glu Asn
 85 90 95
 Val Lys Glu Ile Lys Val Lys Glu Glu Asn Glu Thr Glu Ile Lys Glu
 100 105 110
 Ile Lys Met Glu Glu Glu Arg Asn Ile Ile Pro Arg Glu Glu Lys Pro
 115 120 125
 10 Ile Glu Asp Glu Ile Glu Arg Lys Glu Asn Ile Lys Pro Ser Leu Gly
 130 135 140
 Ser Lys Lys Asn Leu Leu Glu Ser Ile Pro Thr His Ser Asp Gln Glu
 145 150 155 160
 15 Lys Glu Val Asn Ile Lys Lys Pro Glu Asp Asn Glu Asn Leu Asp Asp
 165 170 175
 Lys Asp Asp Asp Thr Thr Arg Val Asp Glu Ser Leu Asn Ile Lys Val
 180 185 190
 Glu Ala Glu Glu Glu Lys Ala Lys Ser Gly Asp Glu Thr Asn Lys Glu
 195 200 205
 20 Glu Asp Glu Asp Asp Glu Glu Ala Glu Glu Glu Glu Glu Glu Glu
 210 215 220
 Xaa Arg Arg Gly
 225
 25 <210> 724
 <211> 109
 <212> PRT
 <213> Homo sapiens
 30 <400> 724
 Thr Ser Phe Xaa His Phe Leu Asn Phe Ser Leu Gly Pro Xaa Arg Xaa
 1 5 10 15
 Leu Asp Phe Xaa Xaa Leu Val Asp Ser Thr Gln Thr Xaa Leu Pro Pro
 20 25 30
 35 Leu Val Gly His His His Leu His Pro Leu Leu Xaa Ser Ser Ser Ser
 35 40 45
 Ser Ser Ser Ser Ala Ser Ser Ser Ser Ser Ser Ser Leu Phe Val
 50 55 60
 Ser Ser Pro Asp Phe Ala Phe Ser Ser Ser Ala Ser Thr Phe Met Leu
 40 65 70 75 80
 Arg Asp Ser Ser Thr Leu Val Val Ser Ser Ser Leu Ser Ser Arg Phe
 85 90 95
 Ser Leu Ser Ser Gly Phe Leu Met Leu Thr Ser Phe Ser
 100 105
 45 <210> 725
 <211> 121
 <212> PRT
 <213> Homo sapiens
 50 <400> 725
 Asp Ile Xaa Ile Phe Asn Thr Ser Phe Ile His Phe Leu Ile Phe Pro
 1 5 10 15
 Ser Ser Ile Pro His Leu Asp Phe His Ala Trp Gly Ile Ala Leu Lys
 20 25 30
 55 Leu Leu Phe Leu Xaa Xaa Gly Ile Ile Ile Phe Ile Xaa Phe Phe Phe
 35 40 45
 Phe Leu Leu Leu Leu Xaa Phe Cys Phe Phe Ile Ile Phe Ile Phe Phe
 50 55 60
 60 Phe Ile Arg Xaa Ile Ser Xaa Phe Cys Phe Phe Phe Leu Ser Phe Tyr
 65 70 75 80
 Leu Tyr Xaa Glu Gly Phe Ile Tyr Pro Ser Xaa Val Ile Ile Phe Gly
 85 90 95
 466

Ala Gln Ile Phe Ile Gly Phe Trp Phe Xaa Asn Xaa Asn Phe Phe Phe
 100 105 110
 Leu Xaa Xaa Met Gly Arg Xaa Xaa Phe
 115 120

5
 <210> 726
 <211> 164
 <212> PRT
 <213> Homo sapiens

10
 <400> 726
 Xaa Gly Xaa Lys Glu Ile Lys Xaa Glu Glu Xaa Gly Xaa Ile Xaa Xaa
 1 5 10 15
 Arg Glu Glu Lys Pro Ile Glu Asp Glu Ile Glu Arg Lys Glu Asn Ile
 20 25 30
 Lys Pro Xaa Xaa Gly Ser Lys Lys Asn Leu Leu Glu Xaa Xaa Pro Thr
 35 40 45
 His Xaa Xaa Gln Glu Lys Glu Val Xaa Ile Xaa Lys Pro Glu Ala Asn
 50 55 60
 Glu Asn Leu Gly Ala Lys Asp Asp Asp Xaa Thr Arg Val Asp Glu Ser
 65 70 75 80
 Leu Xaa Ile Lys Val Glu Ala Glu Glu Glu Lys Ala Lys Xaa Gly Asp
 85 90 95
 Xaa Thr Asn Lys Glu Glu Asp Glu Asp Glu Glu Ala Glu Xaa Glu
 100 105 110
 Glu Glu Glu Glu Glu Glu Glu Xaa Asp Glu Asp Asp Asp Ala Xaa Xaa
 115 120 125
 Glu Glu Glu Glu Phe Glu Cys Tyr Pro Pro Gly Met Lys Val Gln Val
 130 135 140
 Arg Tyr Gly Arg Gly Lys Asn Gln Lys Met Tyr Glu Ala Ser Ile Lys
 145 150 155 160
 Asp Xaa Asp Val

35
 <210> 727
 <211> 207
 <212> PRT
 <213> Homo sapiens

40
 <400> 727
 Trp Phe Pro Ala Leu Val Val Cys Pro Asp Cys Ser Asp Glu Ile Ala
 1 5 10 15
 Val Lys Lys Asp Asn Ile Leu Val Arg Ser Phe Lys Asp Gly Lys Phe
 20 25 30
 Thr Ser Val Pro Arg Lys Asp Val His Glu Ile Thr Ser Asp Thr Ala
 35 40 45
 Pro Lys Pro Asp Ala Val Leu Lys Gln Ala Phe Glu Gln Ala Leu Glu
 50 55 60
 Phe His Lys Ser Arg Thr Ile Pro Ala Asn Trp Lys Thr Glu Leu Lys
 65 70 75 80
 Glu Asp Ser Ser Ser Ser Glu Ala Glu Glu Glu Glu Glu Glu Asp
 85 90 95
 Asp Glu Lys Glu Lys Glu Asp Asn Ser Ser Glu Glu Glu Glu Glu Ile
 100 105 110
 Glu Pro Phe Pro Glu Glu Arg Glu Asn Phe Leu Gln Gln Leu Tyr Lys
 115 120 125
 Phe Met Glu Asp Arg Gly Thr Pro Ile Asn Lys Arg Pro Val Leu Gly
 130 135 140
 Tyr Arg Asn Leu Asn Leu Phe Lys Leu Phe Arg Leu Val His Lys Leu
 145 150 155 160
 Gly Gly Phe Asp Asn Ile Glu Ser Gly Ala Val Trp Lys Gln Val Tyr
 165 170 175
 Gln Asp Leu Gly Ile Pro Val Leu Asn Ser Ala Ala Gly Tyr Asn Val

267

180 185 190
 Lys Cys Ala Tyr Lys Lys Tyr Leu Tyr Gly Phe Glu Gly Val Leu
 195 200 205

5 <210> 728
 <211> 221
 <212> PRT
 <213> Homo sapiens

10 <400> 728
 Met Leu Phe Ala Pro Cys Cys His Gln Cys Gly Glu Phe Ile Ile Gly
 1 5 10 15
 Arg Val Ile Lys Ala Met Asn Asn Ser Trp His Pro Glu Cys Phe Arg
 20 25 30
 15 Cys Asp Leu Cys Gln Glu Val Leu Ala Asp Ile Gly Phe Val Lys Asn
 35 40 45
 Ala Gly Arg His Leu Cys Arg Pro Cys His Asn Arg Glu Lys Ala Arg
 50 55 60
 Gly Leu Gly Lys Tyr Ile Cys Gln Lys Cys His Ala Ile Ile Asp Glu
 20 65 70 75 80
 Gln Pro Leu Ile Phe Lys Asn Asp Pro Tyr His Pro Asp His Phe Asn
 85 90 95
 Cys Ala Asn Cys Gly Lys Glu Leu Thr Ala Asp Ala Arg Glu Leu Lys
 100 105 110
 25 Gly Glu Leu Tyr Cys Leu Pro Cys His Asp Lys Met Gly Val Pro Ile
 115 120 125
 Cys Gly Ala Cys Arg Arg Pro Ile Glu Gly Arg Val Val Asn Ala Met
 130 135 140
 Gly Lys Gln Trp His Val Glu His Phe Val Cys Ala Lys Cys Glu Lys
 30 145 150 155 160
 Pro Phe Leu Gly His Arg His Tyr Glu Arg Lys Gly Leu Ala Tyr Cys
 165 170 175
 Glu Thr His Tyr Asn Gln Leu Phe Gly Asp Val Cys Phe His Cys Asn
 180 185 190
 35 Arg Val Ile Glu Xaa Asp Val Val Ser Ala Leu Asn Lys Ala Trp Cys
 195 200 205
 Val Asn Cys Phe Ala Cys Ser Thr Leu Gln His Leu Asn
 210 215 220

40 <210> 729
 <211> 114
 <212> PRT
 <213> Homo sapiens

45 <400> 729
 Leu Pro Phe Gln Leu Pro Cys Ile Gly Ser Gln Leu Leu Pro Ala Val
 1 5 10 15
 Gly Ala Val Glu Met Val Trp Met Val Gly Val Val Leu Glu Tyr Gln
 20 25 30
 50 Arg Leu Leu Ile Asp Asp Ser Met Ala Phe Leu Ala Asp Val Phe Pro
 35 40 45
 Lys Ala Ser Gly Phe Leu Thr Ile Met Thr Gly Ala Thr Gln Val Ser
 50 55 60
 Pro Ser Ile Leu Asp Lys Pro Asp Ile Cys Gln Asn Phe Leu Ala Glu
 55 65 70 75 80
 Val Thr Ala Glu Ala Leu Arg Met Pro Ala Val Ile His Gly Phe Asp
 85 90 95
 Asn Ser Ala Asn Asp Glu Phe Thr Thr Leu Met Thr Ala Arg Gly Lys
 100 105 110
 60 Glu His

<211> 191
 <212> PRT
 <213> Homo sapiens

5

<400> 730

Arg Arg Pro Ala Ala Gly Leu Arg Asp Xaa Val Xaa Ser Ala Pro Arg
 1 5 10 15
 Gly Met Ala Ser Glu Gly Pro Xaa Glu Pro Glu Ser Glu Gly Ile Lys
 20 25 30
 10 Leu Ser Gly Ile Cys Gln Thr Ile Cys Pro Gln Ile Cys Arg Ala Gln
 35 40 45
 Cys Gly Met Val Arg Val Leu Arg Ser Met Cys Leu Pro Gln Leu Cys
 50 55 60
 15 Ser His Ile Leu Ser Val Cys Ser Gly Thr Thr Ser Asp Arg Asn Xaa
 65 70 75 80
 Tyr Ser Val Pro Gly Ser Gln Tyr Leu Tyr Asn Gln Pro Ser Cys Tyr
 85 90 95
 Arg Gly Phe Gln Thr Xaa Lys His Arg Asn Glu Asn Thr Cys Pro Leu
 100 105 110
 20 Pro Gln Glu Met Lys Ala Leu Phe Lys Lys Lys Thr Xaa Asp Glu Lys
 115 120 125
 Lys Thr Tyr Asp Gln Gln Lys Phe Asp Ser Glu Arg Ala Asp Gly Thr
 130 135 140
 Ile Ser Ser Glu Ile Lys Ser Ala Arg Gly Ser His His Leu Ser Ile
 145 150 155 160
 25 Tyr Ala Glu Asn Ser Leu Lys Ser Asp Gly Tyr His Lys Arg Thr Asp
 165 170 175
 Arg Lys Ser Arg Ile Ile Cys Lys Lys Trp Ile Tyr Leu Gln Thr
 180 185 190

30

<210> 731
 <211> 115
 <212> PRT
 <213> Homo sapiens

35

<400> 731

Asp Gly Pro Leu Leu Ala Ser Val Thr Xaa Ser Xaa Pro Arg Leu Ala
 1 5 10 15
 Ala Trp Arg Arg Arg Gly Xaa Gly Ser Pro Lys Ala Arg Ala Ser Ser
 20 25 30
 40 Tyr Gln Ala Tyr Val Lys Pro Phe Val Pro Arg Phe Ala Gly Leu Asn
 35 40 45
 Val Ala Trp Leu Glu Ser Ser Glu Ala Cys Val Phe Pro Ser Ser Ala
 50 55 60
 45 Ala Thr Tyr Tyr Pro Phe Val Gln Glu Pro Pro Val Thr Glu Met Xaa
 65 70 75 80
 Thr Gln Cys Leu Ala Pro Ser Ile Phe Ile Thr Asn Pro Val Val Thr
 85 90 95
 50 Glu Val Phe Lys Gln Xaa Ser Ile Glu Met Arg Thr His Ala Leu Ser
 100 105 110
 His Lys Lys
 115

55

<210> 732
 <211> 139
 <212> PRT
 <213> Homo sapiens

<400> 732

Ser Ile Ser Arg Phe Asn Ser Tyr Thr Asn Tyr Ile Val Met Lys Asn
 1 5 10 15
 Arg Arg Lys Ser Pro Lys Val Phe Phe Arg Pro Pro Leu Leu Thr Gln
 20 25 30

Asn Thr Asp Thr Gln Ala Arg Thr Leu Ile Asn Ser Asn Ser Ser Phe
 35 40 45
 Glu Arg Leu Lys Pro Pro Arg Ile Leu Leu Ala Pro Gly Tyr Ile His
 50 55 60
 5 Cys Met Leu Pro Asp Val Phe Ser Arg Phe Gln Cys Ser Val Ala Leu
 65 70 75 80
 Leu Phe Leu Ser Gly Leu Gly Gly His Leu Leu Gln Gly Ser Trp Gly
 85 90 95
 Pro Val Trp Val Gly Trp Glu Val Pro Glu Ala Trp Ala Leu Pro Pro
 100 105 110
 10 Ala Pro Ala Ala His Ser Pro Ala Trp Leu Asp Trp Ile Phe Leu Val
 115 120 125
 His Thr Xaa Leu Glu Thr Asp Xaa Phe Phe Glu
 130 135
 15
 <210> 733
 <211> 155
 <212> PRT
 <213> Homo sapiens
 20
 <400> 733
 Gly Gln Ser Leu Lys Lys Xaa Pro Gly Pro Arg Ala Pro Lys Glu Xaa
 1 5 10 15
 Arg Gly Leu Pro Pro Leu Xaa Pro Ile Thr Pro Pro Phe Pro Lys Ile
 20 25 30
 25 His Gln Pro Gln Ile Gln Gly Xaa Leu Gln Pro Asp Ala Leu Val Lys
 35 40 45
 Lys Val Asp Ala Cys Val Thr Asp Pro Thr Gln Arg Xaa Gly Pro Phe
 50 55 60
 30 Pro Xaa Pro Tyr Val Pro Glu Arg Ser Ser Gln Ala Met Leu Glu Asn
 65 70 75 80
 Val Gln Gln Glu Leu Val Gly Glu Pro Arg Pro Gln Ala Pro Pro Ser
 85 90 95
 Leu Pro Thr Gln Gly Pro Ser Cys Pro Ala Glu Asp Gly Pro Pro Ala
 100 105 110
 35 Leu Lys Glu Lys Glu Glu Pro His Tyr Ile Glu Ile Trp Lys Lys His
 115 120 125
 Leu Glu Ala Tyr Ser Gly Cys Thr Leu Glu Leu Glu Glu Ser Leu Glu
 130 135 140
 40 Ala Ser Thr Ser Gln Met Met Asn Leu Asn Leu
 145 150 155
 <210> 734
 <211> 126
 <212> PRT
 <213> Homo sapiens
 45
 <400> 734
 Gly Glu Ala Gly His Trp Ala Gly Arg Ile Ser Arg Tyr Leu Asp Leu
 1 5 10 15
 Tyr Arg Trp Pro Gly Leu Ile Val His Gly Arg Leu Leu Gly Cys Ser
 20 25 30
 50 Glu Cys Lys Gly Ser Leu Ser Lys Pro Phe Ser Leu Val Leu Ser Gly
 35 40 45
 Val Arg Leu Phe Pro Phe Ser Phe Thr Ser Arg Ser Ser Ser Glu Glu
 50 55 60
 Ser Thr Gly Glu Val Val Leu Ala Ser Arg Ser Ser Cys Ser Cys Trp
 65 70 75 80
 Ala Arg Tyr Trp Ala Gly Phe Cys Leu Ala Ser Leu Ala Gln Trp Arg
 85 90 95
 60 Ser Ser Arg Cys Ser Arg Gly Lys Leu Ala Phe Lys Asn Gly Met Thr
 100 105 110
 Lys Gly Leu Ser Gly Lys Leu Val Ala Ser Cys Ser Leu Glu
 115
 120

115 120 125

5 <210> 735
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 735
 10 Thr Lys Thr Gly Arg Gly Glu Leu Gln Thr Glu Pro Lys Lys Met Ala
 1 5 10 15
 Leu Thr Glu Ser Leu Cys Thr Gln Asn Ile Gln Ala Ser Asp His Ala
 20 25 30
 Leu Leu Ala Gln Ala Ser Gly Thr Ser Pro Asn Asn Gly Leu Ser Tyr
 35 40 45
 15 Gln Pro Asn Gly Leu Pro His Pro Thr Pro Pro Pro Xaa His Tyr
 50 55 60
 Arg Leu Asp Asp Met Ala Ile Ala His His Tyr Arg Asp Ser Tyr Arg
 65 70 75 80
 20 His Pro Ser His Arg Gly Pro Xaa Gly Gln Lys Xaa Thr Tyr Gly Val
 85 90 95
 Ala Trp His Thr Ser Arg Arg Asn Asp
 100 105

25 <210> 736
 <211> 124
 <212> PRT
 <213> Homo sapiens

<400> 736
 30 Val Asn Ser Thr Leu Thr Ile Glu Glu Phe His Ser Lys Leu Gln Glu
 1 5 10 15
 Ala Thr Asn Phe Pro Leu Arg Pro Phe Val Ile Pro Phe Leu Lys Ala
 20 25 30
 Asn Leu Pro Leu Leu Gln Arg Glu Leu Leu His Cys Ala Arg Leu Ala
 35 35 40 45
 Lys Gln Asn Pro Ala Gln Tyr Leu Ala Gln His Glu Gln Leu Leu Leu
 50 55 60
 Asp Ala Ser Thr Thr Ser Pro Val Asp Ser Ser Glu Leu Leu Leu Asp
 65 70 75 80
 40 Val Asn Glu Asn Gly Lys Arg Arg Thr Pro Asp Arg Thr Lys Glu Asn
 85 90 95
 Gly Phe Asp Arg Glu Pro Leu His Ser Glu His Pro Ser Lys Arg Pro
 100 105 110
 Cys Thr Ile Ser Pro Gly Gln Arg Tyr Lys Ser Lys
 115 120

50 <210> 737
 <211> 149
 <212> PRT
 <213> Homo sapiens

<400> 737
 55 Leu Gln Val Cys Leu Pro Ala Gly Gly Pro Cys Xaa Val Cys Pro Gln
 1 5 10 15
 Lys Val Met Xaa Leu Leu Pro Ile Phe Xaa Leu Xaa Lys Met Xaa Pro
 20 25 30
 Pro Val Xaa Arg Ala Val Val Thr Ser Pro Trp Xaa Gly Phe Thr Ser
 35 40 45
 60 Leu Leu Xaa Xaa Xaa Asn Phe Gln Thr Asn Xaa Xaa Leu Gly Asn Pro
 50 55 60
 Pro Gly Gly Leu Glu Lys Pro Xaa Gln Val Ala Val Pro Pro Pro Pro
 65 70 75 80
 Leu Pro Phe Xaa Ala Xaa Gly Glu Pro Xaa Pro Ser Ile Phe Trp Ala
 271

5 85 90 95
 Pro Phe Xaa Trp Gly Asn Xaa Val Gly Gly Leu Phe Xaa Ser Pro Leu
 100 105 110
 Lys Lys Xaa Gly Phe Leu Glu Xaa Pro Xaa Ile Xaa Xaa Xaa Pro Leu
 115 120 125
 Xaa Phe Leu Asp Gly Pro Pro Lys Phe Phe Phe Gln Xaa Phe Phe Gly
 130 135 140
 Pro Phe Phe Lys Xaa
 145
 10
 <210> 738
 <211> 202
 <212> PRT
 <213> Homo sapiens
 15
 <400> 738
 Val Asn Ser Thr Leu Thr Ile Glu Glu Phe His Ser Lys Leu Gln Glu
 1 5 10 15
 Ala Thr Asn Phe Pro Leu Arg Pro Phe Val Ile Pro Phe Leu Lys Ala
 20 25 30
 Asn Leu Pro Leu Leu Gln Arg Glu Leu Leu His Cys Ala Arg Leu Ala
 35 40 45
 Lys Gln Asn Pro Ala Gln Tyr Leu Ala Gln His Glu Gln Leu Leu Leu
 50 55 60
 25 Asp Ala Ser Thr Thr Ser Pro Val Asp Ser Ser Ser Glu Leu Leu Leu Asp
 65 70 75 80
 Val Asn Glu Asn Gly Lys Arg Arg Thr Pro Asp Arg Thr Lys Glu Asn
 85 90 95
 Gly Phe Asp Arg Glu Pro Leu His Ser Glu His Pro Ser Lys Arg Pro
 100 105 110
 Cys Thr Ile Ser Pro Gly Gln Arg Tyr Ser Pro Asn Asn Gly Leu Ser
 115 120 125
 Tyr Gln Pro Asn Gly Leu Pro His Pro Thr Pro Pro Pro Gln His
 130 135 140
 35 Tyr Arg Leu Asp Asp Met Ala Ile Ala His His Tyr Arg Asp Ser Tyr
 145 150 155 160
 Arg His Pro Ser His Arg Asp Leu Arg Asp Arg Asn Arg Pro Met Gly
 165 170 175
 40 Leu His Gly Thr Arg Gln Glu Glu Met Ile Asp His Arg Leu Thr Asp
 180 185 190
 Arg Glu Trp Gly Arg Arg Val Glu Thr Ser
 195 200
 45
 <210> 739
 <211> 70
 <212> PRT
 <213> Homo sapiens
 50
 <400> 739
 Arg Gly Val Val Ser Met Val Glu Gly Val Pro Gly Val Val Asp Leu
 1 5 10 15
 Gly Val Ala Ala Gly Gly Val Ser Ile Gly Leu Pro Ala Pro Leu Leu
 20 25 30
 Gly Val Thr Lys Glu Leu Thr Ala Gly Val Ser Pro Cys Cys Trp Ala
 35 40 45
 55 Cys Xaa Val Cys Pro Gln Met Trp Met Gly Leu Xaa Pro Ser Phe Xaa
 50 55 60
 Ala Gly Gln Met Ser Pro
 65 70
 60
 <210> 740
 <211> 105
 <212> PRT

<213> Homo sapiens

<400> 740

5 Trp Ala His Leu Pro Ser Xaa Lys Ala Gly Xaa Lys Pro His Pro His
 1 5 10 15
 Leu Trp Thr Asp Xaa Ala Gly Pro Ala Ala Gly Arg His Pro Cys Ser
 20 25 30
 Gln Leu Phe Cys His Ala Gln Gln Arg Gly Trp Glu Pro Asp Gly His
 35 40 45
 10 Thr Thr Ser Ser His Ser Glu Val Asn His Pro Gly Asn Pro Phe His
 50 55 60
 His Arg Asp Asn Pro Ser Leu Asp Val Asn Ser Glu Leu Ser Glu Glu
 65 70 75 80
 Arg Gln His Asn Gln Arg Glu Thr Asn Ser Ser Ser Asp Ala Gln
 15 85 90 95
 Ser Cys Phe Phe Cys Leu Phe Val Tyr
 100 105

<210> 741

20 <211> 267

<212> PRT

<213> Homo sapiens

<400> 741

25 Met Met Leu Pro Val Leu Thr His His Ile Arg Tyr His Gln Cys Leu
 1 5 10 15
 Met His Leu Asp Lys Leu Ile Gly Tyr Thr Phe Gln Asp Arg Cys Leu
 20 25 30
 Leu Gln Leu Ala Met Thr His Pro Ser His His Leu Asn Phe Gly Met
 30 35 40 45
 Asn Pro Asp His Ala Arg Asn Ser Leu Ser Asn Cys Gly Ile Arg Gln
 50 55 60
 Pro Lys Tyr Gly Asp Arg Lys Val His His Met His Met Arg Lys Lys
 65 70 75 80
 35 Gly Ile Asn Thr Leu Ile Asn Ile Met Ser Arg Leu Gly Gln Asp Asp
 85 90 95
 Pro Thr Pro Ser Arg Ile Asn His Asn Glu Arg Leu Glu Phe Leu Gly
 100 105 110
 Asp Ala Val Val Glu Phe Leu Thr Ser Val His Leu Tyr Tyr Leu Phe
 115 120 125
 40 Pro Ser Leu Glu Glu Gly Gly Leu Ala Thr Tyr Arg Thr Ala Ile Val
 130 135 140
 Gln Asn Gln His Leu Ala Met Leu Ala Lys Lys Leu Glu Leu Asp Arg
 145 150 155 160
 45 Phe Met Leu Tyr Ala His Gly Pro Asp Leu Cys Arg Glu Ser Asp Leu
 165 170 175
 Arg His Ala Met Ala Asn Cys Phe Glu Ala Leu Ile Gly Ala Val Tyr
 180 185 190
 Leu Glu Gly Ser Leu Glu Glu Ala Lys Gln Leu Phe Gly Arg Leu Leu
 195 200 205
 50 Phe Asn Asp Pro Asp Leu Arg Glu Val Trp Leu Asn Tyr Pro Leu His
 210 215 220
 Pro Leu Gln Leu Gln Glu Pro Asn Thr Asp Arg Gln Leu Ile Gly Asn
 225 230 235 240
 55 Phe Phe Gln Phe Tyr Lys Lys Leu Thr Glu Phe Glu Arg Asn Gln Leu
 245 250 255
 Gly Val Asn Phe Leu Leu Ile Gly Ser Asp Phe
 260 265

60 <210> 742

<211> 143

<212> PRT

<213> Homo sapiens

<400> 742

1 Asn Pro Gly Pro Arg Tyr Gly Arg Thr Trp Ala Ser Arg Ser Xaa Pro
 5 1 5 10 15
 Ile Pro Thr Pro Ser Gln Lys Ala Leu Gly Val Ser Pro Gln Ala Xaa
 20 25 30
 Xaa Xaa Leu Leu Glu Ser Phe Ile Ala Ala Leu Xaa Ile Asp Lys Asp
 35 40 45
 10 Leu Xaa Tyr Val His Thr Phe His Glu Cys Leu Phe Leu Ser Xaa Ile
 50 55 60
 Lys Arg Val His Phe Glu Ser Gly Leu Glu Cys Pro Lys Ser Gln Leu
 65 70 75 80
 Gln Gln Cys Cys Leu Pro Leu Gly Arg Arg Lys Arg Ala Arg His Ser
 85 90 95
 15 Phe Val Gln Asp Ser Ala Asp Ser Gly Pro Ile Pro Cys Pro Asn Leu
 100 105 110
 His Cys Gly Cys Leu Phe Gln Gly Arg Lys Asn Arg Leu Trp Glu Arg
 115 120 125
 20 Thr Lys Tyr Ser Ala Ser Gly Asn Gly Ser Ser Asn Gly Cys Ala
 130 135 140

<210> 743

<211> 87

<212> PRT

25 <213> Homo sapiens

<400> 743

1 Lys Thr Gln Ala Gln Gly Thr Glu Glu Leu Gly His Pro Gly Val Xaa
 5 10 15
 30 Gln Tyr Pro Arg Gln Ala Lys Arg Pro Trp Gly Phe Arg Pro Lys Xaa
 20 25 30
 Trp Xaa Xaa Phe Trp Asn His Leu Leu Gln Arg Cys Xaa Leu Ile Arg
 35 35 40 45
 Ile Xaa Asn Met Phe Ile Leu Phe Met Asn Val Cys Phe Phe Xaa Arg
 50 55 60
 35 Leu Lys Glu Phe Ile Leu Asn Gln Asp Trp Asn Ala Pro Asn Pro Ser
 65 70 75 80
 Phe Ser Ser Val Ala Cys Pro
 85

<210> 744

<211> 101

<212> PRT

40 <213> Homo sapiens

<400> 744

1 Leu Leu Ser Val Leu Pro Phe Asp Glu Pro Leu Leu Met Gly His Leu
 5 10 15
 50 Gly Lys Ile Ile Phe Phe Lys Arg Ile His Cys Cys Ser His Phe Arg
 20 25 30
 Leu Leu Asn Thr Trp Ser Phe Pro Thr Ala Tyr Ser Phe Ser Leu Glu
 35 40 45
 Ile Asn Ser His Ser Val Gly Ser Gly Met Gly Trp Ala His Cys Leu
 50 55 60
 55 Gln Ser Leu Val Gln Arg Asn Val Trp Leu Phe Ser Phe Cys Leu Arg
 65 70 75 80
 Ala Ser Asn Thr Ala Glu Ala Gly Ile Trp Gly Ile Pro Ile Leu Ile
 85 90 95
 60 Gln Asn Glu Leu Phe
 100

<210> 745

<211> 277

<212> PRT

<213> Homo sapiens

<400> 745

5 Ile Asn Thr Leu Ile Asn Il Met Ser Arg Leu Gly Gln Asp Asp Pro
 1 5 10 15
 Thr Pro Ser Arg Ile Asn His Asn Glu Arg Leu Glu Phe Leu Gly Asp
 20 25 30
 10 Ala Val Val Glu Phe Leu Thr Ser Val His Leu Tyr Tyr Leu Phe Pro
 35 40 45
 Ser Leu Glu Glu Gly Gly Leu Ala Thr Tyr Arg Thr Ala Ile Val Gln
 50 55 60
 Asn Gln His Leu Ala Met Leu Ala Lys Lys Leu Glu Leu Asp Arg Phe
 65 70 75 80
 15 Met Leu Tyr Ala His Gly Pro Asp Leu Cys Arg Glu Ser Asp Leu Arg
 85 90 95
 His Ala Met Ala Asn Cys Phe Glu Ala Leu Ile Gly Ala Val Tyr Leu
 100 105 110
 20 Glu Gly Ser Leu Glu Glu Ala Lys Gln Leu Phe Gly Arg Leu Leu Phe
 115 120 125
 Asn Asp Pro Asp Leu Arg Glu Val Trp Leu Asn Tyr Pro Leu His Pro
 130 135 140
 Leu Gln Leu Gln Glu Pro Asn Thr Asp Arg Gln Leu Ile Glu Thr Ser
 145 150 155 160
 25 Pro Val Leu Gln Lys Leu Thr Glu Phe Glu Glu Ala Ile Gly Val Ile
 165 170 175
 Phe Thr His Val Arg Leu Leu Ala Arg Ala Phe Thr Leu Arg Thr Val
 180 185 190
 30 Gly Phe Asn His Leu Thr Leu Gly His Asn Gln Arg Met Glu Phe Leu
 195 200 205
 Gly Asp Ser Ile Met Gln Leu Val Pro Gln Ser Thr Tyr Ser Phe Ile
 210 215 220
 Ser Gln Ile Ile Ile Glu Gly His Leu Thr Phe Val Ala Lys Ala Ser
 225 230 235 240
 35 Leu Gly Glu Ile Asn Lys Asn Phe Arg Pro Lys Gly Asn Arg Lys Glu
 245 250 255
 Ala Trp Ala Leu Gln Gly Ser Thr Pro Ile Thr Gln Pro Asp Gln Glu
 260 265 270
 40 Pro Lys Lys Ala Cys
 275

<210> 746

<211> 187

<212> PRT

45 <213> Homo sapiens

<400> 746

Arg Thr Lys Ala Lys Lys Asp Lys Ala Gln Arg Xaa Xaa Xaa Xaa Xaa
 1 5 10 15
 50 Xaa Xaa Gly Xaa Ala Pro His Ser Glu Ser Asp Leu Pro Glu Gln Glu
 20 25 30
 Glu Glu Ile Leu Gly Ser Asp Asp Glu Gln Glu Asp Pro Asn Asp
 35 40 45
 Tyr Cys Lys Gly Gly Tyr His Leu Val Lys Ile Gly Asp Leu Phe Asn
 50 55 60
 55 Gly Arg Tyr His Val Ile Arg Lys Leu Gly Trp Gly His Phe Ser Thr
 65 70 75 80
 Val Trp Leu Ser Trp Asp Ile Gln Gly Lys Lys Phe Val Ala Met Lys
 85 90 95
 60 Xaa Val Lys Ser Ala Glu His Tyr Thr Glu Thr Ala Leu Asp Glu Ile
 100 105 110
 Xaa Leu Leu Lys Ser Val Arg Asn Ser Asp Pro Asn Asp Pro Asn Arg
 115 120 125

Glu Met Val Val Gln Leu Leu Asp Asp Phe Lys Ile Ser Gly Val Asn
 130 135 140
 Gly Thr His Ile Cys Met Val Phe Glu Val Leu Gly His His Leu Leu
 145 150 155 160
 5 Lys Trp Ile Ile Lys Ser Asn Tyr Xaa Gly Leu Pro Leu Pro Cys Xaa
 165 170 175
 Lys Lys Ile Ile Xaa Xaa Val Phe Thr Gly Xaa
 180 185

10 <210> 747
 <211> 89
 <212> PRT
 <213> Homo sapiens

15 <400> 747
 Ile Asp Pro Pro Pro Phe Pro Phe Lys His Phe Pro Leu Pro Phe Ser
 1 5 10 15
 Gly Glu Ala Xaa Pro Ser Lys Val Xaa Arg Ser Cys Phe Phe Phe Asn
 20 25 30
 20 Pro Thr Cys Ser Phe Gly Phe Ala Tyr Leu Thr Leu Xaa Xaa Ser Pro
 35 40 45
 Gln Pro Leu Gly Ile Leu Gly Glu Phe Gly Leu Gly Trp Ala Xaa Pro
 50 55 60
 25 Lys Thr Asn Gly Xaa Lys Cys Glu Thr Ala Ser Cys Xaa Xaa Pro Phe
 65 70 75 80
 Leu Pro Ile Arg Thr Ser Phe Lys Leu
 85

30 <210> 748
 <211> 71
 <212> PRT
 <213> Homo sapiens

35 <400> 748
 Xaa Leu Xaa Ser Met Asn Lys Arg Met Gly Ser Tyr Thr Phe Ile Ala
 1 5 10 15
 Xaa Phe Lys Lys Asp Ala Tyr Asn Leu Lys Asp Val Leu Met Gly Arg
 20 25 30
 40 Lys Gly Xaa Gly Gln Glu Ala Val Ser His Phe Xaa Pro Leu Val Phe
 35 40 45
 Gly Xaa Ala Gln Pro Arg Pro Asn Ser Pro Arg Met Pro Asn Gly Cys
 50 55 60
 Gly Asp Xaa Xaa Arg Val Lys
 65 70

45 <210> 749
 <211> 254
 <212> PRT
 <213> Homo sapiens

50 <400> 749
 Val Cys Lys Gly Ile Leu Glu Tyr Leu Thr Val Ala Glu Val Val Glu
 1 5 10 15
 55 Thr Met Glu Asp Leu Val Thr Tyr Thr Lys Asn Leu Gly Pro Gly Met
 20 25 30
 Thr Lys Met Ala Lys Met Ile Asp Glu Arg Gln Gln Glu Leu Thr His
 35 40 45
 Gln Glu His Arg Val Met Leu Val Asn Ser Met Asn Thr Val Lys Glu
 50 55 60
 60 Leu Leu Pro Val Leu Ile Ser Ala Met Lys Ile Phe Val Thr Thr Lys
 65 70 75 80
 Asn Ser Lys Asn Gln Gly Ile Glu Glu Ala Leu Lys Asn Arg Asn Phe
 85 90 95

Thr Val Glu Lys Met Ser Ala Glu Ile Asn Glu Ile Ile Arg Val Leu
 100 105 110
 Gln Leu Thr Ser Trp Asp Glu Asp Ala Trp Ala Ser Lys Asp Thr Glu
 115 120 125
 5 Ala Met Lys Arg Ala Leu Ala Ser Ile Asp Ser Lys Leu Asn Gln Ala
 130 135 140
 Lys Gly Trp Leu Arg Asp Pro Ser Ala Ser Pro Gly Asp Ala Gly Glu
 145 150 155 160
 10 Gln Ala Ile Arg Gln Ile Leu Asp Glu Ala Gly Lys Val Gly Glu Leu
 165 170 175
 Cys Ala Gly Lys Lys Arg Arg Glu Xaa Leu Gly Asn Leu Gln Asn Ala
 180 185 190
 Xaa Ala Asp Asp Cys Gln Ser Gly Leu Thr Ser Val Pro Arg Gly Gln
 195 200 205
 15 Gly Ser Leu Pro Xaa Gly Pro Cys Xaa Lys Ser Xaa Thr Xaa Tyr Xaa
 210 215 220
 Gln Gly Leu Gly Xaa Cys Ser Pro Ala Lys Xaa Glu Lys Ala Ser Phe
 225 230 235 240
 20 Gln Ser Trp Glu Ser Leu Ala His Xaa Lys Pro Lys His Leu
 245 250

<210> 750

<211> 82

<212> PRT

25 <213> Homo sapiens

<400> 750

Leu Phe Ser Arg Pro Ser Ala Tyr Leu Tyr Ser Cys Leu Pro Asp Ile
 1 5 10 15
 30 Asn Ala Ile Leu Met Pro Leu Lys Tyr Glu Ser Met Pro Lys Ile Thr
 20 25 30
 Cys Cys Phe Thr Lys Glu Arg Leu Leu Arg Gly Asn Lys Lys Asn His
 35 40 45
 Val Cys Ser Pro Gly Ser Ser Ser Gly Leu Arg His Trp Phe Thr Leu
 50 55 60
 35 Tyr Ala Gly Cys Ala Phe Leu Gln Tyr Gln Cys Ser Arg His Ser Glu
 65 70 75 80
 Ala Asn

<210> 751

<211> 162

<212> PRT

40 <213> Homo sapiens

<400> 751

Gln Lys Leu Val Ile Glu Asn Phe Asp Asp Glu Gln Ile Trp Gln Gln
 1 5 10 15
 50 Leu Glu Leu Gln Asn Glu Pro Ile Leu Gln Tyr Phe Gln Asn Ala Val
 20 25 30
 Ser Glu Thr Ile Asn Asp Glu Asp Ile Ser Leu Leu Pro Glu Ser Glu
 35 40 45
 Glu Gln Glu Arg Glu Glu Asp Gly Ser Glu Ile Glu Ala Asp Asp Lys
 50 55 60
 55 Glu Asp Leu Glu Asp Leu Glu Glu Glu Glu Val Ser Asp Met Gly Asn
 65 70 75 80
 Asp Asp Pro Glu Met Gly Glu Arg Ala Glu Asn Ser Ser Lys Ser Asp
 85 90 95
 60 Leu Arg Lys Ser Pro Val Phe Ser Asp Glu Asp Ser Asp Leu Asp Phe
 100 105 110
 Asp Ile Ser Lys Leu Glu Gln Gln Ser Lys Val Gln Asn Lys Gly Gln
 115 120 125
 Gly Lys Pro Arg Glu Lys Ser Ile Val Asp Asp Lys Phe Phe Lys Leu
 177

130 135 140
 Ser Glu Met Glu Ala Tyr Leu Glu Asn Ile Glu Lys Glu Glu Glu Pro
 145 150 155 160
 Lys Arg

5

<210> 752
 <211> 120
 <212> PRT
 <213> Homo sapiens

10

<400> 752
 Ala Ser Ile Ser Glu Ser Leu Lys Asn Leu Ser Ser Thr Met Asp Phe
 1 5 10 15
 15 Ser Leu Gly Phe Pro Cys Pro Leu Phe Cys Thr Leu Leu Cys Cys Ser
 20 25 30
 Asn Leu Leu Ile Ser Lys Ser Arg Ser Glu Ser Ser Ser Leu Lys Thr
 35 40 45
 20 Gly Leu Phe Leu Arg Ser Asp Leu Leu Glu Phe Ser Ala Leu Ser Pro
 50 55 60
 Ile Ser Gly Ser Ser Leu Pro Met Ser Asp Thr Ser Ser Ser Ser Lys
 65 70 75 80
 Ser Ser Arg Ser Ser Leu Ser Ser Ala Ser Ile Ser Glu Pro Ser Ser
 85 90 95
 25 Ser Arg Ser Cys Ser Ser Leu Ser Gly Arg Arg Leu Ile Ser Ser Ser
 100 105 110
 Leu Ile Val Ser Leu Thr Ala Phe
 115 120

30

<210> 753
 <211> 143
 <212> PRT
 <213> Homo sapiens

35

<400> 753
 Xaa Ala Cys Pro Xaa Ile Lys Val Xaa Ser Asn Phe Pro Xaa Ile Xaa
 1 5 10 15
 Met Xaa Glu Xaa Ala Pro Val Xaa Val Ser Xaa Ala Ala Phe Xaa Ala
 20 25 30
 40 Xaa Xaa Xaa Xaa Xaa Xaa Lys Asn Lys Xaa Xaa Xaa Ile Lys Xaa Xaa
 35 40 45
 Ala Glu Lys Xaa Ala Pro Ala Lys Asn Xaa Xaa Xaa Xaa Lys Lys Lys
 50 55 60
 Xaa Gln Xaa Xaa Xaa Lys Ile Lys Xaa Lys Glu Lys Xaa Arg Xaa Xaa
 45 65 70 75 80
 Xaa Xaa Xaa Thr Xaa Val Xaa Gln Ala Gly Lys Ser Ser Lys Xaa Xaa
 85 90 95
 Xaa Trp Xaa Lys Leu Lys Gln Xaa Xaa Lys Xaa Gly Lys Ala Ser Xaa
 100 105 110
 50 Ile Lys Asp Glu Gly Lys Xaa Xaa Xaa Leu Lys Xaa Xaa Gln Ala Phe
 115 120 125
 Phe Phe Xaa Phe Gln Asp Gln Val Lys Met Gln Ile Asn Xaa Ala
 130 135 140

55

<210> 754
 <211> 66
 <212> PRT
 <213> Homo sapiens

60

<400> 754
 Asn Gln Arg His Leu Glu Lys His Met Ile Asp Phe Phe Ala Ser Arg
 1 5 10 15
 Met Pro Glu Thr Leu His Leu Pro His Gly Thr Met Arg Gln Ser Pro

20 25 30
 Asn Pro Met Ser Ala Leu Glu Arg Tyr Ser Tyr Tyr Tyr Ser Cys Lys
 35 40 45
 Thr Ile Asn Gln Leu Ile His Ile Cys Thr Ala Gly Ser Pro Arg Asp
 5 50 55 60
 Lys Ile
 65

 10 <210> 755
 <211> 69
 <212> PRT
 <213> Homo sapiens

 <400> 755
 15 Asn Thr Ser Asn Ile Pro Phe Ile Ala Tyr Val Thr Tyr Ser Asn Glu
 1 5 10 15
 Tyr Asn Lys Leu Leu Phe Lys Lys Val Arg His Met Lys Ser Leu Leu
 20 20 25 30
 Cys Lys Phe His Val Ile Leu Lys Phe Leu Leu Ala Asn Lys Ser Ile
 35 40 45
 Cys Thr Ile Glu Pro Glu Thr Ser Arg Lys Ala His Asp Arg Phe Phe
 50 55 60
 Cys Lys Gln Asn Ala
 65
 25
 <210> 756
 <211> 91
 <212> PRT
 <213> Homo sapiens
 30
 <400> 756
 Trp Phe Cys Asn Cys Asn Ser Ser Cys Ile Val Leu Met Gln Thr Leu
 1 5 10 15
 Asp Leu Val Thr Val Ser Leu Cys His Glu Val Asn Val Met Phe Gln
 35 20 25 30
 Ala Phe Cys Leu Gln Lys Asn Leu Ser Cys Ala Phe Leu Asp Val Ser
 35 40 45
 Gly Ser Ile Val Gln Met Leu Leu Leu Ala Asn Arg Asn Phe Lys Ile
 50 55 60
 40 Thr Trp Asn Leu His Lys Arg Leu Phe Met Cys Leu Thr Phe Leu Lys
 65 70 75 80
 Arg Ser Leu Leu Tyr Ser Leu Glu Tyr Val Thr
 85 90
 45
 <210> 757
 <211> 63
 <212> PRT
 <213> Homo sapiens
 50
 <400> 757
 Asn Ser Tyr Xaa Leu Ile Lys Xaa Phe Ala Leu Xaa Asn Xaa Xaa His
 1 5 10 15
 Xaa Xaa Lys Xaa Met Xaa Asp Phe Phe Ala Ser Xaa Met Pro Glu Thr
 20 25 30
 55 Leu His Leu Pro Tyr Gly Thr Met Arg Gln Xaa Pro Asn Pro Met Xaa
 35 40 45
 Ala Leu Xaa Arg Tyr Ser Tyr Phe Tyr Xaa Xaa Glu Thr Ile Asn
 50 55 60
 60
 <210> 758
 <211> 62
 <212> PRT
 <213> Homo sapiens

<400> 758

Asp Ser Xaa Gln Ile Gln Cys Xaa His Xaa Asn Asp Thr Ala Thr Phe
 1 5 10 15
 5 Thr Xaa Ala Lys Pro Leu Ile Xaa Leu Ser Xaa Tyr Val Gln Xaa Gly
 20 25 30
 Pro His Val Thr Lys Ser Xaa Ala Glu Xaa Phe Gly Ser Xaa Asn Val
 35 40 45
 10 Asp Pro Ala Gly Xaa Arg Xaa Ser Lys Leu Leu Xaa Pro Phe
 50 55 60

<210> 759

<211> 68

<212> PRT

15 <213> Homo sapiens

<400> 759

Thr Xaa Asn Ile Pro Phe Ile Ala Tyr Val Xaa Tyr Ser Asn Glu Tyr
 1 5 10 15
 20 Asn Lys Leu Leu Phe Lys Lys Val Arg Xaa Met Lys Ser Leu Leu Xaa
 20 25 30
 Lys Phe His Val Ile Leu Lys Phe Leu Xaa Ala Asn Lys Ser Xaa Cys
 35 40 45
 25 Thr Ile Xaa Xaa Xaa Thr Xaa Xaa Lys Xaa His Asp Xaa Phe Phe Cys
 50 55 60
 Lys Xaa Asn Ala
 65

<210> 760

30 <211> 91

<212> PRT

<213> Homo sapiens

<400> 760

Trp Phe Arg Xaa Cys Lys Ser Ser Cys Ile Val Xaa Met Xaa Thr Leu
 1 5 10 15
 Asp Leu Xaa Thr Val Ser Leu Cys His Lys Val Asn Val Met Phe Gln
 20 25 30
 40 Ala Xaa Cys Leu Gln Lys Asn Xaa Ser Xaa Ala Phe Xaa Xaa Xaa Xaa
 35 40 45
 Gly Xaa Ile Val Gln Xaa Leu Leu Leu Ala Xaa Arg Asn Phe Lys Ile
 50 55 60
 Thr Trp Asn Leu Xaa Lys Arg Leu Phe Met Xaa Leu Thr Phe Leu Lys
 65 70 75 80
 45 Arg Ser Leu Leu Tyr Ser Leu Glu Tyr Xaa Thr
 85 90

<210> 761

50 <211> 46

<212> PRT

<213> Homo sapiens

<400> 761

His Phe Ser Leu Leu Met Pro Leu Gly Leu Gly Arg Arg Lys Lys Ala
 1 5 10 15
 55 Pro Pro Leu Val Glu Asn Glu Glu Ala Glu Pro Gly Arg Gly Gly Leu
 20 25 30
 Gly Val Gly Glu Pro Gly Pro Leu Gly Gly Gly Gly Ser Gly
 35 40 45
 60

<210> 762

<211> 46

<212> PRT

<213> Homo sapiens

<400> 762

5 Pro Asp Pro Pro Pro Arg Gly Pro Gly Ser Pro Thr Pro Ser Pro
 1 5 10 15
 Pro Arg Pro Gly Ser Ala Ser Ser Phe Ser Thr Arg Gly Gly Ala Phe
 20 25 30
 Phe Arg Arg Pro Ser Pro Ser Gly Met Ser Ser Glu Lys Trp
 35 40 45

<210> 763

<211> 181

<212> PRT

<213> Homo sapiens

<400> 763

15 Ala Ala Gln Gly Gln Trp Xaa Gly Gly Gly Pro Gly Pro Leu Pro Arg
 1 5 10 15
 Ser Asn Gly Thr Ile Pro Ser Leu Val Pro Ser Leu Ala Gly Val Pro
 20 20 25 30
 Gly Pro Pro Val Pro Cys Ser Pro Thr Ser Val Gly Ser Gly Thr
 35 40 45
 Gly Arg Gly Gly Ile Ser Gln Ile Gly Gly Pro Pro Pro Pro Pro
 50 55 60
 25 Leu Ser Thr Ile Ser Cys Gln Thr Gly Pro Ser Val Ser Leu Gly Pro
 65 70 75 80
 Trp Val Leu Phe Gly Gly His Xaa Leu Pro Ser Phe Leu Thr Gln Gly
 85 90 95
 Ile Gln Gly Arg Gly Leu Ser Phe Pro Pro Ala Asn Ala Ile Met Pro
 100 105 110
 30 Ser Pro Leu Leu Arg Gly Ala Pro Ser Leu Xaa Ser Leu Leu Pro Pro
 115 120 125
 His Leu Thr Xaa Val Cys Cys Glu Pro Arg Asn Leu Leu Pro Thr Ser
 130 135 140
 35 Asn Phe Ser Phe Gln Ala His Pro Trp Pro Arg Ala Gly Gly Arg Glu
 145 150 155 160
 Gly Arg Trp Arg Trp Val Phe Val Ser Glu Phe Ala Val Leu Asn Ile
 165 170 175
 40 Lys Asn Gln Ser Ala
 180

<210> 764

<211> 107

<212> PRT

<213> Homo sapiens

<400> 764

50 Pro Pro Asn Arg Thr Gln Gly Pro Arg Glu Thr Glu Gly Pro Val Trp
 1 5 10 15
 Gln Leu Met Val Glu Ser Gly Gly Gly Gly Gly Pro Pro Ile Trp
 20 25 30
 Leu Ile Pro Pro Leu Pro Val Pro Asp Pro Thr Glu Val Gly Gly Glu
 35 40 45
 55 Gln Gly Thr Gly Gly Pro Gly Thr Pro Ala Arg Leu Gly Thr Arg Glu
 50 55 60
 Gly Met Val Pro Leu Glu Arg Gly Lys Gly Pro Gly Pro Pro Pro Xaa
 65 70 75 80
 His Cys Pro Trp Ala Ala Xaa Leu Ala Gln Leu Glu Ala Xaa Val Leu
 85 90 95
 60 Xaa Xaa Xaa Pro Cys Trp Gly Pro Pro Gln Val
 100 105

<210> 765

<211> 114
 <212> PRT
 <213> Homo sapiens

5 <400> 765
 Ala Pro Gly Gly Ala Pro Ser Arg Asp Xaa Xaa Ser Gly Xaa Glu Pro
 1 5 10 15
 Pro Ala Glu Leu Xaa Lys Gln Pro Lys Asp Asn Xaa Arg Glu Val Gly
 20 25 30
 10 Gln Ala Pro Cys Pro Ala Pro Met Gly Pro Ser Pro Pro Trp Phe Pro
 35 40 45
 Val Trp Pro Gly Ser Pro Ala Pro Leu Cys Pro Val Pro His Leu Pro
 50 55 60
 15 Gln Leu Gly Gln Ala Gln Gly Gly Glu Gly Ser Ala Lys Leu Gly Gly
 65 70 75 80
 His Pro Arg Leu His His Phe Pro Pro Ser Ala Ala Lys Leu Val Pro
 85 90 95
 Leu Ser Pro Trp Gly Leu Gly Phe Cys Leu Gly Val Met Xaa Phe Leu
 100 105 110
 20 Val Ser

 <210> 766
 <211> 129
 25 <212> PRT
 <213> Homo sapiens

 <400> 766
 Ser Ser Ser Asn Leu Arg Leu Ser Phe Leu Ile Asn Glu Asn Ile Leu
 30 1 5 10 15
 Gly Lys Cys Phe Arg Ser Gly Pro Ser Cys Ala Gly Pro Arg Ile Ser
 20 25 30
 Pro Leu Ala Ala Gln Tyr Glu Cys Pro Arg Pro Ser Leu Leu Ile Met
 35 40 45
 35 Ala Ser Val Pro Lys Thr Asn Lys Ile Glu Pro Arg Ser Tyr Ser Ile
 50 55 60
 Ile Pro Ser Cys Gly Ile Gln Ala Ala Arg Ala Cys Phe Glu His Ser
 65 70 75 80
 Asn Phe Phe Lys Val Asn Ala Ser Gly Pro Ala Gly His Ser Ala Lys
 85 90 95
 40 Ser Ile Glu Gly Ala Pro Arg Gly Lys Gly Arg Gly Arg Ala Val Ala
 100 105 110
 Arg Leu Ala Ala Asp Arg Pro Pro Ala Pro Lys Ile Gln Leu Arg Ala
 115 120 125
 45 Phe

 <210> 767
 <211> 157
 50 <212> PRT
 <213> Homo sapiens

 <400> 767
 Lys Met Ala Ala Gly Phe Lys Thr Val Glu Pro Xaa Glu Tyr Tyr Arg
 55 1 5 10 15
 Arg Phe Leu Lys Glu Asn Cys Arg Pro Asp Gly Arg Glu Leu Gly Glu
 20 25 30
 Phe Arg Thr Thr Thr Val Asn Ile Gly Ser Ile Ser Thr Ala Asp Gly
 35 40 45
 60 Ser Ala Leu Val Lys Leu Gly Asn Xaa Thr Xaa Ile Cys Gly Val Lys
 50 55 60
 Ala Glu Phe Ala Ala Pro Ser Thr Asp Ala Pro Asp Lys Gly Tyr Val
 65 70 75 80

Val Pro Asn Val Asp Leu Pro Pro Leu Cys Ser Ser Arg Phe Arg Ser
 85 90 95
 Gly Pro Pro Gly Glu Glu Ala Gln Val Ala Ser Gln Phe Ile Ala Asp
 100 105 110
 5 Val Ile Glu Asn Ser Gln Ile Ile Gln Lys Glu Asp Leu Cys Ile Ser
 115 120 125
 Pro Gly Lys Leu Val Trp Val Leu Tyr Cys Asp Leu Ile Cys Leu Asp
 130 135 140
 10 Tyr Asp Gly Asn Ile Leu Asp Ala Cys Thr Phe Ala Leu
 145 150 155

<210> 768

<211> 171

<212> PRT

15 <213> Homo sapiens

<400> 768

Lys Met Ala Ala Gly Phe Lys Thr Val Glu Pro Xaa Glu Tyr Tyr Arg
 1 5 10 15
 20 Arg Phe Leu Lys Glu Asn Cys Arg Pro Asp Gly Arg Glu Leu Gly Glu
 20 25 30
 Phe Arg Thr Thr Thr Val Asn Ile Gly Ser Ile Ser Thr Ala Asp Gly
 35 40 45
 25 Ser Ala Leu Val Lys Leu Gly Asn Xaa Thr Xaa Ile Cys Gly Val Lys
 50 55 60
 Ala Glu Phe Ala Ala Pro Ser Thr Asp Ala Pro Asp Lys Gly Tyr Val
 65 70 75 80
 Val Pro Asn Val Asp Leu Pro Pro Leu Cys Ser Ser Arg Phe Arg Ser
 85 90 95
 30 Gly Pro Pro Gly Glu Glu Ala Gln Val Ala Ser Gln Phe Ile Ala Asp
 100 105 110
 Val Ile Glu Asn Ser Gln Ile Ile Gln Lys Glu Asp Leu Cys Ile Ser
 115 120 125
 35 Pro Gly Lys Leu Val Trp Val Leu Tyr Cys Asp Leu Ile Cys Leu Asp
 130 135 140
 Tyr Asp Gly Asn Ile Leu Asp Ala Cys Thr Phe Xaa Leu Leu Ala Ala
 145 150 155 160
 Leu Lys Asn Val Gln Val Ala Leu Lys Leu Leu
 165 170

<210> 769

<211> 112

<212> PRT

45 <213> Homo sapiens

<400> 769

Gln Leu Pro Glu Val Thr Ile Asn Glu Glu Thr Ala Leu Ala Glu Val
 1 5 10 15
 50 Asn Leu Lys Lys Lys Ser Tyr Leu Asn Ile Arg Thr His Pro Val Ala
 20 25 30
 Thr Ser Phe Ala Val Phe Asp Asp Thr Leu Leu Ile Val Asp Pro Thr
 35 40 45
 Gly Glu Glu Glu His Leu Ala Thr Gly Thr Leu Thr Ile Val Met Asp
 50 55 60
 55 Glu Glu Gly Lys Xaa Cys Cys Xaa His Lys Pro Gly Gly Ser Gly Leu
 65 70 75 80
 Thr Gly Ala Lys Leu Gln Asp Cys Met S r Arg Ala Val Thr Arg His
 85 90 95
 60 Lys Glu Val Lys Lys Leu Met Asp Glu Val Ile Lys Ser Met Lys Pro
 100 105 110

<210> 770

<211> 87

<212> PRT

<213> Homo sapiens

<400> 770

5 Gln His Ala Gly Ser Met Ser Gln Xaa Leu Gln Ala Lys Val Glu
 1 5 10 15
 Ile Phe Xaa Lys Met Phe Ile Ser Ala Gly Xaa Glu Gly Thr Glu Arg
 20 25 30
 Cys Thr Xaa Xaa Xaa Xaa Leu Gly Xaa Xaa Xaa Gly His Ala Ala Pro
 10 35 40 45
 Tyr Asn Arg Trp Ile Leu Xaa Glu Phe Xaa Xaa Asn Xaa Lys Val Xaa
 50 55 60
 Thr Glu Leu Ile Ser Tyr Phe Ser Xaa Thr Xaa Gly Thr Pro Ser Ala
 65 70 75 80
 15 Ser Gly Phe Thr Asn Glu Thr
 85

<210> 771

<211> 151

<212> PRT

<213> Homo sapiens

<400> 771

25 Phe Phe Ile Phe Cys Arg Tyr Glu Val Ser Pro Cys Cys Ser Gly Trp
 1 5 10 15
 Ser Gln Ala Pro Glu Leu Lys Gln Pro Ala Cys Leu Arg Leu Pro Lys
 20 25 30
 Cys Trp Asp His Lys His Glu Pro Leu Cys Pro Ala Trp His Leu Ile
 35 40 45
 30 Cys Glu Ser His Thr Ile Ser Asn Arg Asn Ile Lys Ile Pro Gly His
 50 55 60
 Phe Xaa Ser Pro Arg Leu Gly Gln Leu His Ser Leu Thr Cys Ser Val
 65 70 75 80
 Leu Pro Gln Ser Gln Cys Gly Thr Arg Leu Gln Ala Gln His Trp Gly
 35 85 90 95
 Cys Ala Asp Arg Ser Trp Phe Lys Ser Gln Leu Pro Ala Leu Glu Pro
 100 105 110
 Tyr Ser Asp Leu Ser Ala Pro Arg Leu Pro Gln Arg Val Leu Leu Gln
 115 120 125
 40 Pro Val Ser Gln Cys Thr Cys Pro Ala His Glu Leu Thr Glu Leu Met
 130 135 140
 Ala Ser Glu Ser Glu Cys Leu
 145 150

<210> 772

<211> 159

<212> PRT

<213> Homo sapiens

<400> 772

50 Glu Leu Pro Glu Lys Lys Lys Met Lys Tyr Ile Gln Asp Phe Gln Arg
 1 5 10 15
 Glu Lys Gln Glu Phe Glu Arg Asn Leu Ala Arg Phe Arg Glu Asp His
 20 25 30
 55 Pro Asp Leu Ile Gln Asn Ala Lys Lys Ser Asp Ile Pro Glu Lys Pro
 35 40 45
 Lys Thr Pro Gln Gln Leu Trp Tyr Thr His Glu Lys Lys Val Tyr Leu
 50 55 60
 Lys Val Arg Pro Asp Glu Ile Met Arg Asp Tyr Ile Gln Lys His Pro
 60 65 70 75 80
 Glu Leu Asn Ile Ser Glu Glu Gly Ile Thr Lys Ser Thr Leu Thr Lys
 85 90 95
 Ala Glu Arg Gln Leu Lys Asp Lys Phe Asp Gly Arg Pro Thr Lys Pro

100 105 110
 Pro Pro Asn Ser Tyr Ser Leu Tyr Cys Ala Glu Leu Met Ala Asn Met
 115 120 125
 5 Lys Asp Val Pro Ser Thr Glu Ala His Gly Ala Val Gln Pro Ala Val
 130 135 140
 Glu Ala Ala Val Pro Glu Gly Glu Gly Arg Leu Xaa Gln Glu Val
 145 150 155

 <210> 773
 10 <211> 151
 <212> PRT
 <213> Homo sapiens

 <400> 773
 15 Lys Lys Glu Arg Lys Trp Gly Arg Pro Gly Gly Gln Gly Thr Glu His
 1 5 10 15
 Gly Gly Glu Thr Lys Val Val Ser Trp Gly Gly Glu Leu Leu Gly Ser
 20 20 25 30
 Pro Trp Leu Pro Trp Gly Gly Ala Glu Pro Gln Leu Glu Ser Glu Ser
 35 40 45
 Glu Glu Ser Pro Glu Glu Glu Leu Glu Leu Leu Pro Ser Asp Ser
 50 55 60
 Leu Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
 65 70 75 80
 25 Ser Ser Ser Ser Ser Ser Ser Ser Ser Asp Ser Asp Leu Asp Cys Arg
 85 90 95
 Val Val Arg Leu Asp Leu Gly Phe Gly Pro Arg Ser Leu Val Met Leu
 100 105 110
 Leu Arg Leu Leu Glu Met Tyr Ser Leu Tyr Ala Ala Arg Ser Trp Gly
 115 120 125
 30 Asp Arg Leu Leu Thr Gln Arg Ser Arg Cys Thr Leu Tyr Cys Phe Cys
 130 135 140
 Cys Ser Ser Ala Ser Phe Leu
 145 150

 35 <210> 774
 <211> 140
 <212> PRT
 <213> Homo sapiens

 40 <400> 774
 Gly Gly Gly Ala Gly Ala Ala Ala Leu Gly Leu Ile Ile Phe Ile Leu
 1 5 10 15
 Ile Val Ile Leu Val Val Val Phe Val Leu Val Ile Leu Ile Leu Phe
 20 25 30
 45 Ile Ile Leu Leu Gly Leu Arg Leu Gly Leu Gln Ser Ser Pro Ala Gly
 35 40 45
 Phe Gly Val Trp Ala Ser Gln Leu Gly His Ala Leu Thr Phe Ile Gly
 50 55 60
 Asp Val Leu Phe Ile Cys Cys Thr Val Leu Gly Arg Gln Ala Leu Asn
 65 70 75 80
 Pro Glu Val Gln Val His Leu Val Leu Leu Leu Leu Leu Gly Gln
 85 90 95
 Leu Phe Val Ser Ala Pro Ser Gly Ser Gly Arg Cys Ala Ala Ser Asp
 100 105 110
 55 Cys Arg Ser Pro Pro Cys Ala Pro Ser Ala Ala Gly Gly Ser Xaa Pro
 115 120 125
 His Trp Asn Ser Ser Ser Trp Glu Glu Leu Xaa Xaa
 130 135 140

 60 <210> 775
 <211> 130
 <212> PRT

<213> Homo sapiens

<400> 775

5 Arg Ser Ala Trp Trp Arg Ser Ala Val Ala Gly Ser Ala Ser Pro Arg
 1 5 10 15
 Ala Arg Arg Ser Thr Tyr Lys Lys Leu Ala Glu Glu Gln Gln Lys Gln
 20 25 30
 Tyr Lys Val His Leu Asp Leu Trp Val Lys Ser Leu Ser Pro Gln Asp
 35 40 45
 10 Arg Ala Ala Tyr Lys Glu Tyr Ile Ser Asn Lys Arg Lys Ser Met Thr
 50 55 60
 Lys Leu Arg Gly Pro Asn Pro Lys Ser Ser Arg Thr Thr Leu Gln Ser
 65 70 75 80
 15 Lys Ser Glu Ser Glu Glu Asp Asp Glu Glu Asp Glu Asp Asp Glu Asp
 85 90 95
 Glu Asp Asp Asp Glu Asp Asp Asp Glu Asp Glu Asp Asn Glu Ser Glu
 100 105 110
 Gly Ser Ser Ser Ser Ser Ser Ser Ser Gly Asp Ser Ser Asp Ser Asp
 115 120 125
 20 Ser Asn
 130

<210> 776

<211> 165

<212> PRT

<213> Homo sapiens

<400> 776

30 Pro Pro Ala Leu Pro Leu Pro Val Pro Arg Ser Ala Arg His Glu Ile
 1 5 10 15
 Pro Arg Arg Gly Ala Thr Arg Gly Arg Val Gly Glu Ala Gln Arg Gln
 20 25 30
 Pro Leu Pro Ala Met Glu Glu Glu Ala Arg Gly Ala His Leu Arg Pro
 35 35 40 45
 35 Pro Glu Pro Val Pro Arg Gln Pro Pro Arg Ala Pro Gln Gly Ala Ala
 50 55 60
 Leu Pro Leu His Pro Gln Gly Gly Leu Arg Gly Ala His Gly Gln Val
 65 70 75 80
 40 Arg Val Leu His His Arg His His Arg Pro Gln Gly Asp Arg Leu Pro
 85 90 95
 Leu Arg Gly Arg Glu Leu Leu Glu Arg Gly His Arg Ala Gly Ala His
 100 105 110
 Arg Phe Pro Glu Pro Pro Arg Pro Ala Gly Leu Ser Gln Pro Pro Gly
 115 120 125
 45 Thr His Arg Pro Ala Ala Pro Ala Glu Asp Ala Val Ala Ala Ala Ala
 130 135 140
 Ala Ala Pro Ser Glu Pro Ser Glu Pro Ser Arg Pro Ser Pro Gln Pro
 145 150 155 160
 50 Lys Pro Arg Thr Pro
 165

<210> 777

<211> 158

<212> PRT

<213> Homo sapiens

<400> 777

60 Ala Cys Ser Pro Pr Ala Pro Ala Arg Ala Pro Arg Ser Cys Ala Ser
 1 5 10 15
 Thr Pro Ser Ser Arg Trp Thr Ala Trp Ser Ala Arg Ala Ser Thr Cys
 20 25 30
 Thr Ser Pro Ser Ser Pro Pro Thr Thr Arg Arg Ser Thr Ser Ala Ala
 35 40 45

Arg Ala Arg Ala Ala Gly Thr Arg Pro Ser Arg Trp Arg Ser Ser Ile
 50 55 60
 Ser Arg Thr Ala Ala Pro Cys Arg Thr Phe Ala Ala Ala Arg Asn Ala
 65 70 75 80
 5 Pro Thr Arg Arg Thr Arg Arg Gly Arg Arg Gly Cys Arg Gly Arg Arg
 85 90 95
 Thr Leu Arg Ala Leu Gly Ala Leu Gln Ala Ile Pro Ala Ala Gln Thr
 100 105 110
 10 Pro His Ala Met Ser Pro Pro Arg Ala Ile Arg Trp Thr Ser Arg Thr
 115 120 125
 Glu Ala Arg Thr Trp Pro Ala Leu Leu Gln Pro Cys Ser Xaa Lys Asn
 130 135 140
 Xaa Pro Cys Ala Arg Ile Leu Ala Ser Val Gln Arg Ala Pro
 145 150 155

15
 <210> 778
 <211> 179
 <212> PRT
 <213> Homo sapiens

20
 <400> 778
 Arg Pro His Cys Arg Ser Gln Ser Arg Ala Arg His Asp Met Lys Ser
 1 5 10 15
 25 Pro Asp Glu Val Leu Arg Glu Gly Glu Leu Glu Lys Arg Ser Asp Ser
 20 25 30
 Leu Phe Gln Leu Trp Lys Lys Lys Arg Gly Val Leu Thr Ser Asp Arg
 35 40 45
 Leu Ser Leu Phe Pro Ala Ser Pro Arg Ala Arg Pro Lys Glu Leu Arg
 50 55 60
 30 Phe His Ser Ile Leu Lys Val Asp Cys Val Glu Arg Thr Gly Lys Tyr
 65 70 75 80
 Val Tyr Phe Thr Ile Val Thr Thr Asp His Lys Glu Ile Asp Phe Arg
 85 90 95
 35 Cys Ala Gly Glu Ser Cys Trp Asn Ala Ala Ile Ala Leu Ala Leu Ile
 100 105 110
 Asp Phe Gln Asn Arg Arg Ala Leu Gln Asp Phe Arg Ser Arg Gln Glu
 115 120 125
 Arg Thr Asp Pro Pro His Pro Pro Arg Thr Pro Trp Leu Pro Arg Pro
 130 135 140
 40 Pro His Pro Pro Ser Pro Arg Ser Pro Pro Gly His Pro Arg Ser Pro
 145 150 155 160
 Asn Pro Ala Arg His Glu Pro Ala Ala Gly His Thr Leu Asp Glu Ser
 165 170 175
 Asp Arg Gly

45
 <210> 779
 <211> 179
 <212> PRT
 50 <213> Homo sapiens

<400> 779
 Pro Arg Ser Asp Ser Ser Ser Val Trp Pro Ala Ala Gly Ser Trp Arg
 1 5 10 15
 55 Ala Gly Phe Gly Leu Arg Gly Trp Pro Gly Gly Leu Arg Gly Leu Gly
 20 25 30
 Gly Cys Gly Gly Arg Gly Ser His Gly Val Leu Gly Gly Cys Gly Gly
 35 40 45
 Ser Val Arg Ser Trp Arg Leu Arg Lys Ser Cys Arg Ala Arg Arg Phe
 50 55 60
 60 Trp Lys Ser Met Ser Ala Ser Ala Met Ala Ala Phe Gln Gln Leu Ser
 65 70 75 80
 Pro Ala Gln Arg Lys Ser Ile Ser Leu Trp Ser Val Val Thr Met Val

85 90 95
 Lys Tyr Thr Tyr Leu Pro Val Arg Ser Thr Gln S r Thr Leu Arg Met
 100 105 110
 5 Glu Trp Lys Arg Ser Ser Leu Gly Arg Ala Arg Gly Leu Ala Gly Asn
 115 120 125
 Arg Leu Arg Arg Ser Glu Val Ser Thr Pro Arg Phe Phe Phe His Ser
 130 135 140
 Trp Lys Arg Leu Ser Leu Arg Phe Ser Asn Ser Pro Ser Arg Ser Thr
 145 150 155 160
 10 Ser Ser Gly Asp Phe Met Ser Cys Arg Ala Arg Asp Trp Glu Arg Gln
 165 170 175
 Cys Gly Arg

 15 <210> 780
 <211> 134
 <212> PRT
 <213> Homo sapiens

 20 <400> 780
 Ala Trp Arg Cys Thr Arg Val Ser Glu Ala Leu Leu Leu Ser Ala Arg
 1 5 10 15
 Gln Glu Asp Val Cys Arg Arg Arg Ser Ala Gly Pro Val Ala Phe Thr
 20 25 30
 25 Val Leu Cys Leu Ser Arg Pro Ser Arg Leu Pro Thr Ala Ala Ile Pro
 35 40 45
 Pro Tyr Ser Pro Ser Gly Thr Trp Arg Trp Ser Val Gln Ala Leu Ala
 50 55 60
 30 Cys Asn Gln His Xaa Ser Leu Gly Leu Val Gln Glu Gly Ser Ser Gly
 65 70 75 80
 Lys Ala Pro Ser Ser Phe Pro Ala Arg Leu Gly Pro Ala Thr Val Arg
 85 90 95
 Leu Arg Xaa Gly Leu Lys Glu Xaa Ala Gly Pro Glu Phe Pro Leu Ala
 100 105 110
 35 Arg Xaa Glu Leu Xaa Thr Lys Gly Arg Arg Xaa Pro Pro Gly Arg Xaa
 115 120 125
 Xaa Val Pro Pro Leu Ala
 130

 40 <210> 781
 <211> 130
 <212> PRT
 <213> Homo sapiens

 45 <400> 781
 Gly Gly Met Ala Ala Val Gly Ser Leu Leu Gly Arg Leu Arg Gln Ser
 1 5 10 15
 Thr Val Lys Ala Thr Gly Pro Ala Leu Arg Arg Leu His Thr Ser Ser
 20 25 30
 50 Trp Arg Ala Asp Ser Ser Arg Ala Ser Leu Thr Arg Val His Arg Gln
 35 40 45
 Ala Tyr Ala Arg Leu Tyr Pro Val Leu Leu Val Lys Gln Asp Gly Ser
 50 55 60
 55 Thr Ile His Ile Arg Tyr Arg Glu Pro Arg Arg Met Leu Ala Met Pro
 65 70 75 80
 Ile Asp Leu Asp Thr Leu Ser Pro Glu Glu Arg Arg Ala Arg Leu Arg
 85 90 95
 Lys Arg Glu Ala Gln Leu Gln Ser Arg Lys Glu Tyr Glu Gln Glu Leu
 100 105 110
 60 Ser Asp Asp Leu His Val Glu Arg Tyr Arg Gln Xaa Trp Thr Arg Thr
 115 120 125
 Lys Lys
 130

<210> 782
 <211> 56
 <212> PRT
 5 <213> Homo sapiens

 <400> 782
 Asn Asp Val Pro Asn Gln Phe Leu Val Tyr Ser Phe Pro Lys Ser Lys
 1 5 10 15
 10 Ile Thr Lys Val Leu Lys Val His Lys Thr Asp Leu His Leu Cys Ile
 20 25 30
 Pro Phe Gln Ile Asn Pro Lys Ser Met Tyr Ser Met Phe Asn Ser Met
 35 40 45
 15 Gln Tyr Ala Lys Ala Leu Cys Cys
 50 55

 <210> 783
 <211> 55
 <212> PRT
 20 <213> Homo sapiens

 <400> 783
 Asn Asp Val Pro Asn Gln Phe Leu Val Tyr Ser Phe Pro Lys Ser Lys
 1 5 10 15
 25 Ile Thr Lys Val Leu Lys Val His Lys Thr Asp Leu His Leu Cys Ile
 20 25 30
 Pro Phe Gln Ile Asn Pro Lys Ser Met Tyr Ser Met Phe Asn Ser Met
 35 40 45
 30 Gln Tyr Ala Lys Ala Leu Cys
 50 55

 <210> 784
 <211> 259
 <212> PRT
 35 <213> Homo sapiens

 <400> 784
 Lys Leu Ser Ala Leu Phe Ile Asn Leu Ile Ser Asp Pro Ser Arg Trp
 1 5 10 15
 40 Val Arg Gln Ala Ala Phe Gln Ser Leu Gly Pro Phe Ile Ser Thr Phe
 20 25 30
 Ala Asn Pro Ser Ser Ser Gly Gln Tyr Phe Lys Glu Glu Ser Lys Ser
 35 40 45
 45 Ser Glu Glu Met Ser Val Glu Asn Lys Asn Arg Thr Arg Asp Gln Glu
 50 55 60
 Ala Pro Glu Asp Val Gln Val Arg Pro Glu Asp Thr Pro Ser Asp Leu
 65 70 75 80
 Ser Val Ser Asn Ser Ser Val Ile Leu Glu Asn Thr Met Glu Asp His
 85 90 95
 50 Ala Ala Glu Ala Ser Gly Lys Pro Leu Gly Glu Ile Ser Val Pro Leu
 100 105 110
 Asp Ser Ser Leu Leu Cys Thr Leu Ser Ser Glu Ser His Gln Glu Ala
 115 120 125
 55 Ala Ser Asn Glu Asn Asp Lys Lys Pro Gly Asn Tyr Lys Ser Met Leu
 130 135 140
 Arg Pro Glu Val Gly Thr Thr Ser Gln Asp Ser Ala Leu Leu Asp Gln
 145 150 155 160
 Glu Leu Tyr Asn Ser Phe His Phe Trp Arg Thr Pro Leu Pro Glu Ile
 165 170 175
 60 Asp Leu Asp Ile Glu Leu Glu Gln Asn Ser Gly Gly Lys Pro Ser Pro
 180 185 190
 Glu Gly Pro Glu Glu Glu Ser Glu Gly Pro Val Pro Ser Ser Pro Asn
 195 200 205

Ile Thr Met Ala Thr Arg Lys Glu Leu Glu Glu Met Ile Glu Asn Leu
 210 215 220
 Glu Pro Pro Ile Asp Asp Pro Asp Gly Xaa Ala Gln Val Gly Ser Ala
 225 230 235 240
 5 Val Arg Cys Thr Thr Cys Phe Gln Xaa Trp Asp Xaa His Glu Glu Xaa
 245 250 255
 His Arg Phe

10 <210> 785
 <211> 103
 <212> PRT
 <213> Homo sapiens

15 <400> 785
 Ile Leu Phe Gly Gln Glu Asn Leu Xaa His Asn Ser Leu Asn Ser Met
 1 5 10 15
 Ile Lys Asp Cys Ser Thr Pro Lys Ser Gly His Arg Tyr Val Gln Tyr
 20 20 25 30
 Val Lys Lys Leu His Leu Arg Ala Asp His Asp Gln Val Lys Asn Thr
 35 40 45
 Arg His Thr Leu Tyr Arg Leu Ile Asn Phe Leu Gln Val Met Thr Ser
 50 55 60
 Met Lys Lys Ser Asp Thr Asp Thr Gln Gln Pro Phe Cys Lys Cys Val
 25 65 70 75 80
 Gln Gln Tyr Ala Ala Leu Lys Ser Leu Ser Gln Ser Tyr Leu Xaa Trp
 85 90 95
 His Gln Xaa Leu Xaa Glu Met
 100

30 <210> 786
 <211> 218
 <212> PRT
 <213> Homo sapiens

35 <400> 786
 Glu Leu Glu Asp Lys Val Ala Ala Cys Gln Lys Glu Gln Ala Asp Phe
 1 5 10 15
 Leu Pro Arg Ile Glu Glu Thr Lys Trp Glu Val Cys Gln Lys Ala Gly
 40 20 25 30
 Glu Ile Ser Leu Leu Lys Gln Gln Leu Lys Asp Ser Gln Ala Asp Val
 35 40 45
 Ser Gln Lys Leu Ser Glu Ile Val Gly Leu Arg Ser Gln Leu Arg Glu
 50 55 60
 Gly Arg Ala Ser Leu Arg Glu Lys Glu Glu Gln Leu Leu Ser Leu Arg
 45 65 70 75 80
 Asp Ser Phe Ser Ser Lys Gln Ala Ser Leu Glu Leu Gly Glu Gly Glu
 85 90 95
 Leu Pro Ala Ala Cys Leu Lys Pro Ala Leu Thr Pro Val Asp Pro Ala
 50 100 105 110
 Glu Pro Gln Asp Ala Leu Ala Thr Cys Glu Ser Asp Glu Ala Lys Met
 115 120 125
 Arg Arg Gln Ala Gly Val Ala Ala Ala Ser Leu Val Ser Val Asp
 130 135 140
 55 Gly Glu Ala Glu Ala Gly Gly Glu Ser Gly Thr Arg Ala Leu Arg Arg
 145 150 155 160
 Glu Val Gly Arg Leu Gln Ala Glu Leu Ala Ala Glu Arg Arg Ala Arg
 165 170 175
 Glu Arg Gln Gly Ala Ser Phe Ala Glu Glu Arg Arg Val Trp Leu Glu
 60 180 185 190
 Glu Lys Glu Lys Val Ile Glu Tyr Pro Glu Ser Ser Leu Gln Leu Xaa
 195 200 205
 Leu Arg Xaa Arg Cys Thr Asn Arg Asn Pro

210

215

5 <210> 787
 <211> 208
 <212> PRT
 <213> Homo sapiens

<400> 787

10 Xaa Gln Leu Gln Ala Ala Phe Trp Val Leu Asp His Leu Leu Leu Phe
 1 5 10 15
 Leu Lys Pro Asn Ala Ala Leu Leu Gly Glu Ala Gly Thr Leu Ala Leu
 20 25 30
 Pro Gly Pro Pro Leu Ser Arg Gln Leu Gly Leu Gln Pro Pro His Leu
 35 40 45
 15 Pro Pro Gln Gly Pro Arg Pro Ala Leu Pro Ala Ser Leu Arg Leu Pro
 50 55 60
 Val His Gly Asn Gln Gly Gly Gly Ser Gly His Pro Gly Leu Thr Ala
 65 70 75 80
 20 His Leu Ser Leu Val Ala Leu Ala Gly Gly Gln Ser Ile Leu Trp Leu
 85 90 95
 Gly Arg Val His Gly Gly Gln Arg Arg Leu Glu Ala Gly Gly Arg Gln
 100 105 110
 Leu Ala Phe Ala Gln Leu Gln Ala Gly Leu Leu Ala Ala Glu Gly Val
 115 120 125
 25 Pro Gln Ala Glu Gln Leu Leu Leu Leu Pro Gln Arg Ser Pro Ala
 130 135 140
 Leu Pro Gln Leu Arg Ala Gln Ser His Asp Leu Thr Gln Leu Leu Arg
 145 150 155 160
 30 His Ile Arg Leu Arg Val Leu Gln Leu Leu Gln Glu Gly Asp Leu
 165 170 175
 Ala Ser Leu Leu Ala His Leu Pro Leu Ser Phe Leu Tyr Pro Gly Gln
 180 185 190
 Glu Val Gly Leu Leu Leu Leu Ala Gly Gly His Leu Val Leu Gln Leu
 195 200 205

35 <210> 788
 <211> 130
 <212> PRT
 <213> Homo sapiens

40 <400> 788

Arg Arg Ile Leu Ala Ser Ser Leu Ser Gln Val Ala Arg Ala Ser Cys
 1 5 10 15
 45 Gly Ser Ala Gly Ser Thr Gly Val Ser Ala Gly Leu Arg Gln Ala Ala
 20 25 30
 Gly Ser Ser Pro Ser Pro Ser Ser Arg Leu Ala Cys Leu Leu Lys
 35 40 45
 Glu Ser Arg Arg Leu Ser Ser Cys Ser Ser Phe Ser Arg Ser Glu Ala
 50 55 60
 50 Arg Pro Ser Arg Ser Cys Glu Arg Ser Pro Thr Ile Ser Leu Asn Phe
 65 70 75 80
 Cys Asp Thr Ser Ala Cys Glu Ser Phe Ser Cys Cys Phe Arg Arg Glu
 85 90 95
 55 Ile Ser Pro Ala Phe Trp His Thr Ser His Leu Val Ser Ser Ile Arg
 100 105 110
 Gly Arg Lys Ser Ala Cys Ser Phe Trp Gln Ala Ala Thr Leu Ser Ser
 115 120 125
 Ser Ser
 130

60 <210> 789
 <211> 252
 <212> PRT

<213> Homo sapiens

<400> 789

5 Val Pro Gln Gly Tyr Pro Gly Gly Val Pro Thr Phe Phe Arg Asp Met
 1 5 10 15
 Lys Gln Gly Leu Ser Val Gly Ile Gly Gly Arg Glu Ser Arg Asn
 20 25 30
 Gly Cys Leu Asp Val Glu Lys Asp Cys Ser Ile Thr Lys Phe Leu Asn
 35 40 45
 10 Arg Ile Leu Gly Leu Glu Val His Lys Gln Asn Ala Leu Phe Gln Tyr
 50 55 60
 Phe Ser Asp Thr Phe Asp His Leu Ile Glu Met Asp Lys Arg Glu Gly
 65 70 75 80
 15 Lys Tyr Asp Met Gly Ile Leu Asp Leu Ala Pro Gly Ile Glu Glu Ile
 85 90 95
 Tyr Glu Glu Ser Gln Gln Val Phe Leu Ala Pro Gly His Pro Gln Asp
 100 105 110
 Gly Gln Val Val Phe Tyr Lys Ile Ser Val Asp Arg Gly Leu Lys Trp
 115 120 125
 20 Glu Asp Ala Phe Ala Lys Ser Leu Ala Leu Thr Gly Pro Tyr Asp Gly
 130 135 140
 Phe Tyr Leu Ser Tyr Lys Val Arg Gly Asn Lys Pro Ser Cys Leu Leu
 145 150 155 160
 25 Ala Glu Gln Asn Arg Gly Gln Phe Phe Thr Val Tyr Lys Pro Asn Ile
 165 170 175
 Gly Arg Gln Ser Gln Leu Glu Ala Leu Asp Ser Leu Arg Arg Lys Phe
 180 185 190
 His Arg Val Thr Ala Glu Glu Ala Lys Gly Ala Leu Gly Glu Trp Leu
 195 200 205
 30 Arg Phe Val Ala Asp Ala Leu Gln Ala Thr Ala Pro Gly Thr Gly Thr
 210 215 220
 Cys Arg Leu Ala Gln Glu Gly Xaa Gly Leu Xaa Ala Gly Ala Cys Gly
 225 230 235 240
 35 Leu Arg His Gln Leu His Ala Cys Xaa Ala Pro Leu
 245 250

<210> 790

<211> 94

<212> PRT

40 <213> Homo sapiens

<400> 790

Arg Gly Gln Gly Arg Ala Gly Gly Gly Arg Ile Ala Tyr Ile Ser Arg
 1 5 10 15
 45 Gly Leu Pro His Gly Ala Pro Glu Thr Arg Gly Pro Glu His Leu Gly
 20 25 30
 Phe Pro Glu Phe Leu Ala Leu Gly Thr Thr Arg Phe His Gly Phe Gln
 35 40 45
 50 Gly Phe Gly Pro Thr Glu Pro Leu Trp Val Pro Ser Pro Arg Ala Ala
 50 55 60
 Thr Arg Ser Pro Phe Leu Leu Gly Arg Arg Gly Thr Glu Arg Ala Leu
 65 70 75 80
 Pro Arg Pro Gly Pro Gln Leu Ser Xaa Trp Ala Pro Gln Gly
 85 90

<210> 791

<211> 225

<212> PRT

60 <213> Homo sapiens

<400> 791

Leu Lys Ala Lys Asp Gln Gly Lys Pro Glu Val Gly Glu Tyr Ala Lys
 1 5 10 15

Leu Glu Lys Ile Asn Ala Glu Gln Gln Leu Lys Ile Gln Glu Leu Gln
 20 25 30
 Glu Lys Leu Glu Lys Ala Val Lys Ala Ser Thr Glu Ala Thr Glu Leu
 35 40 45
 5 Leu Gln Asn Ile Arg Gln Ala Lys Glu Arg Ala Glu Arg Glu Leu Glu
 50 55 60
 Lys Leu Gln Asn Arg Glu Asp Ser Ser Glu Gly Ile Arg Lys Lys Leu
 65 70 75 80
 Val Glu Ala Glu Glu Arg Arg His Ser Leu Glu Asn Lys Val Lys Arg
 85 90 95
 10 Leu Glu Thr Met Glu Arg Arg Glu Asn Arg Leu Lys Asp Asp Ile Gln
 100 105 110
 Thr Lys Ser Gln Gln Ile Gln Gln Met Ala Asp Lys Ile Leu Glu Leu
 115 120 125
 15 Glu Glu Lys His Arg Glu Ala Gln Val Ser Ala Gln His Leu Glu Val
 130 135 140
 His Leu Lys Gln Lys Glu Gln His Tyr Glu Glu Lys Ile Lys Val Leu
 145 150 155 160
 Asp Asn Gln Ile Lys Lys Asp Leu Ala Asp Lys Glu Thr Leu Glu Asn
 165 170 175
 20 Met Met Gln Arg His Glu Glu Glu Ala His Glu Lys Gly Lys Ile Leu
 180 185 190
 Ser Glu Gln Lys Ala Met Ile Asn Ala Met Asp Ser Lys Ile Arg Ser
 195 200 205
 25 Leu Glu Gln Xaa Ile Val Glu Leu Ser Glu Ala Asn Lys Leu Ala Ala
 210 215 220
 Lys
 225

 30 <210> 792
 <211> 129
 <212> PRT
 <213> Homo sapiens

 35 <400> 792
 Asn Ala Lys Thr Glu Arg Pro Ile Phe Xaa Asp Leu Ser Lys Tyr Trp
 1 5 10 15
 Gly Pro Arg Xaa Lys Thr Ser Ala Asn Ile Gln Ser Asn Leu Pro Trp
 20 25 30
 40 Gly Arg Glu Gly Arg Glu Tyr Asp Pro Thr Asp Ser Lys Gln His Ile
 35 40 45
 Lys Arg His Ser Arg Thr Phe Ala Lys Gly Ala Thr Thr Trp Arg Phe
 50 55 60
 Val Gly Val Ser Asn Lys Lys Ala Leu Arg Leu Lys His Xaa Xaa Glu
 65 70 75 80
 45 Gly Ala Gly Met Gln Ala Arg Leu Gln Ser Gly Lys Gly Ser Glu Leu
 85 90 95
 Xaa Thr Gln Leu Lys Thr Arg Ser Cys Ser Pro Ala Xaa Gly Glu Thr
 100 105 110
 50 Gly Leu Pro Leu Ser Leu Pro Lys Arg Cys Leu Gly Leu Leu Arg Arg
 115 120 125
 Ala

 55 <210> 793
 <211> 92
 <212> PRT
 <213> Homo sapiens

 60 <400> 793
 Glu Tyr Lys Val Ser Cys Lys Tyr Val Gln Ser Phe Glu Leu Val Leu
 1 5 10 15
 Xaa Ser Arg Lys Gln Phe Thr Asp Xaa Thr His Asn Ile His Phe Gln

20 25 30
 Gly Ser Arg Ser Pro Phe Leu Met Glu Ile Leu Asn Glu Met Pro Arg
 35 40 45
 5 Leu Lys Asp Pro Phe Ser Xaa Thr Phe Pro Asn Thr Gly Asp Gln Xaa
 50 55 60
 Thr Lys Leu Gln Gln Thr Phe Asn Gln Ile Cys Pro Gly Asp Gly Arg
 65 70 75 80
 Gly Gly Ser Thr Thr Pro Gln Thr Pro Ser Asn Thr
 85 90
 10
 <210> 794
 <211> 219
 <212> PRT
 <213> Homo sapiens
 15
 <400> 794
 Ser Ala Met Ser Ser Asp Arg Met Asp Cys Gly Arg Lys Val Arg Val
 1 5 10 15
 20 Glu Ser Gly Tyr Phe Ser Leu Glu Lys Thr Lys Gln Asp Leu Lys Ala
 20 25 30
 Glu Glu Gln Gln Leu Pro Pro Pro Leu Ser Pro Pro Ser Pro Ser Thr
 35 40 45
 Pro Asn His Arg Arg Ser Gln Val Ile Glu Lys Phe Glu Ala Leu Asp
 50 55 60
 25 Ile Glu Lys Ala Glu His Met Glu Thr Asn Ala Val Gly Pro Ser Gln
 65 70 75 80
 Ser Ser Asp Thr Arg Gln Gly Arg Ser Glu Lys Arg Ala Phe Pro Arg
 85 90 95
 30 Lys Arg Asp Phe Thr Asn Glu Ala Pro Pro Ala Pro Leu Pro Asp Ala
 100 105 110
 Ser Ala Ser Pro Leu Ser Pro His Arg Arg Ala Lys Ser Leu Asp Arg
 115 120 125
 Arg Ser Thr Glu Pro Ser Val Thr Pro Asp Leu Leu Asn Phe Lys Lys
 130 135 140
 35 Gly Trp Leu Thr Lys Gln Tyr Glu Asp Gly Gln Trp Lys Lys His Trp
 145 150 155 160
 Phe Val Leu Ala Asp Gln Ser Leu Arg Tyr Tyr Arg Asp Ser Val Ala
 165 170 175
 40 Glu Glu Ala Ala Asp Leu Asp Gly Glu Ile Asp Leu Ser Ala Cys Tyr
 180 185 190
 Asp Val Thr Glu Tyr Pro Val Gln Xaa Lys Leu Trp Leu Pro Asp Thr
 195 200 205
 Tyr Lys Gly Gly Arg Ser Leu Pro Leu Ser Pro
 210 215
 45
 <210> 795
 <211> 77
 <212> PRT
 <213> Homo sapiens
 50
 <400> 795
 Arg Gln Gln Glu Val Asn Thr Ala Glu Ser Gly Val Asp Asn Pro Xaa
 1 5 10 15
 55 Ala Ser Xaa Thr His Xaa Met Pro Thr Val Asn Asp Asp His Asn Arg
 20 25 30
 Asn Xaa Asn Asn Asn Asn Lys Thr Lys Val Gln Val Lys Asn Xaa Ala
 35 40 45
 Trp Gly Val Leu Leu Gln Xaa Trp Gly Lys Arg Val Leu Asn Phe Gly
 50 55 60
 60 Trp Asp Thr Pr Ser Leu Ser Ser Ser Pro Trp Ile Lys
 65 70 75
 <210> 796

<211> 99
 <212> PRT
 <213> Homo sapiens

5 <400> 796
 Leu Ile Gln Gly Leu Glu Glu Arg Leu Gly Val Ser His Pro Lys Leu
 1 5 10 15
 Ser Thr Arg Phe Pro Gln Xaa Cys Ser Ser Thr Pro Gln Ala Xaa Phe
 20 25 30
 10 Phe Thr Trp Thr Phe Val Leu Leu Leu Leu Leu Xaa Leu Arg Leu Trp
 35 40 45
 Ser Ser Leu Thr Val Gly Met Xaa Cys Xaa Arg Leu Ala Xaa Gly Leu
 50 55 60
 Ser Thr Pro Leu Ser Ala Val Leu Thr Ser Cys Cys Leu His Gln Ser
 15 65 70 75 80
 Phe Phe Pro Trp Tyr Ser Lys Ile Arg Pro Xaa Val Gly Val Gly Gly
 85 90 95
 His Leu Cys

20 <210> 797
 <211> 138
 <212> PRT
 <213> Homo sapiens

25 <400> 797
 Ile His Thr Tyr Ile His Thr Tyr Ile His Thr Tyr Ile His Thr Ser
 1 5 10 15
 30 Ile His Ala Tyr Arg Tyr Thr Arg Lys Lys Arg Lys Glu Lys Lys
 20 25 30
 Glu Lys Met Lys Glu Lys Ala Leu Tyr Cys Tyr Trp Ala Arg Ala Phe
 35 40 45
 Ser Leu Ser Val Ser Leu Cys Ser Ser Leu Ser Phe Ser Leu Cys Leu
 50 55 60
 35 Phe Leu Cys Leu Ser Val Ser Phe Phe Leu Ser Val Ser Val Ser Val
 65 70 75 80
 Phe Val Ser Leu Ser Pro Ser Leu Pro Val Ser Leu Cys Leu Ser Ser
 85 90 95
 40 Val Ser Leu Cys Leu Ser Met Ser Phe Ser Val Cys Leu Phe Leu Cys
 100 105 110
 Leu Ser Ala Ser Leu Phe Leu Phe Leu Cys Leu Ser Val Gly Leu Ser
 115 120 125
 Leu Ser Val Cys Leu Ser Val Ser Leu Ser
 130 135

45 <210> 798
 <211> 103
 <212> PRT
 <213> Homo sapiens

50 <400> 798
 Lys Lys Arg His Cys Ile Ala Thr Gly Leu Gly Pro Ser Leu Cys Leu
 1 5 10 15
 55 Phe Leu Ser Val Arg Leu Cys Leu Ser Leu Cys Val Ser Phe Ser Val
 20 25 30
 Cys Leu Ser Leu Ser Phe Ser Leu Ser Leu Ser Leu Ser Leu Ser Leu
 35 40 45
 Ser Leu Pro Leu Cys Leu Ser His Cys Val Cys Leu Leu Ser Leu Ser
 50 55 60
 60 Val Cys Leu Cys Leu Ser Leu Ser Val Ser Phe Ser Val Cys Leu Pro
 65 70 75 80
 Leu Ser Phe Phe Phe Cys Val Ser Leu Ser Val Ser Leu Ser Leu Ser
 85 90 95

Val Cys Leu Ser Leu Ser Leu
100

5 <210> 799
<211> 95
<212> PRT
<213> Homo sapiens

<400> 799
10 Glu Arg Glu Thr Asp Arg Gln Thr Glu Arg Glu Arg Pro Thr Glu Arg
1 5 10 15
His Arg Lys Arg Lys Arg Glu Ala Asp Arg Gln Arg Lys Arg Gln Thr
20 25 30
15 Glu Lys Asp Ile Asp Arg Gln Arg Glu Thr Glu Asp Arg His Ser Glu
35 40 45
Thr Gly Arg Glu Gly Glu Arg Glu Thr Lys Thr Glu Thr Glu Thr Glu
50 55 60
Arg Lys Lys Glu Thr Asp Arg Gln Arg Lys Arg His Arg Glu Lys Asp
65 70 75 80
20 Arg Asp Glu Gln Arg Glu Thr Asp Arg Glu Lys Ala Leu Ala Gln
85 90 95

25 <210> 800
<211> 100
<212> PRT
<213> Homo sapiens

<400> 800
30 Asp Arg Gln Arg Gly Arg Glu Arg Asp Lys Asp Arg Asp Arg Asp Arg
1 5 10 15
Glu Lys Glu Arg Asp Arg Gln Thr Glu Lys Glu Thr Gln Arg Glu Arg
20 25 30
Gln Arg Arg Thr Glu Arg Asn Arg Gln Arg Glu Gly Pro Ser Pro Val
35 40 45
Ala Ile Gln Cys Leu Phe Phe His Phe Leu Phe Leu Phe Phe Ser Phe
50 55 60
Phe Leu Ser Cys Ile Ser Val Cys Met Asp Gly Cys Met Tyr Val Cys
65 70 75 80
Met Tyr Val Cys Met Tyr Val Cys Val Tyr Leu Phe Met Tyr Val Phe
40 85 90 95
Ile Trp Arg Pro
100

45 <210> 801
<211> 185
<212> PRT
<213> Homo sapiens

<400> 801
50 Thr Val Gly Thr Ala Met Ala Pro Val Leu Ser Lys Asp Ser Ala Asp
1 5 10 15
Ile Glu Ser Ile Leu Ala Leu Asn Pro Arg Thr Gln Thr His Ala Thr
20 25 30
Leu Cys Ser Thr Ser Ala Lys Lys Leu Asp Lys Lys His Trp Lys Arg
55 35 40 45
Asn Pro Asp Lys Asn Cys Phe Asn Cys Glu Lys Leu Glu Asn Asn Phe
50 55 60
Asp Asp Ile Lys His Thr Thr Leu Gly Glu Arg Gly Ala Leu Arg Glu
65 70 75 80
60 Ala Met Arg Cys Leu Lys Cys Ala Asp Ala Pro Cys Gln Lys Ser Cys
85 90 95
Pro Thr Asn Leu Asp Ile Lys Ser Phe Ile Thr Ser Ile Ala Asn Lys
100 105 110

Asn Tyr Tyr Gly Ala Ala Lys Met Ile Phe Ser Asp Asn Pro Leu Gly
 115 120 125
 Leu Thr Cys Gly Met Val Cys Pro Thr Ser Asp Leu Cys Val Gly Gly
 130 135 140
 5 Cys Asn Leu Tyr Ala Thr Glu Glu Gly Pro Ile Asn Ile Gly Gly Leu
 145 150 155 160
 Gln Gln Phe Ala Thr Glu Val Cys Met Ile Tyr Thr Val Thr Ser Pro
 165 170 175
 10 His Tyr His His His Ala Gln Ile Ser
 180 185

<210> 802

<211> 155

<212> PRT

15 <213> Homo sapiens

<400> 802

Asp Tyr Arg Xaa Ile Glu Ile Thr Ile Cys Lys Asn Asp Glu Cys Val
 1 5 10 15
 20 Leu Glu Asp Asn Ser Gln Arg Thr Lys Trp Lys Val Ile Ser Pro Thr
 20 25 30
 Gly Asn Glu Ala Xaa Val Pro Xaa Val Cys Phe Leu Ile Pro Pro Pro
 35 40 45
 25 Asn Lys Asp Ala Ile Xaa Met Ala Ser Arg Val Glu Gln Ser Tyr Xaa
 50 55 60
 Lys Val Met Ala Leu Trp His Gln Leu His Val Asn Thr Lys Ser Leu
 65 70 75 80
 Xaa Ser Trp Asn Tyr Leu Arg Lys Asp Leu Asp Leu Val Gln Thr Trp
 85 90 95
 30 Asn Leu Glu Lys Leu Arg Ser Ser Ala Pro Gly Glu Cys His Gln Ile
 100 105 110
 Met Xaa Asn Leu Gln Ala His Tyr Glu Asp Phe Xaa Gln Asp Ser Arg
 115 120 125
 35 Asp Ser Val Leu Val Ser Val Ala Asp Arg Leu Arg Leu Glu Glu Glu
 130 135 140
 Xaa Glu Ala Cys Lys Ala Arg Phe Gln His Leu
 145 150 155

<210> 803

40 <211> 200

<212> PRT

<213> Homo sapiens

<400> 803

45 Arg Gly Asn Xaa Gln Gly Lys Ala Xaa Ser Ser Glu Thr Lys Glu Ser
 1 5 10 15
 Thr Asp Ile Glu Lys Ala Ile Leu Glu Gln Gln Val Leu Ser Glu Glu
 20 25 30
 50 Leu Thr Thr Lys Lys Glu Gln Val Phe Glu Ala Ile Lys Thr Ser Gln
 35 40 45
 Ile Phe Leu Ala Lys His Gly His Lys Leu Ser Glu Lys Glu Lys Lys
 50 55 60
 Gln Ile Ser Glu Gln Leu Asn Ala Leu Asn Lys Ala Tyr His Asp Leu
 65 70 75 80
 55 Cys Asp Gly Ser Ala Asn Gln Leu Gln Gln Leu Gln Ser Gln Leu Ala
 85 90 95
 His Gln Thr Glu Gln Lys Glu Cys Arg Ala Val Ala Gly Val Ile Asp
 100 105 110
 60 Leu Gly Thr Val Glu Ile Phe Pr Ile Phe Lys Ala Met Gln Lys Gly
 115 120 125
 Leu Leu Asp Gln Asp Thr Gly Leu Val Leu Leu Glu Ser Gln Val Ile
 130 135 140
 Met Ser Gly Leu Ile Ala Pro Glu Thr Gly Glu Asn Leu Ser Leu Glu

145 150 155 160
 Glu Gly Val Ala Arg Asn Leu Ile Asn Pro Gln Met Tyr Gln Gln Leu
 165 170 175
 Arg Glu Leu Gln Asp Ala Leu Ala Leu Il Ser Arg Leu Thr Glu Ser
 5 180 185 190
 Arg Gly Pro Leu Ser Val Val Glu
 195 200

 <210> 804
 10 <211> 204
 <212> PRT
 <213> Homo sapiens

 <400> 804
 15 Ala Val Glu Gly Arg Arg Val Gln Ala Leu Glu Glu Val Leu Gly Asp
 1 5 10 15
 Leu Arg Ala Glu Ser Arg Glu Gln Glu Lys Ala Leu Leu Ala Leu Gln
 20 25 30
 Gln Gln Cys Ala Glu Gln Ala Gln Glu His Glu Val Glu Thr Arg Ala
 20 35 40 45
 Leu Gln Asp Ser Trp Leu Gln Ala Gln Ala Val Leu Lys Glu Arg Asp
 50 55 60
 Gln Glu Leu Glu Ala Leu Arg Ala Glu Ser Gln Ser Ser Arg His Gln
 65 70 75 80
 25 Glu Glu Ala Ala Arg Ala Arg Ala Glu Ala Leu Gln Glu Ala Leu Gly
 85 90 95
 Lys Ala His Ala Ala Leu Gln Gly Lys Glu Gln His Leu Leu Glu Gln
 100 105 110
 Ala Glu Leu Ser Arg Ser Leu Glu Ala Ser Thr Ala Thr Leu Gln Ala
 30 115 120 125
 Ser Leu Asp Ala Cys Gln Ala His Ser Arg Gln Leu Glu Glu Ala Leu
 130 135 140
 Arg Ile Gln Glu Gly Glu Ile Gln Asp Gln Asp Leu Arg Tyr Gln Glu
 145 150 155 160
 35 Asp Val Gln Gln Leu Gln Gln Ala Leu Ala Gln Arg Asp Glu Glu Leu
 165 170 175
 Arg His Gln Xaa Gly Thr Gly Ala Ser Cys Trp Lys Lys Ser Phe Gly
 180 185 190
 Pro Lys Gly Xaa Lys Lys Asn Met Ile Gln Glu Glu
 40 195 200

 <210> 805
 <211> 187
 <212> PRT
 45 <213> Homo sapiens

 <400> 805
 Phe Phe Leu Asp His Ile Leu Leu Xaa Pro Phe Trp Ala Lys Arg Leu
 1 5 10 15
 50 Phe Pro Ala Ala Cys Ser Arg Ser Xaa Leu Met Ser Gln Leu Phe Ile
 20 25 30
 Pro Leu Gly Lys Cys Leu Leu Gln Leu Leu His Ile Leu Leu Val Ser
 35 40 45
 Glu Ile Leu Val Leu Asp Leu Thr Phe Leu Tyr Pro Gln Ser Leu Leu
 55 50 55 60
 Gln Leu Pro Thr Val Cys Leu Ala Gly Ile Gln Gly Gly Leu Gln Gly
 65 70 75 80
 Cys Ser Ala Gly Leu Gln Thr Ala Ala Gln Phe Cys Leu Leu Glu Glu
 85 90 95
 60 Met Leu Leu Phe Pro Leu Gln Gly Ser Met Ser Leu Ala Lys Gly Leu
 100 105 110
 Leu Gln Ser Leu Ser Pro Gly Pro Gly Ser Leu Leu Leu Met Pro Gly
 115 120 125

Gly Leu Thr Phe Cys Pro Gln Ser Phe Gln Leu Leu Val Pro Phe Leu
 130 135 140
 Glu His Cys Leu Gly Leu Gln Pro Ala Val Leu Gln Gly Pro Gly Leu
 145 150 155 160
 5 His Leu Met Leu Leu Cys Leu Leu Ser Thr Leu Leu Leu Glu Gly Gln
 165 170 175
 Gln Ser Phe Leu Leu Leu Pro Arg Leu Ser Pro
 180 185
 10 <210> 806
 <211> 105
 <212> PRT
 <213> Homo sapiens
 15 <400> 806
 Asp Lys Lys Asn Ser Arg Trp Pro Ser Val Gly Leu Lys Leu Gln Lys
 1 5 10 15
 Xaa Arg Trp Ser Cys Cys Lys Ala Gln Leu Thr Leu Glu Arg Lys Gln
 20 25 30
 Lys Gln Asp Tyr Ile Thr Arg Ser Ala Gln Thr Ser Arg Glu Leu Ala
 35 40 45
 Gly Leu His His Ser Leu Ser His Ser Leu Leu Ala Val Ala Gln Ala
 50 55 60
 Pro Glu Ala Thr Val Leu Glu Ala Glu Thr Arg Arg Leu Asp Glu Ser
 25 65 70 75 80
 Leu Thr Gln Ser Leu Thr Ser Pro Gly Pro Val Leu Leu His Pro Ser
 85 90 95
 Pro Ser Thr Thr Gln Ala Ala Ser Arg
 100 105
 30 <210> 807
 <211> 256
 <212> PRT
 <213> Homo sapiens
 35 <400> 807
 Phe Glu Lys Asp Ala Asp Ser Ser Glu Arg Ile Ile Ala Pro Met Arg
 1 5 10 15
 Trp Gly Leu Val Pro Ser Trp Phe Lys Glu Ser Asp Pro Ser Lys Leu
 40 20 25 30
 Gln Phe Asn Thr Thr Asn Cys Arg Ser Asp Thr Val Met Glu Lys Arg
 35 40 45
 Ser Phe Lys Val Pro Leu Gly Lys Gly Arg Arg Cys Val Val Leu Ala
 50 55 60
 Asp Gly Phe Tyr Glu Trp Gln Arg Cys Gln Gly Thr Asn Gln Arg Gln
 45 65 70 75 80
 Pro Tyr Phe Ile Tyr Phe Pro Gln Ile Lys Thr Glu Lys Ser Gly Ser
 85 90 95
 Ile Gly Ala Ala Asp Ser Pro Glu Asn Trp Glu Lys Val Trp Asp Asn
 50 100 105 110
 Trp Arg Leu Leu Thr Met Ala Gly Ile Phe Asp Cys Trp Glu Pro Pro
 115 120 125
 Glu Gly Gly Asp Val Leu Tyr Ser Tyr Thr Ile Ile Thr Val Asp Ser
 130 135 140
 55 Cys Lys Gly Leu Ser Asp Ile His His Arg Met Pro Ala Ile Leu Asp
 145 150 155 160
 Gly Glu Glu Ala Val Ser Lys Trp Leu Asp Phe Gly Glu Val Ser Thr
 165 170 175
 Xaa Glu Ala Leu Lys Leu Ile His Pro Thr Glu Asn Ile Thr Phe His
 60 180 185 190
 Ala Val Ser Ser Val Xaa Asn Asn Ser Arg Asn Asn Thr Ser Glu Cys
 195 200 205
 Leu Ala Xaa Val Asp Leu Val Val Lys Xaa Glu Leu Lys Ala Ser Gly

210 215 220
 Asn Xaa Pro Lys Asp Val Ala Met Gly Trp Xaa Gln Ser Xaa Pro Lys
 225 230 235 240
 Lys Glu Asp Ser Lys Thr Leu Gln Lys Glu Lys Val Arg Cys Xaa Pro
 5 245 250 255

 <210> 808
 <211> 88
 <212> PRT
 10 <213> Homo sapiens

 <400> 808
 Lys Ser Glu Arg Ala Gln Trp Leu Ser Arg Lys Gln Leu Thr Thr Arg
 1 5 10 15
 15 Ser Thr Arg Ser Gly Gln Arg Leu Pro Ser Trp Val Arg His Ala Leu
 20 25 30
 Arg Glu Asp Ser Thr Ser Pro Ala Arg Lys Gly Gln Gln Ala Gln Cys
 35 40 45
 20 Pro Tyr Gly Ala His Met Ala Gly Asn Ser Ser Arg Thr Pro Leu Pro
 50 55 60
 Lys Leu Ser Thr Ser Pro Thr Arg Gly Ser Tyr Ser Trp Gln Lys Arg
 65 70 75 80
 Leu His Glu Pro Thr Thr Val Asn
 85
 25
 <210> 809
 <211> 96
 <212> PRT
 30 <213> Homo sapiens

 <400> 809
 Gly Lys Thr Pro Pro Ala Leu Pro Gly Lys Gly Ser Arg Arg Ser Ala
 1 5 10 15
 35 Pro Met Gly Pro Thr Trp Leu Val Thr Ala Ala Gly His Leu Phe Gln
 20 25 30
 Ser Cys Pro Pro Ala Pro Leu Gly Ala Pro Thr His Gly Lys Lys Asp
 35 40 45
 Tyr Met Ser Pro Gln Leu Ser Thr Asn Thr Val Pro Pro Pro Pro Lys
 50 55 60
 40 Ala Asn Thr Tyr Thr Tyr Asn Val Lys Asn Leu Leu Ser Glu Gln Gln
 65 70 75 80
 Cys Ser Arg Pro Trp Pro Trp Ser Leu Lys Val Leu Cys His Trp Leu
 85 90 95
 45
 <210> 810
 <211> 178
 <212> PRT
 <213> Homo sapiens

 50 <400> 810
 Gln Ser Asn Ser Pro Val Leu Leu Ser Arg Leu His Phe Glu Lys Asp
 1 5 10 15
 Ala Asp Ser Ser Glu Arg Ile Ile Ala Pro Met Arg Trp Gly Leu Val
 20 25 30
 55 Pro Ser Trp Phe Lys Glu Ser Asp Pro Ser Lys Leu Gln Phe Asn Thr
 35 40 45
 Thr Asn Cys Arg Ser Asp Thr Val Met Glu Lys Arg Ser Phe Lys Val
 50 55 60
 60 Pr Leu Gly Lys Gly Arg Arg Cys Val Val Leu Ala Asp Gly Phe Tyr
 65 70 75 80
 Glu Trp Gln Arg Cys Gln Gly Thr Asn Gln Arg Gln Pro Tyr Phe Ile
 85 90 95
 Tyr Phe Pro Gln Ile Lys Thr Glu Lys Ser Gly Ser Ile Gly Ala Ala

100 105 110
 Asp Ser Pro Glu Asn Trp Glu Lys Val Trp Asp Asn Trp Arg Leu Leu
 115 120 125
 5 Thr Met Ala Gly Ile Phe Asp Cys Trp Glu Pro Pro Glu Gly Gly Asp
 130 135 140
 Val Leu Tyr Ser Tyr Thr Ile Ile Thr Val Asp Ser Cys Lys Gly Leu
 145 150 155 160
 Ser Asp Ile His His Arg Met Pro Ala Ile Leu Asp Gly Glu Glu Ala
 165 170 175
 10 Ser Phe

<210> 811
 <211> 294
 15 <212> PRT
 <213> Homo sapiens

<400> 811
 20 Arg Met Cys Gly Arg Thr Ser Cys His Leu Pro Arg Asp Val Leu Thr
 1 5 10 15
 Arg Ala Cys Ala Tyr Gln Asp Arg Arg Gly Gln Gln Arg Leu Pro Glu
 20 25 30
 Trp Arg Asp Pro Asp Lys Tyr Cys Pro Ser Tyr Asn Lys Ser Pro Gln
 35 40 45
 25 Ser Asn Ser Pro Val Leu Leu Ser Arg Leu His Phe Glu Lys Asp Ala
 50 55 60
 Asp Ser Ser Glu Arg Ile Ile Ala Pro Met Arg Trp Gly Leu Val Pro
 65 70 75 80
 30 Ser Trp Phe Lys Glu Ser Asp Pro Ser Lys Leu Gln Phe Asn Thr Thr
 85 90 95
 Asn Cys Arg Ser Asp Thr Val Met Glu Lys Arg Ser Phe Lys Val Pro
 100 105 110
 Leu Gly Lys Gly Arg Arg Cys Val Val Leu Ala Asp Gly Phe Tyr Glu
 115 120 125
 35 Trp Gln Arg Cys Gln Gly Thr Asn Gln Arg Gln Pro Tyr Phe Ile Tyr
 130 135 140
 Phe Pro Gln Ile Lys Thr Glu Lys Ser Gly Ser Ile Gly Ala Ala Asp
 145 150 155 160
 Ser Pro Glu Asn Trp Glu Lys Val Trp Asp Asn Trp Arg Leu Leu Thr
 165 170 175
 40 Met Ala Gly Ile Phe Asp Cys Trp Glu Pro Pro Glu Gly Gly Asp Val
 180 185 190
 Leu Tyr Ser Tyr Thr Ile Ile Thr Val Asp Ser Cys Lys Gly Leu Ser
 195 200 205
 45 Asp Ile His His Xaa Met Pro Ala His Ile Xaa Met Glu Lys Glu Ala
 210 215 220
 Val Ser Lys Met Ala Trp Thr Leu Val Lys Val Phe Asn Leu Arg Lys
 225 230 235 240
 Leu Leu Lys Phe Asn Pro Pro Asn Lys Arg Lys Phe Thr Phe Pro Cys
 245 250 255
 50 Gln Xaa Phe Xaa Gly Gly Thr Asn Leu Arg Lys Gln His Phe Pro Glu
 260 265 270
 Trp Phe Gly Phe Leu Ser Thr Leu Gly Gly Xaa Lys Xaa Asn Leu Xaa
 275 280 285
 55 Ala Lys Trp Glu Xaa Pro
 290

<210> 812
 <211> 96
 60 <212> PRT
 <213> Homo sapiens

<400> 812

Gly Lys Thr Pro Pro Ala Leu Pro Gly Lys Gly Ser Arg Arg Ser Ala
 1 5 10 15
 Pro Met Gly Pro Thr Trp Leu Val Thr Ala Ala Gly His Leu Phe Gln
 20 25 30
 5 Ser Cys Pro Pro Ala Pro Leu Gly Ala Pro Thr His Gly Lys Lys Asp
 35 40 45
 Tyr Met Ser Pro Gln Leu Ser Thr Asn Thr Xaa Pro Pro Pro Lys
 50 55 60
 10 Ala Asn Thr Tyr Thr Tyr Asn Val Lys Asn Leu Leu Ser Glu Gln Gln
 65 70 75 80
 Cys Ser Arg Pro Trp Pro Trp Ser Leu Lys Val Leu Cys His Trp Leu
 85 90 95

15 <210> 813
 <211> 235
 <212> PRT
 <213> Homo sapiens

<400> 813
 20 Ala Val Ser Val Ser Cys Ile Thr Tyr Leu Arg Gly Ile Phe Pro Glu
 1 5 10 15
 Cys Ala Tyr Gly Thr Arg Tyr Leu Asp Asp Leu Cys Val Lys Ile Leu
 20 25 30
 25 Arg Glu Asp Lys Asn Cys Pro Gly Ser Thr Gln Leu Val Lys Trp Met
 35 40 45
 Leu Gly Cys Tyr Asp Ala Leu Gln Lys Lys Tyr Leu Arg Met Val Val
 50 55 60
 Leu Ala Val Tyr Thr Asn Pro Glu Asp Pro Gln Thr Ile Ser Glu Cys
 65 70 75 80
 30 Tyr Gln Phe Lys Phe Lys Tyr Thr Asn Asn Gly Pro Leu Met Asp Phe
 85 90 95
 Ile Ser Lys Asn Gln Ser Asn Glu Ser Ser Met Leu Ser Thr Asp Thr
 100 105 110
 35 Lys Lys Ala Ser Ile Leu Leu Ile Arg Lys Ile Tyr Ile Leu Met Gln
 115 120 125
 Asn Leu Gly Pro Leu Pro Asn Asp Val Cys Leu Thr Met Lys Leu Phe
 130 135 140
 Tyr Tyr Asp Glu Val Thr Pro Pro Asp Tyr Gln Pro Pro Gly Phe Lys
 145 150 155 160
 40 Asp Gly Asp Cys Glu Gly Val Ile Phe Glu Gly Glu Pro Met Tyr Leu
 165 170 175
 Asn Val Gly Glu Val Ser Thr Pro Phe His Ile Phe Lys Val Lys Val
 180 185 190
 45 Thr Thr Glu Arg Glu Arg Met Glu Asn Ile Asp Ser Thr Xaa Leu Ser
 195 200 205
 Pro Lys Gln Ile Lys Thr Pro Phe Gln Lys Ile Leu Arg Asp Lys Asp
 210 215 220
 Val Xaa Xaa Glu Gln Asp Xaa Tyr Ile Ser Gly
 225 230 235

50 <210> 814
 <211> 59
 <212> PRT
 <213> Homo sapiens

55 <400> 814
 Leu Asn Asn Ile Leu Phe Met Leu Gln Lys Met Pro Tyr Phe Lys Asn
 1 5 10 15
 60 Gln Ser Phe Cys Pro Val Lys Lys Ser Ile Val Lys Val Lys His Gln
 20 25 30
 Phe Leu Asn Cys Thr Leu Tyr Ile Lys Met Leu Ile His Tyr Val Lys
 35 40 45
 Ile Leu Lys Asn Ile Val Leu Ile Thr Ala Gln

50

55

5 <210> 815
 <211> 148
 <212> PRT
 <213> Homo sapiens

<400> 815
 10 Leu Cys Leu Val Tyr Val Tyr Met Pro Asn Gly Ser Leu Leu Asp Arg
 1 5 10 15
 Leu Ser Cys Leu Asp Gly Thr Pro Pro Leu Ser Trp His Met Arg Cys
 20 25 30
 Lys Ile Ala Gln Gly Ala Ala Asn Gly Ile Asn Phe Leu His Glu Asn
 35 40 45
 15 His His Ile His Arg Asp Ile Lys Ser Ala Asn Ile Leu Leu Asp Glu
 50 55 60
 Ala Phe Thr Ala Lys Ile Ser Asp Phe Gly Leu Ala Arg Ala Ser Glu
 65 70 75 80
 20 Lys Phe Ala Gln Thr Val Met Thr Ser Arg Ile Val Gly Thr Thr Ala
 85 90 95
 Tyr Met Ala Pro Glu Ala Leu Arg Gly Glu Ile Thr Pro Lys Ser Asp
 100 105 110
 Ile Tyr Ser Phe Gly Val Val Leu Leu Glu Ile Ile Thr Gly Leu Pro
 115 120 125
 25 Ala Val Asp Glu His Arg Glu Pro Gln Leu Leu Leu Asp Ile Lys Arg
 130 135 140
 Arg Asn Xaa Arg
 145

30 <210> 816
 <211> 77
 <212> PRT
 <213> Homo sapiens

35 <400> 816
 Asn Val Thr His Leu Phe Ile Tyr Leu Phe Met Met Glu Ser His Ser
 1 5 10 15
 Val Thr Gln Ala Gly Val Gln Trp His Asp Leu Ser Ser Leu Gln Pro
 20 25 30
 40 Leu Pro Pro Trp Phe Gln Leu Val Ser Cys Leu Ser Leu Pro Ser Ser
 35 40 45
 Trp Asp Tyr Arg Cys Pro Pro Pro Arg Ser Ser Asn Phe Cys Ile Phe
 50 55 60
 Ser Lys Asp Gly Val Ser Pro Cys Trp Pro Gly Arg Ser
 45 65 70 75

50 <210> 817
 <211> 83
 <212> PRT
 <213> Homo sapiens

<400> 817
 55 Ser Pro Ala Ser Ala Ser Gln Val Ala Gly Thr Thr Gly Val His His
 1 5 10 15
 His Ala Arg Leu Ile Phe Val Phe Leu Val Lys Thr Gly Phe His His
 20 25 30
 Val Gly Gln Ala Gly Leu Glu Leu Leu Thr Ser Gly Asp Leu Pro Ala
 35 40 45
 60 Ser Ala Ser Gln Ser Ala Gly Ile Tyr Arg Tyr Glu Pro Pro His Pro
 50 55 60
 Ala Asn Val Thr His Tyr Leu Thr Val Leu Tyr Ile Arg Ser Pro Ala
 65 70 75 80
 Gln Asn Arg

5 <210> 818
 <211> 169
 <212> PRT
 <213> Homo sapiens

 <400> 818
 10 Lys Glu Gln Arg Lys Glu Asn Glu Pro Glu Ala Glu Lys Thr His Leu
 1 5 10 15
 Phe Ala Lys Gln Glu Lys Ala Phe Tyr Pro Lys Ser Phe Lys Ser Lys
 20 25 30
 Lys Gln Lys Pro Ser Arg Val Leu Tyr Ser Ser Thr Glu Ser Ser Asp
 35 40 45
 15 Glu Glu Ala Leu Gln Asn Lys Lys Ile Ser Thr Ser Cys Ser Val Ile
 50 55 60
 Pro Glu Thr Ser Asn Ser Asp Met Gln Thr Lys Lys Glu Tyr Val Val
 65 70 75 80
 Ser Gly Glu His Lys Gln Lys Gly Lys Val Lys Arg Lys Leu Lys Asn
 85 90 95
 20 Gln Asn Lys Asn Lys Glu Asn Gln Glu Leu Lys Gln Glu Lys Glu Gly
 100 105 110
 Lys Glu Asn Thr Arg Ile Thr Asn Leu Thr Val Asn Thr Gly Leu Asp
 115 120 125
 25 Cys Ser Glu Lys Thr Arg Glu Glu Gly Asn Phe Arg Lys Ser Phe Ser
 130 135 140
 Pro Lys Asp Asp Thr Ser Leu His Leu Phe His Ile Ser Thr Gly Lys
 145 150 155 160
 Ser Pro Lys His Ser Cys Gly Leu Lys
 30 165

35 <210> 819
 <211> 139
 <212> PRT
 <213> Homo sapiens

 <400> 819
 40 Ala Phe Leu Phe Pro Ser Xaa Tyr Ala Ser Ile Tyr Val Phe Leu Met
 1 5 10 15
 Xaa Tyr Leu Xaa Tyr Pro Phe Phe Ser Xaa Gly Asn Leu Asn Phe Gln
 20 25 30
 Met Xaa Asp Tyr Asp Leu His Pro Leu Phe Trp His Leu Ile Phe His
 35 40 45
 45 Gln Ile Leu Xaa Gly Asn Leu Ser Asp Val Xaa Phe Phe Pro Tyr Ala
 50 55 60
 Tyr Xaa Ile Leu Xaa Leu Asn Phe Xaa Ala Xaa Ile Gln Ile Leu Xaa
 65 70 75 80
 Tyr His Xaa Xaa Gln Xaa Gln Ala Val Met Thr Phe Gln Asn Phe Leu
 85 90 95
 50 Gly Ile Asn Met Phe Xaa Tyr Val Leu Xaa Leu Gly Gly Xaa Thr Xaa
 100 105 110
 Phe His Leu Ile Xaa Xaa Asn Val Trp Xaa Ile Tyr Xaa Xaa Lys Tyr
 115 120 125
 55 Glu Ile Asn Val Met Lys Xaa His Xaa Leu Gly
 130 135

60 <210> 820
 <211> 168
 <212> PRT
 <213> Homo sapiens

 <400> 820
 Pro Arg Xaa Pro Thr Leu Pro Val Asn Thr Xaa Xaa Asp Cys Ser Glu

1 5 10 15
 Lys Thr Arg Glu Glu Gly Asn Phe Arg Lys Xaa Phe Ser Pro Lys Xaa
 20 25 30
 Xaa Thr Ser Leu His Leu Phe His Ile Ser Xaa Gly Lys Xaa Pro Lys
 35 40 45
 5 His Xaa Xaa Gly Leu Ser Glu Xaa Gln Ser Xaa Pro Leu Xaa Gln Glu
 50 55 60
 His Xaa Lys Thr Cys Leu Ser Pro Gly Ser Phe Glu Met Ser Leu Gln
 65 70 75 80
 10 Pro Asp Xaa Val Xaa Xaa Asp Xaa Thr Glu Phe Glu Xaa Leu Pro Xaa
 85 90 95
 Ser Ser Xaa Val Lys Xaa Cys Lys His Lys Glu Lys Ser Xaa His Gln
 100 105 110
 Lys Asp Phe Xaa Leu Glu Phe Gly Glu Lys Ser Asn Ala Lys Ile Lys
 115 120 125
 15 Asp Glu Asp His Ser Pro Xaa Phe Glu Asn Ser Asp Cys Xaa Leu Lys
 130 135 140
 Lys Met Asp Lys Xaa Gly Lys Xaa Leu Lys Lys His Lys Leu Lys His
 145 150 155 160
 20 Lys Xaa Arg Glu Lys Glu Lys His
 165

<210> 821

<211> 176

25 <212> PRT

<213> Homo sapiens

<400> 821

30 Leu Ser Phe Val Lys Glu Ile Lys Glu Cys Arg Arg Ile Glu Asn Leu
 1 5 10 15
 Trp Lys Asn Arg Met His Glu Lys Ala Arg Lys Ala Glu Glu Met Arg
 20 25 30
 Arg Gln Gln Lys Leu Lys Gln Ala Lys Leu Val Glu Gln Tyr Arg Glu
 35 35 40 45
 35 Gln Ser Trp Met Thr Met Ala Asn Leu Glu Lys Glu Leu Gln Glu Met
 50 55 60
 Glu Ala Arg Tyr Glu Lys Glu Phe Gly Asp Gly Ser Asp Glu Asn Glu
 65 70 75 80
 Met Glu Glu His Glu Leu Lys Asp Glu Glu Asp Gly Lys Asp Ser Asp
 85 90 95
 40 Glu Ala Glu Asp Ala Glu Leu Tyr Asp Asp Leu Tyr Cys Pro Ala Cys
 100 105 110
 Asp Lys Ser Phe Lys Thr Glu Xaa Ala Met Lys Asn His Glu Lys Ser
 115 120 125
 45 Lys Lys His Arg Glu Met Val Ala Leu Leu Lys Gln Gln Leu Glu Glu
 130 135 140
 Glu Glu Xaa Asn Phe Ser Xaa Pro Gln Ile Asp Glu Asn Pro Leu Asp
 145 150 155 160
 Asp Asn Ser Glu Glu Glu Met Glu Asp Ala Pro Lys Gln Lys Leu Ser
 50 165 170 175

<210> 822

<211> 193

55 <212> PRT

<213> Homo sapiens

<400> 822

60 Ile Arg Xaa Lys Ala Arg Lys Glu Lys Asn Glu Leu Val Arg Gln Leu
 1 5 10 15
 Val Ala Phe Ile Arg Lys Arg Asp Lys Arg Val Gln Ala His Arg Lys
 20 25 30
 Leu Val Glu Glu Gln Asn Ala Glu Lys Ala Arg Lys Ala Glu Glu Met
 35 40 45

Arg Arg Gln Gln Lys Leu Lys Gln Ala Lys Leu Val Glu Gln Tyr Arg
 50 55 60
 Glu Gln Ser Trp Met Thr Met Ala Asn Leu Glu Lys Glu Leu Gln Glu
 65 70 75 80
 5 Met Glu Ala Arg Tyr Glu Lys Glu Phe Gly Asp Gly Ser Asp Glu Asn
 85 90 95
 Glu Met Glu Glu His Glu Leu Lys Asp Glu Glu Asp Gly Lys Asp Ser
 100 105 110
 10 Asp Glu Ala Glu Asp Ala Glu Leu Tyr Asp Asp Leu Tyr Cys Pro Ala
 115 120 125
 Cys Asp Lys Ser Phe Lys Thr Glu Lys Ala Met Lys Asn His Glu Lys
 130 135 140
 Ser Lys Lys His Arg Glu Met Val Ala Leu Leu Lys Gln Gln Leu Glu
 145 150 155 160
 15 Glu Glu Glu Glu Asn Phe Ser Arg Pro Gln Ile Asp Glu Asn Pro Leu
 165 170 175
 Asp Asp Asn Ser Glu Glu Glu Met Glu Asp Ala Pro Lys Gln Lys Leu
 180 185 190
 Ser
 20
 <210> 823
 <211> 253
 <212> PRT
 25 <213> Homo sapiens
 <400> 823
 Ala Val Gln Ala Ser Ser Gly Ser Pro Lys Ala Arg Thr Thr Glu Gly
 1 5 10 15
 30 Pro Val Asp Ser Met Pro Cys Leu Asp Arg Met Pro Leu Leu Ala Lys
 20 25 30
 Gly Lys Gln Ala Thr Gly Glu Glu Lys Ala Ala Thr Ala Pro Gly Ala
 35 35 40 45
 Gly Ala Lys Ala Ser Gly Glu Gly Met Ala Gly Asp Ala Ala Gly Glu
 50 55 60
 35 Thr Glu Gly Ser Met Glu Arg Met Gly Glu Pro Ser Gln Asp Pro Lys
 65 70 75 80
 Gln Gly Thr Ser Gly Gly Val Asp Thr Ser Ser Glu Gln Ile Ala Thr
 85 90 95
 40 Leu Thr Gly Phe Pro Asp Phe Arg Glu His Ile Ala Lys Ile Phe Glu
 100 105 110
 Lys Pro Val Leu Gly Ala Leu Ala Thr Pro Gly Glu Lys Ala Gly Ala
 115 120 125
 45 Gly Arg Ser Ala Val Gly Lys Asp Leu Thr Arg Pro Leu Gly Pro Glu
 130 135 140
 Lys Leu Leu Asp Gly Pro Pro Gly Val Asp Val Thr Leu Leu Pro Ala
 145 150 155 160
 Pro Pro Ala Arg Leu Gln Val Glu Lys Lys Gln Gln Leu Ala Gly Glu
 165 170 175
 50 Ala Glu Ile Ser His Leu Ala Leu Gln Asp Pro Ala Ser Asp Lys Leu
 180 185 190
 Leu Gly Pro Ala Gly Leu Thr Trp Glu Arg Asn Leu Pro Gly Ala Gly
 195 200 205
 55 Val Gly Lys Glu Met Ala Gly Cys Pro Thr His Thr Glu Gly Arg Xaa
 210 215 220
 Xaa Gly Gln Lys Gly Leu Gly Gln Pro Gly Gln Ala Trp Lys Ala Arg
 225 230 235 240
 Leu Thr Tyr Ser Leu Glu Lys Asn Xaa Gln Glu Leu Leu
 245 250
 60
 <210> 824
 <211> 242
 <212> PRT

<213> Homo sapiens

<400> 824

5 Val Ser Leu Ala Phe Gln Ala Trp Pro Gly Cys Pro Arg Pro Phe Trp
 1 5 10 15
 Pro Xaa Xaa Leu Pro Ser Val Trp Val Gly Gln Pro Ala Ile Ser Phe
 20 25 30
 Pro Thr Pro Ala Pro Gly Lys Phe Arg Ser Gln Val Ser Pro Ala Gly
 35 40 45
 10 Pro Arg Ser Leu Ser Glu Ala Gly Ser Cys Arg Ala Arg Trp Glu Ile
 50 55 60
 Ser Ala Ser Pro Ala Asn Cys Cys Phe Phe Ser Thr Trp Ser Arg Ala
 65 70 75 80
 15 Gly Gly Ala Gly Arg Val Thr Ser Thr Pro Gly Gly Pro Ser Arg
 85 90 95
 Ser Phe Ser Gly Pro Asn Gly Leu Val Arg Ser Leu Pro Thr Ala Leu
 100 105 110
 Leu Pro Ala Pro Ala Phe Ser Pro Gly Val Ala Arg Ala Pro Ser Thr
 115 120 125
 20 Gly Phe Ser Lys Ile Leu Ala Met Cys Ser Leu Lys Ser Gly Lys Pro
 130 135 140
 Val Arg Val Ala Ile Cys Ser Glu Leu Val Ser Thr Pro Pro Asp Val
 145 150 155 160
 25 Pro Cys Phe Gly Ser Trp Glu Gly Ser Pro Ile Leu Ser Met Leu Pro
 165 170 175
 Ser Val Ser Pro Ala Ala Ser Pro Ala Met Pro Ser Pro Leu Ala Leu
 180 185 190
 Ala Pro Ala Pro Gly Ala Val Ala Ala Phe Ser Ser Pro Val Ala Cys
 195 200 205
 30 Leu Pro Leu Ala Arg Ser Gly Ile Arg Ser Arg His Gly Met Glu Ser
 210 215 220
 Thr Gly Pro Ser Val Val Leu Ala Leu Gly Leu Pro Leu Leu Ala Cys
 225 230 235 240
 Thr Ala

<210> 825

<211> 82

<212> PRT

<213> Homo sapiens

<400> 825

45 Phe Tyr Asn Leu Lys Xaa Leu Lys Gln Gln Val Met Lys Tyr Leu Leu
 1 5 10 15
 Tyr Tyr Tyr Thr Ser Gly Pro Ala Phe Ser Lys Lys Xaa Leu Thr Cys
 20 25 30
 Leu Arg Thr Leu Lys Lys Lys Ala Leu Ile Trp Ser Phe Leu Gly Trp
 35 40 45
 50 Gly Arg Leu Phe Gln Ala Arg Gln Ile Phe Leu Leu Pro Leu Asn Trp
 50 55 60
 Glu Tyr Lys Lys Tyr Ile Thr Ala Lys Ala Ala Gly Asn Cys Ile Leu
 65 70 75 80
 Ser Gln

<210> 826

<211> 64

<212> PRT

<213> Homo sapiens

<400> 826

60 Pro Leu Val Leu Cys Xaa Ser Cys Xaa Pro Arg Phe His Pro Phe Gly
 1 5 10 15

Lys Arg Gly Xaa Cys Ala Arg Thr Gln Thr His Arg Asn Lys Leu Ser
 20 25 30
 Ala Ser Xaa Ala Phe Gly Cys Xaa Gly Ala Val Cys Ala His Ile Tyr
 35 40 45
 5 Met His Thr Thr Leu Val Cys Met Ser Arg Gly Asn Gln Xaa Leu Asn
 50 55 60

 <210> 827
 <211> 157
 10 <212> PRT
 <213> Homo sapiens

 <400> 827
 15 Ala Trp Pro Ala Leu Ala Pro Gly Ser Pro Val Pro Ala Ala Arg Pro
 1 5 10 15
 Pro Arg Ser Arg Ala Pro Phe Arg Pro Gly Arg Ser Pro Ala Gly Met
 20 25 30
 Gln Xaa Ser Pro Xaa Gly Tyr Gly Ala Gln Asp Asp Pro Pro Ala Arg
 35 40 45
 20 Arg Asp Cys Ala Trp Ala Pro Gly His Gly Ala Ala Ala Asp Thr Arg
 50 55 60
 Gly Leu Thr Ala Gly Pro Ala Ala Leu Ala Ala Pro Ala Xaa Pro Ala
 65 70 75 80
 Xaa Xaa Pro Ser Pro Gln Arg Xaa Pro Pro Arg Asn Xaa Glu Pro Gly
 25 85 90 95
 Arg Tyr Gly Leu Ser Pro Ala Gly Arg Gly Glu Arg Xaa Ala Xaa Tyr
 100 105 110
 Glu Xaa Xaa Ile Pro Leu Ala His Glu Arg Leu Xaa Gly Val Gly Lys
 115 120 125
 30 Xaa Thr Xaa Ser Lys Leu Xaa Gly Xaa Xaa Xaa Thr Arg Xaa Cys Xaa
 130 135 140
 Asn Ala Val Xaa Gln Xaa Arg Cys Trp Xaa Lys Ser Val
 145 150 155

 35 <210> 828
 <211> 138
 <212> PRT
 <213> Homo sapiens

 40 <400> 828
 Pro Gly Leu Pro Leu Arg Pro Ala Pro Gln Cys Pro Pro Pro Ala Arg
 1 5 10 15
 Arg Ala Pro Ala Leu Arg Ser Ala Gln Ala Ala Ala Gln Leu Glu Cys
 20 25 30
 45 Lys Xaa Arg Xaa Pro Ala Thr Ala His Arg Thr Thr Arg Pro Pro Ala
 35 40 45
 Ala Thr Val His Gly Pro Arg Asp Thr Gly Pro Pro Leu Thr Arg Ala
 50 55 60
 Ala Ser Pro Pro Ala Pro Pro Pro Ser Pro Arg Pro Xaa Xaa Pro Pro
 65 70 75 80
 Xaa Arg Pro Ala Arg Ser Ala Xaa Pro Arg Ala Thr Xaa Ser Arg Gly
 85 90 95
 Ala Met Ala Ser Ala Arg Pro Ala Ala Gly Asn Ala Xaa Arg Xaa Thr
 100 105 110
 55 Ser Xaa Ala Ser Arg Trp Pro Met Asn Ala Xaa Met Gly Trp Ala Xaa
 115 120 125
 Gly Arg Xaa Ala Ser Xaa Leu Ala Xaa Xaa
 130 135

 60 <210> 829
 <211> 164
 <212> PRT
 <213> Homo sapiens

<400> 829
 Arg Xaa Val Xaa Ala Pro Ser His Ala Phe Xaa Pro Ala Ser Xaa Leu
 1 5 10 15
 5 Xaa His Arg Val Xaa Ala Xaa Pro Gly Xaa Xaa Xaa Ala Xaa Gln Leu
 20 25 30
 Ala Xaa Arg Xaa Phe Ala His Pro Xaa Lys Ala Phe Met Gly Gln Arg
 35 40 45
 10 Asp Xaa Xaa Leu Val Xaa Arg Xaa Ala Phe Pro Ala Ala Gly Arg Ala
 50 55 60
 Glu Ala Ile Ala Pro Arg Leu Xaa Val Ala Arg Gly Xaa Ala Leu Arg
 65 70 75 80
 Ala Gly Xaa Xaa Gly Gly Xaa Gly Gly Arg Gly Glu Gly Gly Gly Ala
 85 90 95
 15 Gly Gly Glu Ala Ala Arg Val Ser Gly Gly Pro Val Ser Arg Gly Pro
 100 105 110
 Cys Thr Val Ala Ala Gly Gly Arg Val Val Leu Cys Ala Val Ala Xaa
 115 120 125
 20 Arg Arg Xaa Leu His Ser Ser Trp Ala Ala Ala Trp Ala Glu Arg Ser
 130 135 140
 Ala Gly Ala Arg Arg Ala Gly Gly Gly His Trp Gly Ala Gly Arg Lys
 145 150 155 160
 Gly Arg Pro Gly

25

<210> 830
 <211> 179
 <212> PRT
 <213> Homo sapiens

30

<400> 830
 Pro Ala Phe Ile Gly Glu Val Asn His Lys Glu Ile Lys Met Ser Lys
 1 5 10 15
 35 Ser Lys Asp Asp Ala Pro His Glu Leu Glu Ser Gln Phe Ile Leu Arg
 20 25 30
 Leu Pro Pro Glu Tyr Ala Ser Thr Val Arg Arg Ala Val Gln Ser Gly
 35 40 45
 His Val Asn Leu Lys Asp Arg Leu Thr Ile Glu Leu His Pro Asp Gly
 50 55 60
 40 Arg His Gly Ile Val Arg Val Asp Arg Val Pro Leu Ala Ser Lys Leu
 65 70 75 80
 Val Asp Leu Pro Cys Val Met Glu Ser Leu Lys Thr Ile Asp Lys Lys
 85 90 95
 Thr Phe Tyr Lys Thr Ala Asp Ile Cys Gln Met Leu Val Ser Thr Val
 100 105 110
 45 Asp Gly Asp Leu Tyr Pro Pro Val Glu Glu Pro Val Ala Ser Thr Asp
 115 120 125
 Pro Lys Ala Ser Lys Lys Lys Asp Lys Asp Lys Glu Lys Lys Phe Ile
 130 135 140
 50 Trp Asn His Gly Ile Thr Leu Pro Leu Lys Asn Val Arg Lys Lys Lys
 145 150 155 160
 Val Pro Glu Asp Ser Gln Arg Arg Asn Ile Leu Asn Leu Gln Met Leu
 165 170 175
 Lys Lys Lys

55

<210> 831
 <211> 135
 <212> PRT
 <213> Homo sapiens

60

<400> 831
 Leu Gly Asn Arg Lys Ala Asn Gly Gly Ser Pro Gly Thr Val Phe Gly

1 5 10 15
 Pro Glu Ser Pro Ala Glu Ile Leu Ser Thr His Lys Leu Ser Arg Asn
 20 25 30
 Lys Asp Thr Gln Lys Ile Arg Ala Gln Arg Ala Leu Phe Ala Ser Gly
 5 35 40 45
 Thr Tyr Asn Pro Val Thr Ile Ile Ser Ser Val Ser Pro Gly Arg Ser
 50 55 60
 Glu Gly Lys Arg Arg Pro Gln Gly Ala Lys Arg Glu Arg Ala Glu Arg
 65 70 75 80
 10 Leu Leu Val Val Ser Leu Ile Leu Pro Ala Ala Trp Gln Ser Asp Pro
 85 90 95
 Leu Pro Ile Thr Asp Glu Arg Ala Arg Asp Gly Gln Arg Glu Ile Leu
 100 105 110
 15 Pro Arg Gly Ala Ala Arg Ile Thr Arg Pro Arg Thr Ser Pro Ala Leu
 115 120 125
 Arg Pro Gly Arg Leu Pro Ser
 130 135

20 <210> 832
 <211> 113
 <212> PRT
 <213> Homo sapiens

25 <400> 832
 Pro Ala Phe Ile Gly Glu Val Asn His Lys Glu Ile Lys Met Ser Lys
 1 5 10 15
 Ser Lys Asp Asp Ala Pro His Glu Leu Glu Ser Gln Phe Ile Leu Arg
 20 25 30
 30 Leu Pro Pro Glu Tyr Ala Ser Thr Val Arg Arg Ala Val Gln Ser Gly
 35 40 45
 His Val Asn Leu Lys Asp Arg Leu Thr Ile Glu Leu His Pro Asp Gly
 50 55 60
 Arg His Gly Ile Val Arg Val Asp Arg Val Pro Leu Ala Ser Lys Leu
 65 70 75 80
 35 Val Asp Leu Pro Cys Val Met Glu Ser Leu Lys Thr Ile Asp Lys Lys
 85 90 95
 Thr Phe Tyr Lys Thr Ala Asp Ile Cys Gln Met Leu Val Ser Thr Val
 100 105 110
 Asp

40 <210> 833
 <211> 134
 <212> PRT
 45 <213> Homo sapiens

50 <400> 833
 Ala His Pro Val Ser Leu Lys Ser Val Leu Arg Ala Arg Phe Ser Thr
 1 5 10 15
 Phe Met Met Arg Pro Leu Xaa Val Leu Pro Cys Pro Gly Leu Leu Glu
 20 25 30
 Leu Ala Phe His Val Gly Asn Leu Xaa Xaa Asn Ser Ile Thr Ser Trp
 35 40 45
 55 Met Gly Pro Ser Xaa Ser Trp Gly Trp Ser Ser Glu Xaa Ile Asn Leu
 50 55 60
 Gly Leu Asp Xaa Xaa Ser Lys Thr Ser Ser Gly Xaa Glu Gly Xaa Ile
 65 70 75 80
 Phe Leu Ser Gly Arg Xaa Gly Leu Phe Tyr Pro Thr Gly Xaa Xaa Xaa
 85 90 95
 60 Gly Trp Lys Ser Xaa Gln Xaa Ile Cys Xaa Lys Asn Met Ala Cys Arg
 100 105 110
 Asp Lys Ile Leu Xaa Lys Lys Xaa Gly Leu Ile Xaa Pro Phe Val Ile
 115 120 125

Ser His Xaa Xaa Pro Xaa
130

5 <210> 834
<211> 128
<212> PRT
<213> Homo sapiens

10 <400> 834
Leu Gly Asn Arg Lys Ala Asn Gly Gly Ser Pro Gly Thr Val Phe Gly
1 5 10 15
Pro Glu Ser Pro Ala Glu Ile Leu Ser Thr His Lys Leu Ser Arg Asn
20 25 30
15 Lys Asp Thr Gln Lys Ile Arg Ala Gln Arg Ala Leu Phe Ala Ser Gly
35 40 45
Thr Tyr Asn Pro Val Thr Ile Ile Ser Ser Val Ser Pro Gly Arg Ser
50 55 60
Glu Gly Lys Arg Arg Pro Gln Gly Ala Lys Arg Glu Arg Ala Glu Arg
65 70 75 80
20 Leu Leu Val Val Ser Leu Ile Leu Pro Ala Ala Trp Gln Ser Asp Pro
85 90 95
Leu Pro Ile Thr Asp Glu Arg Ala Arg Asp Gly Gln Arg Glu Ile Leu
100 105 110
25 Pro Arg Gly Ala Ala Arg Ile Thr Arg Pro Arg Thr Ser Pro Ala Leu
115 120 125

<210> 835
<211> 78
<212> PRT
30 <213> Homo sapiens

<400> 835
Arg Ala Gly Glu Val Arg Gly Leu Val Met Arg Ala Ala Pro Leu Gly
1 5 10 15
35 Lys Ile Ser Arg Cys Pro Ser Arg Ala Leu Ser Ser Val Ile Gly Ser
20 25 30
Gly Ser Leu Cys Gln Ala Ala Gly Arg Ile Lys Glu Thr Thr Arg Arg
35 40 45
40 Arg Ser Ala Leu Ser Arg Leu Ala Pro Cys Gly Leu Leu Phe Pro Ser
50 55 60
Leu Arg Pro Gly Glu Thr Glu Leu Ile Ile Val Thr Gly Leu
65 70 75

<210> 836
45 <211> 107
<212> PRT
<213> Homo sapiens

<400> 836
50 Leu Leu Leu Gln Arg Ala Glu Leu Leu Leu Phe Ser Xaa Phe Leu Leu
1 5 10 15
Val Glu Leu Ile Gln Tyr Ser Leu Lys Ser Val Leu Glu Ser Gln Ile
20 25 30
Ser Thr Phe Met Met Arg Pro Leu Xaa Gly Leu Pro Cys Pro Gly Leu
35 40 45
55 Leu Gly Ala Trp Leu Tyr Gly Gly Asn Leu Leu Xaa Lys Xaa His Asn
50 55 60
Xaa Leu Asp Xaa Val Leu Xaa Phe Pro Gly Ala Gly His Leu Asp Gln
65 70 75 80
60 Leu Thr Trp Xaa Gly Thr Xaa Phe Ser Lys Xaa Ser Ser Xaa Gln Arg
85 90 95
Arg Leu Tyr Leu Leu Xaa Leu Gly Gly Xaa Gly
100 105

<210> 837
 <211> 87
 <212> PRT
 5 <213> Homo sapiens

 <400> 837
 Leu Ile Gln Met Thr Ser Pro Arg Lys Xaa Lys Asp Xaa Ile Gln Xaa
 1 5 10 15
 10 Val Met Xaa Phe Xaa Lys Gln Ile Ala Thr Ile Lys Pro Ser Ser Gln
 20 25 30
 Glu Pro Arg Thr Gly Gln Thr Xaa Lys Arg Ser His His Glu Ser Gly
 35 40 45
 15 Asn Leu Ala Leu Lys Asn Arg Phe Gln Ala Val Leu Asp Glu Leu Asn
 50 55 60
 Gln Lys Glu Xaa Arg Glu Lys Glu Gln Leu Ser Ser Leu Gln Glu Glu
 65 70 75 80
 Leu Glu Ser Leu Leu Glu Lys
 85
 20
 <210> 838
 <211> 183
 <212> PRT
 25 <213> Homo sapiens

 <400> 838
 Pro Ala Phe Ile Gly Glu Val Asn His Lys Glu Ile Lys Met Ser Lys
 1 5 10 15
 30 Ser Lys Asp Asp Ala Pro His Glu Leu Glu Ser Gln Phe Ile Leu Arg
 20 25 30
 Leu Pro Pro Glu Tyr Ala Ser Thr Val Arg Arg Ala Val Gln Ser Gly
 35 40 45
 His Val Asn Leu Lys Asp Arg Leu Thr Ile Glu Leu His Pro Asp Gly
 50 55 60
 35 Arg His Gly Ile Val Arg Val Asp Arg Val Pro Leu Ala Ser Lys Leu
 65 70 75 80
 Val Asp Leu Pro Cys Val Met Glu Ser Leu Lys Thr Ile Asp Lys Lys
 85 90 95
 Thr Phe Tyr Lys Thr Ala Asp Ile Cys Gln Met Leu Val Ser Thr Val
 100 105 110
 40 Asp Gly Asp Leu Tyr Pro Pro Val Glu Glu Pro Val Ala Ser Thr Asp
 115 120 125
 Pro Lys Ala Ser Lys Lys Lys Asp Lys Asp Lys Glu Lys Lys Phe Ile
 130 135 140
 45 Trp Asn His Gly Ile Thr Leu Pro Leu Lys Asn Val Xaa Glu Glu Lys
 145 150 155 160
 Gly Ser Gly Arg Gln Pro Lys Lys Lys Xaa Xaa Glu Ser Xaa Asp Val
 165 170 175
 Glu Lys Glu Val Lys Arg Cys
 180
 50
 <210> 839
 <211> 64
 <212> PRT
 55 <213> Homo sapiens

 <400> 839
 Leu Leu Leu Gln Arg Ala Glu Leu Leu Leu Phe Ser Xaa Phe Leu Leu
 1 5 10 15
 60 Phe Glu Leu Ile Pro Val Gln Ala Trp Lys Xaa Val Leu Glu Lys Pro
 20 25 30
 Asp Phe Pro Leu Ser Trp Met Arg Xaa Leu Leu Ser Phe Leu Pro Cys
 35 40 45

Pro Gly Ser Phe Gly Ala Leu Pro Phe His Gly Xaa Asn Leu Ala Ser
50 55 60

5 <210> 840
<211> 79
<212> PRT
<213> Homo sapiens

10 <400> 840
Glu Ala Arg Phe Ser Thr Phe Met Asp Glu Xaa Pro Leu Val Val Phe
1 5 10 15
Ala Leu Ser Trp Val Phe Trp Ser Leu Ala Leu Ser Trp Xaa Gln Ser
20 25 30
15 Gly Phe Leu Asn Ser His Asn Pro Ala Xaa Xaa Gly Pro Phe Ile Phe
35 40 45
Xaa Gly Xaa Gly His Phe Gly Phe His Leu Asn Leu Xaa Pro Gly Xaa
50 55 60
Leu Ala Xaa Ser Xaa Xaa Phe Ser Ser Arg Xaa Xaa Lys Glu Gly
65 70 75

20 <210> 841
<211> 57
<212> PRT
<213> Homo sapiens

25 <400> 841
Lys Gly Lys Ala Pro Lys Asp Pro Gly Gln Gly Lys Asn Asp Lys Arg
1 5 10 15
Xaa Leu Ile His Glu Ser Gly Lys Ser Gly Phe Ser Arg Thr Xaa Phe
20 25 30
30 Gln Ala Cys Thr Gly Met Ser Ser Asn Lys Arg Lys Xaa Glu Lys Arg
35 40 45
Ser Asn Ser Ala Leu Cys Lys Arg Ser
50 55

35 <210> 842
<211> 57
<212> PRT
<213> Homo sapiens

40 <400> 842
Thr Pro Gly Thr Gly Gln Asn Arg Gln Glu Xaa Ser His His Glu Ser
1 5 10 15
Gly Asn Leu Ala Leu Lys Thr Asp Phe Gln Gly Leu Tyr Trp Asp Glu
20 25 30
45 Leu Lys Gln Lys Glu Xaa Arg Glu Lys Glu Gln Leu Ser Ser Leu Gln
35 40 45
Glu Glu Leu Glu Ser Leu Leu Glu Lys
50 55

50 <210> 843
<211> 50
<212> PRT
<213> Homo sapiens

55 <400> 843
Pro Gln Gly Gln Gly Lys Thr Asp Lys Arg Xaa Leu Ile Met Lys Val
1 5 10 15
Glu Ile Trp Leu Ser Arg Gln Ile Phe Arg Ala Cys Thr Gly Met Ser
20 25 30
60 Ser Asn Lys Arg Lys Xaa Glu Lys Arg Ser Asn Ser Ala Leu Cys Lys
35 40 45
Arg Ser

50

<210> 844

<211> 85

5

<212> PRT

<213> Homo sapiens

<400> 844

10 Leu Gly Arg Arg Pro Gly Arg Arg Ala Gly Glu Val Arg Gly Leu Val
 1 5 10 15
 Met Arg Ala Ala Pro Leu Gly Lys Ile Ser Arg Cys Pro Ser Arg Ala
 20 25 30
 Leu Ser Ser Val Ile Gly Ser Gly Ser Leu Cys Gln Ala Ala Gly Arg
 35 40 45
 15 Ile Lys Glu Thr Thr Arg Arg Arg Ser Ala Leu Ser Arg Leu Ala Pro
 50 55 60
 Cys Gly Leu Leu Phe Pro Ser Leu Arg Pro Gly Glu Thr Glu Leu Ile
 65 70 75 80
 20 Ile Val Thr Gly Leu
 85

<210> 845

<211> 95

25

<212> PRT

<213> Homo sapiens

<400> 845

30 Leu Ala Arg Glu Gln Glu Ser Lys Trp Arg Leu Pro Arg Asn Gly Phe
 1 5 10 15
 Arg Pro Arg Lys Pro Ser Arg Asp Thr Phe Asn Ser Gln Thr Leu Pro
 20 25 30
 Glu Gln Arg His Ser Lys Asn Gln Gly Ser Ala Ser Ser Leu Arg Leu
 35 40 45
 Gly Tyr Leu Gln Ser Ser Asp Asp Tyr Lys Phe Ser Phe Thr Gly Pro
 50 55 60
 35 Glu Arg Arg Glu Glu Glu Ala Ala Arg Ser Gln Ala Gly Glu Ser Arg
 65 70 75 80
 Ala Ser Pro Cys Arg Phe Leu Asn Ser Ser Cys Arg Leu Ala Glu
 85 90 95
 40

<210> 846

<211> 135

<212> PRT

45

<213> Homo sapiens

<400> 846

50 Leu Gly Asn Arg Lys Ala Asn Gly Gly Ser Pro Gly Thr Val Phe Gly
 1 5 10 15
 Pro Glu Ser Pro Ala Glu Ile Leu Ser Thr His Lys Leu Ser Arg Asn
 20 25 30
 Lys Asp Thr Gln Lys Ile Arg Ala Gln Arg Ala Leu Phe Ala Ser Gly
 35 40 45
 Thr Tyr Asn Pro Val Thr Ile Ser Ser Val Ser Pro Gly Arg Ser
 50 55 60
 55 Glu Gly Lys Arg Arg Pro Gln Gly Ala Lys Arg Glu Arg Ala Glu Arg
 65 70 75 80
 Leu Leu Val Val Ser Leu Ile Leu Pro Ala Ala Trp Gln Ser Asp Pro
 85 90 95
 Leu Pro Ile Thr Asp Glu Arg Ala Arg Asp Gly Gln Arg Glu Ile Leu
 100 105 110
 60 Pro Arg Gly Ala Ala Arg Ile Thr Arg Pro Arg Thr Ser Pro Ala Leu
 115 120 125
 Arg Pro Gly Arg Leu Pro Ser

130 135

<210> 847
 <211> 133
 5 <212> PRT
 <213> Homo sapiens

<400> 847
 10 Leu Gly Asn Arg Lys Ala Asn Gly Gly Ser Pro Gly Thr Val Phe Gly
 1 5 10 15
 Pro Glu Ser Pro Ala Glu Ile Leu Ser Thr His Lys Leu Ser Arg Asn
 20 25 30
 Lys Asp Thr Gln Lys Ile Arg Ala Gln Arg Ala Leu Phe Ala Ser Gly
 35 40 45
 15 Thr Tyr Asn Pro Val Thr Ile Ile Ser Ser Val Ser Pro Gly Arg Ser
 50 55 60
 Glu Gly Lys Arg Arg Pro Gln Gly Ala Lys Arg Glu Arg Ala Glu Arg
 65 70 75 80
 20 Leu Leu Val Val Ser Leu Ile Leu Pro Ala Ala Trp Gln Ser Asp Pro
 85 90 95
 Leu Pro Ile Thr Asp Glu Arg Ala Arg Asp Gly Gln Arg Glu Ile Leu
 100 105 110
 Pro Arg Gly Ala Ala Arg Ile Thr Arg Pro Arg Thr Ser Pro Ala Leu
 115 120 125
 25 Arg Pro Gly Arg Leu
 130

<210> 848
 <211> 84
 30 <212> PRT
 <213> Homo sapiens

<400> 848
 35 Gly Arg Arg Pro Gly Arg Arg Ala Gly Glu Val Arg Gly Leu Val Met
 1 5 10 15
 Arg Ala Ala Pro Leu Gly Lys Ile Ser Arg Cys Pro Ser Arg Ala Leu
 20 25 30
 Ser Ser Val Ile Gly Ser Gly Ser Leu Cys Gln Ala Ala Gly Arg Ile
 35 40 45
 40 Lys Glu Thr Thr Arg Arg Arg Ser Ala Leu Ser Arg Leu Ala Pro Cys
 50 55 60
 Gly Leu Leu Phe Pro Ser Leu Arg Pro Gly Glu Thr Glu Leu Ile Ile
 65 70 75 80
 Val Thr Gly Leu

<210> 849
 <211> 73
 50 <212> PRT
 <213> Homo sapiens

<400> 849
 55 Ala Gln Pro Met Lys Arg Ala Lys Gly Ser Xaa Lys Lys Thr Pro Xaa
 1 5 10 15
 Gly Pro Gly Ala Lys Asn Arg Pro Xaa Arg Xaa Phe Ser Phe His Glu
 20 25 30
 Lys Xaa Lys Ile Trp Ala Xaa Gln Glu Xaa Ile Ser Gly Xaa Tyr Leu
 35 40 45
 Asp Glu Leu Asn Gln Lys Glu Ala Arg Xaa Lys Glu Gln Leu Ser Xaa
 50 55 60
 60 Leu Gln Glu Glu Leu Glu Ile Pro Pro
 65 70

<210> 850
 <211> 129
 <212> PRT
 <213> Homo sapiens

5

<400> 850
 Leu Gly Asn Arg Lys Ala Asn Gly Gly Ser Pro Gly Thr Val Phe Gly
 1 5 10 15
 Pro Glu Ser Pro Ala Glu Ile Leu Ser Thr His Lys Leu Ser Arg Asn
 10 20 25 30
 Lys Asp Thr Gln Lys Ile Arg Ala Gln Arg Ala Leu Phe Ala Ser Gly
 35 40 45
 Thr Tyr Asn Pro Val Thr Ile Ile Ser Ser Val Ser Pro Gly Arg Ser
 50 55 60
 15 Glu Gly Lys Arg Arg Pro Gln Gly Ala Lys Arg Glu Arg Ala Glu Arg
 65 70 75 80
 Leu Leu Val Val Ser Leu Ile Leu Pro Ala Ala Trp Gln Ser Asp Pro
 85 90 95
 20 Leu Pro Ile Thr Asp Glu Arg Ala Arg Asp Gly Gln Arg Glu Ile Leu
 100 105 110
 Pro Arg Gly Ala Ala Arg Ile Thr Arg Pro Arg Thr Ser Pro Ala Leu
 115 120 125
 Arg

25

<210> 851
 <211> 95
 <212> PRT
 <213> Homo sapiens

30

<400> 851
 Leu Ala Arg Glu Gln Glu Ser Lys Trp Arg Leu Pro Arg Asn Gly Phe
 1 5 10 15
 Arg Pro Arg Lys Pro Ser Arg Asp Thr Phe Asn Ser Gln Thr Leu Pro
 35 20 25 30
 Glu Gln Arg His Ser Lys Asn Gln Gly Ser Ala Ser Ser Leu Arg Leu
 35 40 45
 Gly Tyr Leu Gln Ser Ser Asp Asp Tyr Lys Phe Ser Phe Thr Gly Pro
 50 55 60
 40 Glu Arg Arg Glu Glu Glu Ala Ala Arg Ser Gln Ala Gly Glu Ser Arg
 65 70 75 80
 Ala Ser Pro Cys Arg Phe Leu Asn Ser Ser Cys Arg Leu Ala Glu
 85 90 95

45

<210> 852
 <211> 80
 <212> PRT
 <213> Homo sapiens

50

<400> 852
 Gly Arg Arg Ala Gly Glu Val Arg Gly Leu Val Met Arg Ala Ala Pro
 1 5 10 15
 Leu Gly Lys Ile Ser Arg Cys Pro Ser Arg Ala Leu Ser Ser Val Ile
 20 25 30
 55 Gly Ser Gly Ser Leu Cys Gln Ala Ala Gly Arg Ile Lys Glu Thr Thr
 35 40 45
 Arg Arg Arg Ser Ala Leu Ser Arg Leu Ala Pro Cys Gly Leu Leu Phe
 50 55 60
 60 Pro Ser Leu Arg Pro Gly Glu Thr Glu Leu Ile Val Thr Gly Leu
 65 70 75 80

<210> 853
 <211> 166

<212> PRT

<213> Homo sapiens

<400> 853

5 Pro Gln Gly Phe Phe Pro Xaa Xaa Ser Phe Ile Asn Ser Asn Pro Met
 1 5 10 15
 Pro Val Pro Thr Phe Xaa Cys Arg Xaa Arg Thr Thr Arg Lys Lys Xaa
 20 25 30
 Xaa Xaa Xaa Val Arg Asn Xaa Lys Xaa Xaa Gly Xaa Phe Pro Gly Thr
 10 35 40 45
 Gly Phe Xaa Pro Xaa Lys Pro Xaa Xaa Xaa Thr Phe Xaa Xaa Gln Leu
 50 55 60
 Ser Arg Asn Lys Asp Thr Gln Lys Ile Arg Xaa Gln Xaa Ala Phe Phe
 65 70 75 80
 15 Arg Leu Arg Gly Leu Ser Ile Pro Val Thr Ile Ile Ser Ser Val Ser
 85 90 95
 Pro Gly Arg Ser Glu Gly Lys Arg Arg Pro Gln Gly Ala Lys Arg Glu
 100 105 110
 Arg Ala Glu Arg Leu Leu Val Val Ser Leu Ile Leu Pro Ala Ala Trp
 115 120 125
 20 Gln Ser Asp Pro Leu Pro Ile Thr Asp Glu Arg Ala Arg Asp Gly Gln
 130 135 140
 Arg Glu Ile Leu Pro Arg Gly Ala Ala Arg Ile Thr Arg Pro Arg Thr
 145 150 155 160
 25 Ser Pro Ala Leu Arg Pro
 165

<210> 854

<211> 91

<212> PRT

<213> Homo sapiens

<400> 854

35 Pro Gly Arg Arg Ala Gly Glu Val Arg Gly Leu Val Met Arg Ala Ala
 1 5 10 15
 Pro Leu Gly Lys Ile Ser Arg Cys Pro Ser Arg Ala Leu Ser Ser Val
 20 25 30
 Ile Gly Ser Gly Ser Leu Cys Gln Ala Ala Gly Arg Ile Lys Glu Thr
 35 40 45
 40 Thr Arg Arg Arg Ser Ala Leu Ser Arg Leu Ala Pro Cys Gly Leu Leu
 50 55 60
 Phe Pro Ser Leu Arg Pro Gly Glu Thr Glu Leu Ile Ile Val Thr Gly
 65 70 75 80
 45 Met Glu Arg Pro Arg Arg Lys Lys Ala Xaa
 85 90

<210> 855

<211> 130

<212> PRT

<213> Homo sapiens

<400> 855

55 Ser Xaa Arg Xaa Ile Thr Xaa Ser Phe Xaa Pro Gly Xaa Lys Xaa Trp
 1 5 10 15
 Glu Lys Xaa Ser Xaa Gln Gly Pro Xaa Xaa Xaa Xaa Phe Gln Met Gly
 20 25 30
 Xaa Ala Pro Arg Xaa Asn Glu Gly Thr Xaa Ile Pro Xaa Xaa Val Xaa
 35 40 45
 60 Gly Ile Xaa Xaa Ser Gln Asp Cys Xaa Thr Xaa Lys Arg Ala Xaa Phe
 50 55 60
 Gln Lys Ala Xaa Arg Thr Gly Xaa Asn Gly Pro Lys Gly Xaa Ser Phe
 65 70 75 80
 Xaa Lys Gly Gly Lys Phe Xaa Xaa Ser Lys Asn Lys Phe Ser Gly Cys

85 90 95
 Xaa Gly Xaa Ala Gln Xaa Lys Gly Ser Pro Arg Lys Gly Ala Thr Gln
 100 105 110
 5 Leu Phe Ala Arg Xaa Ala Arg Ile Thr Pro Arg Glu Val Lys Xaa Thr
 115 120 125
 Asp Ile
 130
 <210> 856
 10 <211> 119
 <212> PRT
 <213> Homo sapiens
 <400> 856
 15 Pro Xaa Pro Xaa Xaa Pro Gly Xaa Xaa Phe Gly Lys Asn Xaa Val Xaa
 1 5 10 15
 Arg Ala Gln Xaa Xaa Xaa Tyr Ser Arg Trp Ala Xaa Pro Pro Xaa Lys
 20 20 25 30
 Met Lys Gly Pro Xaa Phe Xaa Xaa Gly Xaa Trp Glu Phe Xaa Xaa Ala
 35 40 45
 20 Arg Ile Ala Xaa Pro Xaa Lys Gly Gln Xaa Ser Lys Lys Pro Xaa Gly
 50 55 60
 Gln Xaa Lys Thr Asp Gln Arg Xaa Ser Leu Ser Xaa Lys Gly Glu Asn
 65 70 75 80
 25 Leu Xaa Phe Gln Arg Thr Asn Phe Gln Ala Val Xaa Xaa Glu Leu Asn
 85 90 95
 Xaa Lys Glu Ala Arg Glu Lys Glu Gln Leu Ser Ser Leu Gln Glu Xaa
 100 105 110
 Leu Glu Ser Leu Leu Glu Lys
 115
 30 <210> 857
 <211> 79
 <212> PRT
 35 <213> Homo sapiens
 <400> 857
 Arg Asp Pro Xaa Ser Xaa Xaa Gly Xaa Gly Asn Phe Xaa Lys Pro Gly
 1 5 10 15
 40 Leu Pro Xaa His Xaa Lys Gly Lys Xaa Pro Lys Ser Pro Xaa Asp Arg
 20 25 30
 Xaa Lys Arg Thr Lys Gly Xaa Leu Phe Xaa Glu Arg Gly Lys Ile Trp
 35 40 45
 Xaa Phe Lys Glu Gln Ile Phe Arg Leu Xaa Trp Xaa Ser Ser Thr Xaa
 50 55 60
 45 Arg Lys Pro Glu Lys Arg Ser Asn Ser Ala Leu Cys Lys Xaa Ser
 65 70 75
 <210> 858
 50 <211> 63
 <212> PRT
 <213> Homo sapiens
 <400> 858
 55 Xaa Leu Leu Gln Xaa Ala Glu Leu Pro Leu Phe Ser Gly Phe Leu Leu
 1 5 10 15
 Xaa Glu Leu Xaa Pro Val Gln Pro Trp Lys Xaa Val Xaa Glu Asn Xaa
 20 25 30
 Xaa Phe Pro Pro Phe Met Glu Arg Lys Thr Pro Trp Ala Val Phe Xaa
 35 40 45
 60 Pro Gly Xaa Gly Ala Phe Trp Glu Pro Gly Pro Phe Asn Gly Gly
 50 55 60

<210> 859
 <211> 76
 <212> PRT
 <213> Homo sapiens

5

<400> 859
 Xaa Ser Gly Leu Phe Thr Ser Leu Gly Xaa Asp Xaa Ser Xaa Ser Cys
 1 5 10 15
 Lys Xaa Leu Ser Cys Pro Phe Ser Arg Ala Ser Phe Xaa Xaa Ser Ser
 20 25 30
 Xaa Gln Tyr Ser Pro Gly Asn Xaa Xaa Leu Lys Thr Xaa Xaa Phe Pro
 35 40 45
 Leu Ser Trp Lys Glu Lys Pro Leu Gly Arg Phe Leu Xaa Leu Ala Xaa
 50 55 60
 Gly Leu Phe Gly Asn Leu Ala Leu Leu Met Gly Gly
 65 70 75

10

<210> 860
 <211> 71
 <212> PRT
 <213> Homo sapiens

20

<400> 860
 Ala Pro Pro Leu Lys Gly Pro Gly Ser Gln Lys Ala Xaa Gly Pro Gly
 1 5 10 15
 Xaa Lys Thr Ala Gln Gly Val Phe Leu Ser Met Lys Gly Gly Xaa Phe
 20 25 30
 Xaa Phe Ser Xaa Thr Xaa Phe Gln Gly Cys Thr Xaa Met Ser Xaa Xaa
 35 40 45
 Lys Arg Lys Pro Glu Lys Arg Gly Asn Ser Ala Xaa Cys Lys Arg Xaa
 50 55 60
 Xaa Asn Xaa Leu Leu Glu Lys
 65 70

30

<210> 861
 <211> 138
 <212> PRT
 <213> Homo sapiens

35

<400> 861
 Met Ala Gly Gly Asp Val Ala Met Leu Glu Leu Thr Gly Gln Asn Phe
 1 5 10 15
 Thr Pro Asn Leu Arg Val Trp Phe Gly Asp Val Glu Ala Glu Thr Met
 20 25 30
 Tyr Arg Cys Gly Glu Ser Met Leu Cys Val Val Pro Asp Ile Ser Ala
 35 40 45
 Phe Arg Glu Gly Trp Arg Trp Val Arg Gln Pro Val Gln Val Pro Val
 50 55 60
 Thr Leu Val Arg Asn Asp Gly Ile Ile Tyr Ser Thr Ser Leu Thr Phe
 65 70 75 80
 Thr Tyr Thr Pro Glu Pro Gly Pro Arg Pro His Cys Ser Ala Ala Gly
 85 90 95
 Ala Ile Leu Arg Ala Asn Ser Ser Gln Val Pro Pro Asn Glu Ser Asn
 100 105 110
 Thr Asn Ser Glu Gly Ser Tyr Thr Asn Ala Ser Thr Asn Ser Thr Ser
 115 120 125
 Val Thr Ser Ser Thr Ala Thr Val Val Ser
 130 135

40

<210> 862
 <211> 82
 <212> PRT
 <213> Homo sapiens

45

<210> 862
 <211> 82
 <212> PRT
 <213> Homo sapiens

50

<210> 862
 <211> 82
 <212> PRT
 <213> Homo sapiens

55

<210> 862
 <211> 82
 <212> PRT
 <213> Homo sapiens

60

<400> 862
 Leu Trp Ser Glu Met Met Glu Ser Phe Ile Pro Pro Ala Leu Pro Leu
 1 5 10 15
 5 Pro Thr His Gln Asn Gln Gly Arg Gly His Ile Ala Val Gln Gln Glu
 20 25 30
 Gln Ser Phe Glu Pro Ile Gln Ala Arg Cys Pro Leu Thr Asn Gln Thr
 35 40 45
 Gln Thr Ala Arg Glu Val Thr Gln Thr Pro Ala Gln Ile Gln Pro Val
 10 50 55 60
 Ser His His Leu Gln Pro Gln Trp Tyr Pro Asn Tyr Arg Leu Phe Ala
 65 70 75 80
 Arg Thr
 15
 <210> 863
 <211> 84
 <212> PRT
 <213> Homo sapiens
 20
 <400> 863
 Met Ile Pro Ser Phe Arg Thr Lys Val Thr Gly Thr Trp Thr Gly Cys
 1 5 10 15
 25 Arg Thr His Leu Gln Pro Ser Arg Asn Ala Glu Met Ser Gly Thr Thr
 20 25 30
 Gln Ser Ile Leu Ser Pro His Leu Tyr Ile Val Ser Ala Ser Thr Ser
 35 40 45
 Pro Asn His Thr Arg Lys Phe Gly Val Lys Phe Cys Pro Val Ser Ser
 50 55 60
 30 Ser Ile Ala Thr Ser Pro Pro Ala Ile Gln Leu Lys Ala Leu Tyr His
 65 70 75 80
 Xaa Xaa Gln Xaa
 35
 <210> 864
 <211> 138
 <212> PRT
 <213> Homo sapiens
 40
 <400> 864
 Met Ala Gly Gly Asp Val Ala Met Leu Glu Leu Thr Gly Gln Asn Phe
 1 5 10 15
 Thr Pro Asn Leu Arg Val Trp Phe Gly Asp Val Glu Ala Glu Thr Met
 20 25 30
 45 Tyr Arg Cys Gly Glu Ser Met Leu Cys Val Val Pro Asp Ile Ser Ala
 35 40 45
 Phe Arg Glu Gly Trp Arg Trp Val Arg Gln Pro Val Gln Val Pro Val
 50 55 60
 Thr Leu Val Arg Asn Asp Gly Ile Ile Tyr Ser Thr Ser Leu Thr Phe
 50 65 70 75 80
 Thr Tyr Thr Pro Glu Pro Gly Pro Arg Pro His Cys Ser Ala Ala Gly
 85 90 95
 Ala Ile Leu Arg Ala Asn Ser Ser Gln Val Pro Pro Asn Glu Ser Asn
 100 105 110
 55 Thr Asn Ser Glu Gly Ser Tyr Thr Asn Ala Ser Thr Asn Ser Thr Ser
 115 120 125
 Val Thr Ser Ser Thr Ala Thr Val Val Ser
 130 135
 60
 <210> 865
 <211> 218
 <212> PRT
 <213> Homo sapiens

<400> 865

	Phe	Lys	Gly	Phe	Pro	Glu	Lys	Glu	Asn	Gly	Ile	Xaa	Ala	Leu	Phe	Ser
	1				5					10					15	
5	Lys	Lys	Lys	Asn	Ile	Ser	Asn	Xaa	Gln	Ala	His	Ser	His	Val	Gln	Lys
				20					25					30		
	Asp	Pro	Asn	Lys	Glu	Met	Ile	Asn	Asp	Gly	Arg	Phe	Leu	Xaa	Asn	Ser
			35					40					45			
10	Leu	Xaa	Gln	Ile	Xaa	Gln	Glu	Tyr	Thr	Phe	Tyr	Glu	Gly	Met	Gly	Pro
		50					55					60				
	Val	Leu	Ala	Pro	Val	Thr	Pro	Val	Pro	Val	Val	Glu	Ser	Leu	Gln	Leu
	65					70					75				80	
	Asn	Gly	Gly	Gly	Asp	Val	Ala	Met	Leu	Glu	Leu	Thr	Gly	Gln	Asn	Phe
					85					90					95	
15	Thr	Pro	Asn	Leu	Arg	Val	Trp	Phe	Gly	Asp	Val	Glu	Ala	Glu	Thr	Met
				100					105					110		
	Tyr	Arg	Cys	Gly	Glu	Ser	Met	Leu	Cys	Val	Val	Pro	Asp	Ile	Ser	Ala
			115					120					125			
20	Phe	Arg	Glu	Gly	Trp	Arg	Trp	Val	Arg	Gln	Pro	Val	Gln	Val	Pro	Val
		130					135					140				
	Thr	Leu	Val	Arg	Asn	Asp	Gly	Ile	Ile	Tyr	Ser	Thr	Ser	Leu	Thr	Phe
	145				150					155					160	
	Thr	Tyr	Thr	Pro	Glu	Pro	Gly	Pro	Arg	Pro	His	Cys	Ser	Ala	Ala	Gly
				165					170					175		
25	Ala	Ile	Leu	Arg	Ala	Asn	Ser	Ser	Gln	Val	Pro	Pro	Asn	Glu	Ser	Asn
				180					185					190		
	Thr	Asn	Ser	Glu	Gly	Ser	Tyr	Thr	Asn	Ala	Ser	Thr	Asn	Ser	Thr	Ser
		195						200					205			
30	Val	Thr	Ser	Ser	Thr	Ala	Thr	Val	Val	Ser						
		210					215									

<210> 866
 <211> 109
 <212> PRT
 35 <213> Homo sapiens

<400> 866

	Asn	Tyr	Val	Gln	Val	Trp	Xaa	Lys	Val	Cys	Xaa	Cys	Val	Val	Pro	Xaa
	1				5					10					15	
40	Ile	Phe	Ala	Phe	Arg	Xaa	Gly	Trp	Xaa	Trp	Val	Arg	Gln	Pro	Val	Gln
				20					25					30		
	Val	Pro	Val	Thr	Leu	Val	Arg	Asn	Asp	Gly	Ile	Ile	Tyr	Ser	Thr	Ser
			35					40					45			
45	Leu	Thr	Phe	Thr	Tyr	Thr	Pro	Glu	Pro	Gly	Pro	Arg	Pro	His	Cys	Ser
		50					55					60				
	Ala	Ala	Gly	Ala	Ile	Leu	Arg	Ala	Asn	Ser	Ser	Gln	Xaa	Pro	Pro	Asn
	65				70					75					80	
	Glu	Ser	Asn	Xaa	Asn	Ser	Glu	Gly	Ser	Tyr	Xaa	Asn	Ala	Ser	Thr	Asn
				85					90					95		
50	Ser	Thr	Xaa	Val	Thr	Ser	Xaa	Thr	Ala	Xaa	Xaa	Val	Ser			
				100					105							

<210> 867
 <211> 98
 55 <212> PRT
 <213> Homo sapiens

<400> 867

	Gly	Glu	Asn	Gly	Ala	Pro	Trp	Ser	Phe	Gly	Pro	Xaa	Val	His	Phe	Leu
	1				5					10					15	
60	Gly	Ala	Leu	Gly	Xaa	Lys	Xaa	Pro	Phe	Lys	Phe	Lys	Trp	Arg	Val	Gly
			20						25					30		
	Thr	Xaa	Gln	Met	Leu	Glu	Leu	Thr	Gly	Gln	Asn	Phe	Thr	Pro	Asn	Leu

35 40 45
 Xaa Ser Val Val Trp Gly Xaa Xaa Ser Leu Lys Leu Cys Thr Gly Val
 50 55 60
 Xaa Lys Ser Met Xaa Leu Cys Arg Pro Xaa His Phe Cys Ile Pro Xaa
 5 65 70 75 80
 Arg Leu Xaa Met Gly Pro Ala Thr Ser Pro Gly Ser Ser Asn Phe Gly
 85 90 95
 Pro Lys
 10
 <210> 868
 <211> 102
 <212> PRT
 <213> Homo sapiens
 15
 <400> 868
 Phe His His Phe Gly Pro Lys Leu Leu Glu Pro Gly Leu Val Ala Gly
 1 5 10 15
 Pro Xaa Ser Asn Leu Xaa Gly Met Gln Lys Cys Xaa Gly Arg His Xaa
 20 20 25 30
 Ser Ile Leu Xaa Ser Thr Pro Val His Ser Phe Lys Leu Xaa His Pro
 35 40 45
 Gln Thr Thr Leu Xaa Lys Phe Gly Val Lys Phe Cys Pro Val Ser Ser
 50 55 60
 25 Ser Ile Xaa Tyr Val Pro Thr Arg His Leu Asn Leu Lys Xaa Phe Phe
 65 70 75 80
 Xaa Pro Lys Ala Pro Arg Lys Trp Thr Xaa Gly Pro Lys Asp Gln Gly
 85 90 95
 Ala Pro Phe Ser Pro Gln
 30 100
 <210> 869
 <211> 115
 <212> PRT
 35 <213> Homo sapiens
 <400> 869
 Met Ile Pro Ser Phe Arg Thr Lys Val Thr Gly Thr Trp Thr Gly Cys
 1 5 10 15
 40 Arg Thr His Phe Gln Pro Xaa Arg Asn Ala Lys Met Ser Gly Thr Thr
 20 25 30
 Gln Ser Ile Xaa Xaa Pro His Leu Tyr Ile Val Ser Ala Xaa Thr Ser
 35 40 45
 Pro Asn His Thr Arg Lys Ile Xaa Ser Glu Asn Ser Val Leu Val Ser
 45 50 55 60
 Ser Ser Ile Ala Thr Ser Xaa Pro Ala Ile Xaa Thr Gly Arg Xaa Xaa
 65 70 75 80
 Leu Xaa Gln Gly Pro Xaa Asn Glu Leu Gly Gly Lys Gly Pro Xaa Ala
 85 90 95
 50 Pro Phe Pro Ser Xaa Lys Xaa Val Leu Pro Leu Gly Pro Tyr Phe Trp
 100 105 110
 Gly Pro Lys
 115
 55 <210> 870
 <211> 174
 <212> PRT
 <213> Homo sapiens
 60 <400> 870
 Gly Pro Arg Gly Asn Xaa Phe Xaa Ile Glu Gly Asn Gly Ala Xaa Gly
 1 5 10 15
 Pro Leu Pro Pro Ser Ser Phe Xaa Gly Pro Xaa Gly Lys Xaa Xaa Leu
 322

20 25 30
 Pro Val Xaa Met Ala Xaa Gly Asp Val Ala Met Leu Glu Leu Thr Arg
 35 40 45
 5 Thr Glu Phe Ser Leu Xaa Ile Leu Arg Val Trp Phe Gly Asp Val Xaa
 50 55 60
 Ala Glu Thr Met Tyr Arg Cys Gly Xaa Ser Met Leu Cys Val Val Pro
 65 70 75 80
 Asp Ile Phe Ala Phe Arg Xaa Gly Trp Lys Trp Val Arg Gln Pro Val
 85 90 95
 10 Gln Val Pro Val Thr Leu Val Arg Asn Asp Gly Ile Ile Tyr Ser Thr
 100 105 110
 Ser Leu Thr Phe Thr Tyr Thr Pro Glu Pro Gly Pro Arg Pro His Cys
 115 120 125
 Ser Ala Ala Gly Ala Thr Leu Arg Ala Asn Ser Ser Gln Xaa Pro Pro
 130 135 140
 15 Asn Glu Ser Asn Xaa Asn Ser Glu Gly Ser Tyr Thr Asn Ala Ser Thr
 145 150 155 160
 Asn Ser Thr Ser Val Thr Ser Xaa Thr Ala Xaa Val Val Ser
 165 170

20

<210> 871
 <211> 237
 <212> PRT
 <213> Homo sapiens

25

<400> 871
 Lys Thr Leu Tyr Ile Ser Asp Ser Asp Lys Arg Lys His Phe Met Leu
 1 5 10 15
 30 Ser Val Lys Met Phe Tyr Gly Asn Ser Asp Asp Ile Gly Val Phe Leu
 20 25 30
 Ser Lys Arg Ile Lys Val Ile Ser Lys Pro Ser Lys Lys Lys Gln Ser
 35 40 45
 Leu Lys Asn Ala Asp Leu Cys Ile Ala Ser Gly Thr Lys Val Ala Leu
 50 55 60
 35 Phe Asn Arg Leu Arg Ser Gln Thr Val Ser Thr Arg Tyr Leu His Val
 65 70 75 80
 Glu Gly Gly Asn Phe His Ala Ser Ser Gln Gln Trp Gly Ala Phe Phe
 85 90 95
 40 Ile His Leu Leu Asp Asp Asp Glu Ser Glu Gly Glu Glu Phe Thr Val
 100 105 110
 Arg Asp Gly Tyr Ile His Tyr Gly Gln Thr Val Lys Leu Val Cys Ser
 115 120 125
 Val Thr Gly Met Ala Leu Pro Arg Leu Ile Ile Arg Lys Val Asp Lys
 130 135 140
 45 Gln Thr Ala Leu Leu Asp Ala Asp Asp Pro Val Ser Gln Leu His Lys
 145 150 155 160
 Cys Ala Phe Tyr Leu Lys Asp Thr Glu Arg Met Tyr Leu Cys Leu Ser
 165 170 175
 Gln Glu Arg Ile Ile Gln Phe Gln Ala Thr Pro Cys Pro Lys Glu Pro
 180 185 190
 50 Asn Lys Glu Met Ile Asn Asp Gly Ala Xaa Trp Thr Ile Ile Ser Thr
 195 200 205
 Asp Lys Ala Glu Tyr Thr Phe Tyr Xaa Gly Met Gly Pro Val Leu Ala
 210 215 220
 55 Pro Ile Thr Pro Val Pro Val Val Lys Lys Ala Phe Xaa
 225 230 235

60

<210> 872
 <211> 179
 <212> PRT
 <213> Homo sapiens

<400> 872

Leu Asn Asp Gly Ala Ser Trp Pro Phe Ile Ser Xaa Asp Lys Ala Glu
 1 5 10 15
 Tyr Thr Phe Tyr Glu Gly Met Gly Pro Val Xaa Ala Pro Val Thr Pro
 20 25 30
 5 Val Pro Val Val Glu Ser Leu Gln Leu Asn Gly Gly Gly Asp Val Ala
 35 40 45
 Met Leu Glu Leu Thr Gly Gln Asn Phe Thr Pro Asn Leu Arg Val Trp
 50 55 60
 Phe Gly Asp Val Glu Ala Glu Thr Met Tyr Arg Cys Gly Glu Ser Met
 65 70 75 80
 10 Leu Cys Val Val Pro Asp Ile Ser Ala Phe Arg Glu Gly Trp Arg Trp
 85 90 95
 Val Arg Gln Pro Val Gln Val Pro Val Thr Leu Val Arg Asn Asp Gly
 100 105 110
 15 Ile Ile Tyr Ser Thr Ser Leu Thr Phe Thr Tyr Thr Pro Glu Pro Gly
 115 120 125
 Pro Arg Pro His Cys Ser Ala Ala Gly Ala Ile Leu Arg Ala Asn Ser
 130 135 140
 Ser Gln Val Pro Pro Asn Glu Ser Asn Thr Asn Ser Glu Gly Ser Tyr
 145 150 155 160
 20 Thr Asn Ala Ser Thr Asn Ser Thr Ser Val Thr Ser Ser Thr Ala Thr
 165 170 175
 Val Val Ser

25

<210> 873
 <211> 170
 <212> PRT
 <213> Homo sapiens

30

<400> 873
 Pro Arg Ile Gly Gln Ser Xaa His Phe Tyr Glu Gly Met Gly Pro Cys
 1 5 10 15
 Pro Cys Pro Ser His Xaa Cys Ala Cys Gly Xaa Glu Pro Ser Val Glu
 20 25 30
 35 Trp Arg Val Gly Thr Val Ala Met Leu Glu Leu Thr Gly Gln Asn Phe
 35 40 45
 Thr Pro Asn Leu Arg Val Trp Phe Gly Asp Val Glu Ala Glu Thr Met
 50 55 60
 40 Tyr Arg Cys Gly Glu Ser Met Leu Cys Val Val Pro Asp Ile Ser Ala
 65 70 75 80
 Phe Arg Glu Gly Trp Arg Trp Val Arg Gln Pro Val Gln Val Pro Val
 85 90 95
 Thr Leu Val Arg Asn Asp Gly Ile Ile Tyr Ser Thr Ser Leu Thr Phe
 100 105 110
 45 Thr Tyr Thr Pro Glu Pro Gly Pro Arg Pro His Cys Ser Ala Ala Gly
 115 120 125
 Ala Ile Leu Arg Ala Asn Ser Ser Gln Val Pro Pro Asn Glu Ser Asn
 130 135 140
 50 Thr Asn Ser Glu Gly Ser Tyr Thr Asn Ala Ser Thr Asn Ser Thr Ser
 145 150 155 160
 Val Thr Ser Ser Thr Ala Thr Val Val Ser
 165 170

55

<210> 874
 <211> 132
 <212> PRT
 <213> Homo sapiens

60

<400> 874
 Gln Cys Leu Asn Phe Thr Xaa Gln Asn Phe Thr Pro Asn Leu Arg Val
 1 5 10 15
 Trp Phe Gly Asp Val Glu Ala Glu Thr Met Tyr Arg Cys Gly Glu Ser

20 25 30
 Met Leu Cys Val Val Pro Asp Ile Xaa Ala Phe Arg Glu Gly Trp Arg
 35 40 45
 Trp Val Arg Gln Pro Val Gln Val Pro Val Thr Leu Val Arg Asn Asp
 5 50 55 60
 Gly Ile Ile Tyr Ser Thr Ser Leu Thr Phe Thr Tyr Thr Pro Glu Pro
 65 70 75 80
 Gly Pro Arg Pro His Cys Ser Ala Ala Gly Ala Ile Leu Arg Ala Asn
 85 90 95
 10 Ser Ser Gln Val Pro Pro Asn Glu Ser Asn Thr Asn Ser Glu Gly Ser
 100 105 110
 Tyr Thr Asn Ala Ser Thr Asn Ser Thr Ser Val Thr Ser Ser Thr Ala
 115 120 125
 Thr Val Val Ser
 15 130

<210> 875

<211> 160

<212> PRT

20 <213> Homo sapiens

<400> 875

Ile Gly Ser Lys Asp Cys Ser Cys Cys Thr Ala Met Trp Pro Arg Pro
 1 5 10 15
 25 Trp Phe Trp Cys Val Gly Lys Gly Lys Ala Gly Gly Ile Asn Asp Ser
 20 25 30
 Ile Ile Ser Asp Gln Ser Tyr Trp Asn Leu Asp Trp Leu Pro Asp Pro
 35 40 45
 Ser Pro Thr Xaa Ser Glu Cys Lys Asn Val Trp Asp Asp Thr Lys His
 50 55 60
 Thr Xaa Ser Thr Pro Xaa His Lys Phe Gln Ala Xaa Thr Ser Pro Asn
 65 70 75 80
 His Thr Arg Lys Phe Gly Val Lys Phe Cys Pro Val Ser Ser Lys His
 85 90 95
 35 Trp Tyr Val Pro Thr Ala Ile Gln Leu Xaa Xaa Xaa Phe His Xaa Pro
 100 105 110
 Xaa Xaa Asp Trp Gly Lys Asp Xaa Xaa His Ser Leu Xaa Lys Gly Tyr
 115 120 125
 Ser Gly Xaa Ser Gly Xaa Lys Xaa Gly Gln Xaa Xaa Pro His Leu Ser
 40 130 135 140
 Thr Xaa Tyr Leu Gly Leu Leu Glu Ile Gly Gly Ala Xaa Asn Xaa Ile
 145 150 155 160

<210> 876

45 <211> 129

<212> PRT

<213> Homo sapiens

<400> 876

50 Thr Tyr Arg Thr Glu Phe His Ser Lys Phe Thr Ser Val Val Trp Gly
 1 5 10 15
 Cys Xaa Ser Leu Lys Leu Met Xaa Arg Cys Gly Xaa Ser Met Leu Cys
 20 25 30
 Val Val Pro Asp Ile Phe Ala Phe Arg Xaa Gly Trp Arg Trp Val Arg
 55 35 40 45
 Gln Pro Val Gln Val Pro Val Thr Leu Val Arg Asn Asp Gly Ile Ile
 50 55 60
 Tyr Ser Thr Ser Leu Thr Phe Thr Tyr Thr Pro Glu Pro Gly Pro Arg
 65 70 75 80
 60 Pro His Cys Ser Ala Ala Gly Ala Ile Leu Arg Ala Asn Ser Ser Gln
 85 90 95
 Xaa Pro Pro Asn Glu Ser Asn Thr Asn Ser Glu Gly Ser Tyr Xaa Asn
 100 105 110

Ala Ser Xaa Asn Ser Thr Ser Val Thr Ser Xaa Thr Ala Xaa Val Val
 115 120 125
 Ser

5

<210> 877
 <211> 126
 <212> PRT
 <213> Homo sapiens

10

<400> 877
 Xaa Asn Xaa Gly Pro Leu Gln Phe Pro Lys Asp Pro Asn Lys Xaa Leu
 1 5 10 15
 Ile Asn Glu Xaa Leu Xaa Gly Xaa Ser Xaa Ala Gln Ile Xaa Gln Ser
 15 20 25 30
 Ile Leu Xaa Ile Arg Asn Xaa Xaa Cys Pro Cys Pro Ser Xaa Xaa Trp
 35 40 45
 Xaa Cys Gly Lys Xaa Xaa Ser Val Glu Trp Arg Trp Gly Arg Thr Asn
 50 55 60
 20 Ala Leu Asn Leu Gln Asp Arg Ile Ser Leu Gln Ile Tyr Glu Cys Gly
 65 70 75 80
 Leu Gly Met Xaa Lys Leu Glu Thr Tyr Xaa Gln Val Trp Xaa Glu Tyr
 85 90 95
 Ala Leu Cys Arg Pro Arg His Phe Cys Ile Pro Xaa Arg Leu Glu Met
 100 105 110
 25 Gly Pro Ala Thr Ser Pro Gly Ser Ser Asn Phe Gly Pro Lys
 115 120 125

30

<210> 878
 <211> 159
 <212> PRT
 <213> Homo sapiens

<400> 878
 35 Gly Lys Trp Ala Xaa Ser Xaa Ala Pro Val Ile Leu Val Pro Val Glu
 1 5 10 15
 Lys Xaa Xaa Gln Leu Asn Gly Gly Gly Asp Val Pro Met Leu Glu Leu
 20 25 30
 Thr Gly Xaa Asn Phe Thr Pro Asn Leu Arg Val Trp Phe Gly Asp Val
 40 35 40 45
 Xaa Ala Glu Thr Met Tyr Arg Cys Gly Xaa Ser Met Xaa Cys Val Val
 50 55 60
 Pro Asp Ile Xaa Ala Phe Arg Xaa Gly Trp Arg Trp Val Arg Gln Pro
 65 70 75 80
 45 Val Gln Val Pro Val Thr Leu Val Arg Asn Asp Gly Ile Ile Tyr Ser
 85 90 95
 Thr Ser Leu Thr Phe Thr Tyr Thr Pro Glu Pro Gly Pro Arg Pro His
 100 105 110
 Cys Ser Ala Ala Gly Ala Ile Leu Arg Ala Asn Ser Ser Gln Val Pro
 115 120 125
 50 Pro Asn Glu Ser Asn Thr Asn Ser Glu Gly Ser Tyr Xaa Asn Ala Ser
 130 135 140
 Thr Asn Ser Thr Ser Val Thr Ser Xaa Thr Ala Xaa Val Val Ser
 145 150 155

55

<210> 879
 <211> 111
 <212> PRT
 <213> Homo sapiens

60

<400> 879
 Lys Leu Lys Leu Met Tyr Arg Cys Gly Xaa Ser Met Xaa Cys Val Val
 1 5 10 15

Pro Xaa Ile Xaa Ala Phe Arg Xaa Gly Trp Arg Trp Val Arg Gln Pro
 20 25 30
 Val Gln Val Pro Val Thr Leu Val Arg Asn Asp Gly Ile Ile Tyr Ser
 35 40 45
 5 Xaa Ser Leu Thr Phe Thr Tyr Thr Pro Xaa Pro Gly Pro Arg Pro His
 50 55 60
 Cys Ser Ala Ala Gly Ala Ile Leu Arg Ala Asn Ser Ser Gln Xaa Pro
 65 70 75 80
 10 Pro Asn Glu Ser Asn Thr Asn Ser Glu Gly Ser Tyr Xaa Asn Ala Ser
 85 90 95
 Thr Asn Ser Thr Ser Val Thr Ser Xaa Thr Ala Xaa Val Val Ser
 100 105 110

15 <210> 880
 <211> 96
 <212> PRT
 <213> Homo sapiens

20 <400> 880
 Gly Gln Ser Ile Leu Xaa Ile Arg Xaa Trp Ala Xaa Xaa Leu Pro Gln
 1 5 10 15
 Ser Phe Leu Gly Xaa Gly Lys Xaa Pro Ser Val Glu Trp Arg Gly Asp
 20 25 30
 25 Val Xaa Met Phe Glu Leu Thr Xaa Gln Asn Phe Thr Pro Asn Leu Arg
 35 40 45
 Val Trp Phe Gly Asp Val Lys Ala Glu Thr Tyr Val Gln Val Trp Xaa
 50 55 60
 Glu Tyr Ala Xaa Cys Arg Pro Xaa His Xaa Cys Ile Pro Xaa Arg Leu
 65 70 75 80
 30 Glu Met Gly Pro Ala Thr Ser Pro Gly Ser Ser Asn Phe Gly Pro Lys
 85 90 95

35 <210> 881
 <211> 247
 <212> PRT
 <213> Homo sapiens

40 <400> 881
 Thr Val Phe Arg Gln Met Arg Pro Val Ser Arg Val Leu Ala Pro His
 1 5 10 15
 Leu Thr Arg Ala Tyr Ala Lys Asp Val Lys Phe Gly Ala Asp Ala Arg
 20 25 30
 Ala Leu Met Leu Gln Gly Val Asp Leu Leu Ala Asp Ala Val Ala Val
 35 40 45
 45 Thr Met Gly Pro Lys Gly Arg Thr Val Ile Ile Glu Gln Ser Trp Gly
 50 55 60
 Ser Pro Lys Val Thr Lys Asp Gly Val Thr Val Ala Lys Ser Ile Asp
 65 70 75 80
 Leu Lys Asp Lys Tyr Lys Asn Ile Gly Ala Lys Leu Val Gln Asp Val
 85 90 95
 50 Ala Asn Asn Thr Asn Glu Glu Ala Gly Asp Gly Thr Thr Thr Ala Thr
 100 105 110
 Val Leu Ala Arg Ser Ile Ala Lys Glu Gly Phe Glu Lys Ile Ser Lys
 115 120 125
 55 Gly Ala Asn Pro Val Glu Ile Xaa Arg Gly Val Met Leu Ala Val Asp
 130 135 140
 Ala Val Ile Ala Glu Leu Lys Lys Gln Ser Lys Pro Val Thr Thr Pro
 145 150 155 160
 Glu Glu Ile Ala Gln Val Ala Thr Ile Ser Ala Asn Gly Asp Lys Glu
 165 170 175
 60 Ile Gly Asn Ile Ile Ser Asp Ala Met Lys Lys Val Gly Arg Lys Gly
 180 185 190
 Val Ile Thr Val Lys Asp Gly Lys Thr Leu Asn Asp Glu Leu Glu Ile

195 200 205
 Ile Glu Gly Met Lys Phe Asp Arg Gly Tyr Ile Ser Pro Tyr Phe Ile
 210 215 220
 Asn Thr Ser Lys Gly Gln Lys Cys Glu Xaa Gln Asp Ala Tyr Val Leu
 5 225 230 235 240
 Val Ser Glu Lys Xaa Asn Xaa
 245

 <210> 882
 10 <211> 123
 <212> PRT
 <213> Homo sapiens

 <400> 882
 15 Pro Arg Ser Asn Phe Met Pro Ser Ile Ile Ser Asn Ser Ser Phe Ser
 1 5 10 15
 Val Phe Pro Ser Phe Thr Val Met Thr Pro Phe Leu Pro Thr Phe Phe
 20 20 25 30
 Ile Ala Ser Glu Met Ile Leu Pro Ile Ser Leu Ser Pro Phe Ala Glu
 35 40 45
 Ile Val Ala Thr Cys Ala Ile Ser Ser Gly Val Val Thr Gly Leu Asp
 50 55 60
 Cys Phe Leu Ser Ser Ala Ile Thr Ala Ser Thr Ala Asn Ile Thr Pro
 65 70 75 80
 25 Leu Xaa Ile Ser Thr Gly Leu Ala Pro Leu Leu Ile Phe Ser Lys Pro
 85 90 95
 Ser Leu Ala Ile Glu Arg Ala Ser Thr Val Ala Val Val Val Pro Ser
 100 105 110
 Pro Ala Ser Ser Phe Val Leu Leu Ala Thr Ser
 30 115 120

 <210> 883
 <211> 96
 <212> PRT'
 35 <213> Homo sapiens

 <400> 883
 Lys Lys Cys Arg Val Leu Lys Asp Leu Leu Lys Ser Xaa Arg Lys Ile
 1 5 10 15
 40 Met Gln Lys Phe Leu Gln Lys Val Gly Tyr Asp Ala Lys Gly Xaa Arg
 20 25 30
 Phe Cys Glu Tyr Gly Glu Lys Gly Ser Phe Asp Pro Pro Lys Val Val
 35 40 45
 Arg Thr Ala Leu Leu Asp Ala Ala Gly Val Ala Ser Leu Leu Thr Thr
 45 50 55 60
 Ala Xaa Val Val Val Thr Glu Ile Pro Lys Glu Lys Asp Pro Gly
 65 70 75 80
 Met Gly Ala Met Gly Gly Met Gly Gly Gly Met Gly Gly Gly Met Phe
 85 90 95
 50

 <210> 884
 <211> 212
 <212> PRT
 <213> Homo sapiens
 55

 <400> 884
 Leu Ala Glu Arg Thr Pr Cys Arg Arg Pro Ala Glu Met Leu Arg Leu
 1 5 10 15
 Pro Thr Val Phe Arg Gln Met Arg Pro Val Ser Arg Val Leu Ala Pro
 20 25 30
 His Leu Thr Arg Ala Tyr Ala Lys Asp Val Lys Phe Gly Ala Asp Ala
 35 40 45
 Arg Ala Leu Met Leu Gln Gly Val Asp Leu Leu Ala Asp Ala Val Ala
 328

	50		55		60												
	Val	Thr	Met	Gly	Pro	Lys	Gly	Arg	Thr	Val	Ile	Ile	Glu	Gln	Ser	Trp	
	65					70					75					80	
5	Gly	Ser	Pro	Lys	Val	Thr	Lys	Asp	Gly	Val	Thr	Val	Ala	Lys	Ser	Ile	
				85						90					95		
	Asp	Leu	Lys	Asp	Lys	Tyr	Lys	Asn	Ile	Gly	Ala	Lys	Leu	Val	Gln	Asp	
				100					105						110		
	Val	Ala	Asn	Asn	Thr	Asn	Glu	Glu	Ala	Gly	Asp	Gly	Thr	Thr	Thr	Ala	
			115				120						125				
10	Thr	Val	Leu	Ala	Arg	Ser	Ile	Ala	Lys	Glu	Gly	Phe	Glu	Lys	Ile	Ser	
	130						135					140					
	Lys	Gly	Ala	Asn	Pro	Val	Glu	Ile	Arg	Arg	Gly	Val	Met	Leu	Ala	Val	
	145					150					155					160	
	Asp	Ala	Val	Ile	Ala	Glu	Leu	Lys	Lys	Gln	Ser	Lys	Pro	Val	Thr	Thr	
15				165						170					175		
	Pro	Glu	Glu	Ile	Ala	Gln	Val	Ala	Thr	Ile	Ser	Ala	Asn	Gly	Asp	Lys	
				180					185					190			
	Glu	Ile	Gly	Asn	Ile	Ile	Ser	Asp	Ala	Met	Lys	Lys	Val	Gly	Arg	Xaa	
			195				200						205				
20	Gly	Val	Ile	Gln													
	210																

<210> 885

<211> 123

25 <212> PRT

<213> Homo sapiens

<400> 885

30	Gly	Ser	Lys	Phe	Asn	Ala	Phe	Lys	Asn	Phe	Leu	Ile	His	Pro	Phe	Arg	
	1				5					10					15		
	Val	Xaa	Pro	Ser	Phe	Tyr	Trp	Met	Thr	Xaa	Phe	Leu	Pro	Thr	Phe	Phe	
				20					25					30			
	Ile	Ala	Ser	Glu	Met	Ile	Leu	Pro	Ile	Ser	Leu	Ser	Pro	Phe	Ala	Glu	
			35				40						45				
35	Ile	Val	Ala	Thr	Cys	Ala	Ile	Ser	Ser	Gly	Val	Val	Thr	Gly	Leu	Asp	
	50						55				60						
	Cys	Phe	Leu	Ser	Ser	Ala	Ile	Thr	Ala	Ser	Thr	Ala	Asn	Ile	Thr	Pro	
	65				70					75					80		
	Leu	Leu	Ile	Ser	Thr	Gly	Leu	Ala	Pro	Leu	Leu	Ile	Phe	Ser	Lys	Pro	
40				85						90					95		
	Ser	Leu	Ala	Ile	Glu	Arg	Ala	Ser	Thr	Val	Ala	Val	Val	Val	Pro	Ser	
				100					105					110			
	Pro	Ala	Ser	Ser	Phe	Val	Leu	Leu	Ala	Thr	Ser						
			115					120									

45

<210> 886

<211> 107

<212> PRT

<213> Homo sapiens

50

<400> 886

	Thr	Val	Thr	Gly	Ser	Pro	Arg	Gln	Cys	Ser	Ser	Pro	Ile	Thr	Ser	Glu	
	1				5					10					15		
	Lys	Ser	Val	Gly	Glu	Asn	Glu	Glu	Lys	Gly	Trp	Leu	Lys	Ile	Thr	Ile	
55				20					25					30			
	Thr	Ile	Ser	Tyr	Trp	Phe	Gln	Leu	Thr	Lys	Tyr	Ile	Met	Val	Tyr	Cys	
			35				40						45				
	Cys	His	Cys	Pro	Cys	Leu	Gln	Ile	Ile	Tyr	Phe	Val	Phe	Leu	Asn	Lys	
	50					55				60							
60	Lys	His	Leu	Tyr	Ile	Pro	Asp	Thr	Gly	Tyr	Lys	Ser	His	Val	Pro	Val	
	65				70					75					80		
	Tyr	Cys	Phe	Gln	Leu	Lys	Ser	Leu	Arg	His	Phe	Tyr	Tyr	Tyr	Ser	Val	
				85					90						95		

Lys Ile Arg Ile Leu Val Leu Ala Thr Thr Arg
 100 105
 <210> 887
 5 <211> 107
 <212> PRT
 <213> Homo sapiens
 <400> 887
 10 Thr Val Thr Gly Ser Pro Arg Gln Cys Ser Ser Pro Ile Thr Ser Glu
 1 5 10 15
 Lys Ser Val Gly Glu Asn Glu Glu Lys Gly Trp Leu Lys Ile Thr Ile
 20 25 30
 Thr Ile Ser Tyr Trp Phe Gln Leu Thr Lys Tyr Ile Met Val Tyr Cys
 15 35 40 45
 Cys His Cys Pro Cys Leu Gln Ile Ile Tyr Phe Val Phe Leu Asn Lys
 50 55 60
 Lys His Leu Tyr Ile Pro Asp Thr Gly Tyr Lys Ser His Val Pro Val
 65 70 75 80
 20 Tyr Cys Phe Gln Leu Lys Ser Leu Arg His Phe Tyr Tyr Tyr Ser Val
 85 90 95
 Lys Ile Arg Ile Leu Val Leu Ala Xaa Thr Arg
 100 105
 25 <210> 888
 <211> 88
 <212> PRT
 <213> Homo sapiens
 30 <400> 888
 Asn Met Pro Pro Ile Pro Pro Ser Ile Pro Pro Ile Ala Pro Ile
 1 5 10 15
 Pro Gly Ser Phe Ser Ser Leu Gly Ile Ser Val Thr Thr Thr Ser Ala
 20 25 30
 35 Val Val Asn Lys Arg Gly Pro Thr Gln Gln His Pro Ile Lys Ala Val
 35 40 45
 Leu Thr Thr Phe Gly Trp Gly Asn Asp Ser Phe Phe Xaa Pro Tyr Ser
 50 55 60
 Pro Lys Ile Xaa Pro Ala Xaa Ser Ile Ile Thr Xaa Leu Xaa Gly Gly
 40 65 70 75 80
 Lys Leu Cys Ile Asn Phe Leu Asn
 85
 45 <210> 889
 <211> 107
 <212> PRT
 <213> Homo sapiens
 <400> 889
 50 Thr Val Thr Gly Ser Pro Arg Gln Cys Ser Ser Pro Ile Thr Ser Glu
 1 5 10 15
 Lys Ser Val Gly Glu Asn Glu Glu Lys Gly Trp Leu Lys Ile Thr Ile
 20 25 30
 Thr Ile Ser Tyr Trp Phe Gln Leu Thr Lys Tyr Ile Met Val Tyr Cys
 55 35 40 45
 Cys His Cys Pro Cys Leu Gln Ile Ile Tyr Phe Val Phe Leu Asn Lys
 50 55 60
 Lys His Leu Tyr Ile Pro Asp Thr Gly Tyr Lys Ser His Val Pro Val
 65 70 75 80
 60 Tyr Cys Phe Gln Leu Lys Ser Leu Arg His Phe Tyr Tyr Tyr Ser Val
 85 90 95
 Lys Ile Arg Ile Leu Val Leu Ala Thr Thr Arg
 100 105

<210> 890
 <211> 68
 <212> PRT
 5 <213> Homo sapiens

<400> 890
 Ser Thr Ser Leu Gly Val Arg Thr Cys His Leu Pro Tyr His Leu Pro
 1 5 10 15
 10 Phe His Pro Leu His Pro Phe Gln Gly Pro Phe Ser Ser Phe Xaa Asn
 20 25 30
 Phe Trp Gly Leu Gln Leu Leu Leu Val Val Asn Arg Glu Gly Pro His
 35 40 45
 15 Gln Ala Ala Phe Pro Ile Lys Pro Val Xaa His Gln Pro Phe Gly Trp
 50 55 60
 Gly Gln Arg Ile
 65

20 <210> 891
 <211> 107
 <212> PRT
 <213> Homo sapiens

<400> 891
 25 Thr Val Thr Gly Ser Pro Arg Gln Cys Ser Ser Pro Ile Thr Ser Glu
 1 5 10 15
 Lys Ser Val Gly Glu Asn Glu Glu Lys Gly Trp Leu Lys Ile Thr Ile
 20 25 30
 30 Thr Ile Ser Tyr Trp Phe Gln Leu Thr Lys Tyr Ile Met Val Tyr Cys
 35 40 45
 Cys His Cys Pro Cys Leu Gln Ile Ile Tyr Phe Val Phe Leu Asn Lys
 50 55 60
 Lys His Leu Tyr Ile Pro Asp Thr Gly Tyr Lys Ser His Val Pro Val
 65 70 75 80
 35 Tyr Cys Phe Gln Leu Lys Ser Leu Arg His Phe Tyr Tyr Tyr Ser Val
 85 90 95
 Lys Ile Arg Ile Leu Val Leu Ala Thr Thr Arg
 100 105

40 <210> 892
 <211> 66
 <212> PRT
 <213> Homo sapiens

45 <400> 892
 Asp Phe Gly Glu Tyr Gly Glu Lys Gly Ile Ile Asp Xaa Thr Lys Gly
 1 5 10 15
 Cys Glu Asn Cys Phe Tyr Trp Met Leu Leu Gly Val Xaa Ser Leu Leu
 20 25 30
 50 Thr Thr Ala Glu Val Val Val Thr Glu Ile Pro Lys Glu Glu Lys Asp
 35 40 45
 Pro Gly Met Gly Ala Met Gly Gly Met Gly Gly Gly Met Gly Gly Gly
 50 55 60
 Met Phe
 55 65

60 <210> 893
 <211> 217
 <212> PRT
 <213> Homo sapiens

<400> 893
 Met Ala Met Ala Tyr Leu Ala Trp Arg Leu Ala Arg Arg Ser Cys Pro

1 5 10 15
 Ser Ser Leu Gln Val Thr Ser Phe Pro Val Val Gln Leu His Met Asn
 20 25 30
 Arg Thr Ala Met Arg Ala Ser Gln Lys Asp Phe Glu Asn Ser Met Asn
 35 40 45
 5 Gln Val Lys Leu Leu Lys Lys Asp Pro Gly Asn Glu Val Lys Leu Lys
 50 55 60
 Leu Tyr Ala Leu Tyr Lys Gln Ala Thr Glu Gly Pro Cys Asn Met Pro
 65 70 75 80
 10 Lys Pro Gly Val Phe Asp Leu Ile Asn Lys Ala Lys Trp Asp Ala Trp
 85 90 95
 Asn Ala Leu Gly Ser Leu Pro Lys Glu Ala Ala Arg Gln Asn Tyr Val
 100 105 110
 Asp Leu Val Ser Ser Leu Ser Pro Ser Leu Glu Ser Ser Ser Gln Val
 115 120 125
 15 Glu Pro Gly Thr Asp Arg Lys Ser Thr Gly Phe Glu Thr Leu Val Val
 130 135 140
 Thr Ser Glu Asp Gly Ile Thr Lys Ile Met Phe Asn Arg Pro Lys Lys
 145 150 155 160
 20 Lys Asn Ala Ile Asn Thr Glu Met Tyr His Glu Ile Met Arg Ala Leu
 165 170 175
 Lys Ala Ala Ser Lys Asp Asp Ser Ile Ile Thr Val Leu Thr Gly Asn
 180 185 190
 Gly Asp Tyr Tyr Ser Ser Gly Asn Asp Leu Thr Asn Phe Thr Asp Ile
 195 200 205
 25 Pro Pro Gly Gly Val Glu Glu Lys Ala
 210 215

30 <210> 894
 <211> 156
 <212> PRT
 <213> Homo sapiens

35 <400> 894
 Leu Gln Gly Gly Asn Gly Pro Ala Val Gly Ile Ser Val Thr Leu Leu
 1 5 10 15
 Gly Leu Phe Asp Ala Val Tyr Ala Ser Asp Arg Ala Thr Phe His Thr
 20 25 30
 40 Pro Phe Ser His Leu Gly Gln Ser Pro Glu Gly Cys Ser Ser Tyr Thr
 35 40 45
 Phe Pro Lys Ile Met Ser Pro Ala Lys Ala Thr Glu Met Leu Ile Phe
 50 55 60
 Gly Lys Lys Leu Thr Ala Gly Glu Ala Cys Ala Gln Gly Leu Val Thr
 65 70 75 80
 45 Glu Val Phe Pro Asp Ser Thr Phe Gln Lys Glu Val Trp Thr Arg Leu
 85 90 95
 Lys Ala Phe Ala Lys Leu Pro Pro Asn Ala Leu Arg Ile Ser Lys Glu
 100 105 110
 Val Ile Arg Lys Arg Glu Arg Glu Lys Leu His Ala Val Asn Ala Glu
 115 120 125
 50 Glu Cys Asn Val Leu Gln Gly Arg Trp Leu Ser Asp Glu Cys Thr Asn
 130 135 140
 Ala Val Val Asn Phe Leu Ser Arg Lys Ser Lys Leu
 145 150 155

55 <210> 895
 <211> 195
 <212> PRT
 <213> Homo sapiens

60 <400> 895
 Val Leu Gly Leu Glu Thr Gly Ala Ala Phe Val Ser Glu Val Thr Ser
 1 5 10 15

Phe Pro Val Val Gln Leu His Met Asn Arg Thr Ala Met Arg Ala Ser
 20 25 30
 Gln Lys Asp Phe Glu Asn Ser Met Asn Gln Val Lys Leu Leu Lys Lys
 35 40 45
 5 Asp Pro Gly Asn Glu Val Lys Leu Lys Leu Tyr Ala Leu Tyr Lys Gln
 50 55 60
 Ala Thr Glu Gly Pro Cys Asn Met Pro Lys Pro Gly Val Phe Asp Leu
 65 70 75 80
 10 Ile Asn Lys Ala Lys Trp Asp Ala Trp Asn Ala Leu Gly Ser Leu Pro
 85 90 95
 Lys Glu Ala Ala Arg Gln Asn Tyr Val Asp Leu Val Ser Ser Leu Ser
 100 105 110
 Pro Ser Leu Glu Ser Ser Ser Gln Val Glu Pro Gly Thr Asp Arg Lys
 115 120 125
 15 Ser Thr Gly Phe Glu Thr Leu Val Val Thr Ser Glu Asp Gly Ile Thr
 130 135 140
 Lys Ile Met Phe Asn Arg Pro Lys Lys Lys Asn Ala Ile Asn Thr Glu
 145 150 155 160
 20 Met Tyr His Glu Ile Met Arg Ala Leu Lys Ser Xaa Xaa Gln Xaa Met
 165 170 175
 Thr Gln Ser Ser Leu Val Leu Thr Arg Lys Trp Xaa Thr Ile Thr Ser
 180 185 190
 Lys Trp Glu
 195
 25
 <210> 896
 <211> 176
 <212> PRT
 <213> Homo sapiens
 30
 <400> 896
 Asn Asn Xaa Val Leu Leu Arg Xaa Phe Val Xaa Cys Phe Ile Asp Phe
 1 5 10 15
 35 Pro Lys Pro Leu Ile Ala Val Val Asn Gly Pro Ala Val Gly Ile Xaa
 20 25 30
 Val Thr Leu Leu Gly Leu Phe Asp Xaa Val Tyr Ala Ser Asp Arg Ala
 35 40 45
 Thr Phe His Thr Pro Phe Ser His Leu Gly Gln Ser Pro Glu Gly Cys
 50 55 60
 40 Ser Ser Tyr Thr Phe Pro Lys Ile Met Ser Pro Ala Lys Ala Thr Glu
 65 70 75 80
 Met Leu Ile Phe Gly Lys Lys Leu Thr Ala Gly Glu Ala Cys Ala Gln
 85 90 95
 45 Gly Leu Val Thr Glu Val Phe Pro Asp Ser Thr Phe Gln Lys Glu Val
 100 105 110
 Trp Thr Arg Leu Lys Ala Phe Ala Lys Leu Pro Pro Asn Ala Leu Arg
 115 120 125
 Ile Ser Lys Glu Val Ile Arg Lys Arg Glu Arg Glu Lys Leu His Ala
 130 135 140
 50 Val Asn Ala Glu Glu Cys Asn Val Leu Gln Gly Arg Trp Leu Ser Asp
 145 150 155 160
 Glu Cys Thr Asn Ala Val Val Asn Phe Leu Ser Arg Lys Ser Lys Leu
 165 170 175
 55
 <210> 897
 <211> 217
 <212> PRT
 <213> Homo sapiens
 60
 <400> 897
 Met Ala Met Ala Tyr Leu Ala Trp Arg Leu Ala Arg Arg Ser Cys Pro
 1 5 10 15
 Ser Ser Leu Gln Val Thr Ser Phe Pro Val Val Gln Leu His Met Asn
 20 25 30

20 25 30
 Arg Thr Ala Met Arg Ala Ser Gln Lys Asp Phe Glu Asn Ser Met Asn
 35 40 45
 5 Gln Val Lys Leu Leu Lys Lys Asp Pro Gly Asn Glu Val Lys Leu Lys
 50 55 60
 Leu Tyr Ala Leu Tyr Lys Gln Ala Thr Glu Gly Pro Cys Asn Met Pro
 65 70 75 80
 Lys Pro Gly Val Phe Asp Leu Ile Asn Lys Ala Lys Trp Asp Ala Trp
 85 90 95
 10 Asn Ala Leu Gly Ser Leu Pro Lys Glu Ala Ala Arg Gln Asn Tyr Val
 100 105 110
 Asp Leu Val Ser Ser Leu Ser Pro Ser Leu Glu Ser Ser Ser Gln Val
 115 120 125
 15 Glu Pro Gly Thr Asp Arg Lys Ser Thr Gly Phe Glu Thr Leu Val Val
 130 135 140
 Thr Ser Glu Asp Gly Ile Thr Lys Ile Met Phe Asn Arg Pro Lys Lys
 145 150 155 160
 Lys Asn Ala Ile Asn Thr Glu Met Tyr His Glu Ile Met Arg Ala Leu
 165 170 175
 20 Lys Ala Ala Ser Lys Asp Asp Ser Ile Ile Thr Val Leu Thr Gly Asn
 180 185 190
 Gly Asp Tyr Tyr Ser Ser Gly Asn Asp Leu Thr Asn Phe Thr Asp Ile
 195 200 205
 Xaa Pro Gly Gly Val Xaa Glu Lys Ala
 210 215

<210> 898

<211> 158

<212> PRT

30 <213> Homo sapiens

<400> 898

Ala Ser Asp Xaa Ser Gly Asn Gly Pro Ala Val Gly Ile Xaa Val Thr
 1 5 10 15
 35 Leu Leu Gly Leu Phe Asp Xaa Val Tyr Ala Ser Asp Arg Ala Thr Phe
 20 25 30
 His Thr Pro Phe Ser His Xaa Gly Gln Ser Pro Glu Gly Cys Ser Ser
 35 40 45
 Tyr Thr Phe Pro Lys Ile Met Ser Pro Ala Lys Ala Thr Glu Met Leu
 50 55 60
 Ile Phe Gly Lys Lys Leu Thr Ala Gly Glu Ala Cys Ala Gln Gly Leu
 65 70 75 80
 Val Thr Glu Val Phe Pro Asp Ser Thr Phe Gln Lys Glu Val Trp Thr
 85 90 95
 45 Arg Leu Lys Ala Phe Ala Lys Leu Pro Pro Asn Ala Leu Arg Ile Ser
 100 105 110
 Lys Glu Val Ile Arg Lys Arg Glu Arg Glu Lys Leu His Ala Val Asn
 115 120 125
 Ala Glu Glu Cys Asn Val Leu Gln Gly Arg Trp Leu Ser Asp Glu Cys
 130 135 140
 50 Thr Asn Ala Val Val Asn Phe Leu Ser Arg Lys Ser Lys Leu
 145 150 155

<210> 899

55 <211> 156

<212> PRT

<213> Homo sapiens

<400> 899

60 Leu Gln Trp Ser Met Val Gln Leu Trp Ala Ser Pro Ser Pro Ser Leu
 1 5 10 15
 Gly Leu Phe Asp Ala Val Tyr Ala Ser Asp Arg Ala Thr Phe His Thr
 20 25 30

Pro Phe Ser His Leu Gly Gln Ser Pro Glu Gly Cys Ser Ser Tyr Thr
 35 40 45
 Phe Pro Lys Ile Met Ser Pro Ala Lys Ala Thr Glu Met Leu Ile Phe
 50 55 60
 5 Gly Lys Lys Leu Thr Ala Gly Glu Ala Cys Ala Gln Gly Leu Val Thr
 65 70 75 80
 Glu Val Phe Pro Asp Ser Thr Phe Gln Lys Glu Val Trp Thr Arg Leu
 85 90 95
 10 Lys Ala Phe Ala Lys Leu Pro Pro Asn Ala Leu Arg Ile Ser Lys Glu
 100 105 110
 Val Ile Arg Lys Arg Glu Arg Glu Lys Leu His Ala Val Asn Ala Glu
 115 120 125
 Glu Cys Asn Val Leu Gln Gly Arg Trp Leu Ser Asp Glu Cys Thr Asn
 130 135 140
 15 Ala Val Val Asn Phe Leu Ser Arg Lys Ser Lys Leu
 145 150 155

 <210> 900
 <211> 108
 20 <212> PRT
 <213> Homo sapiens

 <400> 900
 25 Leu Leu Lys Asn His Thr Asp Lys Gln Leu Ser Asn Lys Thr Gly Leu
 1 5 10 15
 Val Gly Phe Leu Ala Cys Leu Thr Asn Met Thr Asp Phe Leu Ser Gln
 20 25 30
 Ala Leu Leu Xaa Lys Thr Ser Cys Gly Asn Gln Ala Arg Asp Lys Asn
 35 40 45
 30 Ser Ser Leu Met Gln Leu Gly Glu Arg Glu Arg Leu Glu Thr Ser Leu
 50 55 60
 Ala Ser Asn Ser Thr His Ser His Leu Cys Val Ser Ala Leu Leu Gln
 65 70 75 80
 Ala Gln Tyr Ala Xaa Cys Arg Asp Gly Gln Met Phe Arg Val Gly Ser
 85 90 95
 35 Gly Thr Phe Gln Pro Ala Lys Ser Ala Glu Val Ile
 100 105

 <210> 901
 40 <211> 77
 <212> PRT
 <213> Homo sapiens

 <400> 901
 45 Phe Tyr Asn Ala Leu Tyr Leu Ile Lys Glu Phe Ala Phe Phe Val Tyr
 1 5 10 15
 Thr Gly Met Leu Tyr Ser Leu Cys Ile Leu Gln Gly Tyr Lys Met Ser
 20 25 30
 Leu Ile Leu Asn Ile Thr Pro Lys Val Ile Ser Glu Lys Lys Gly Phe
 35 40 45
 50 Leu Lys Leu Asn Leu Thr Phe Lys Lys Ser Tyr Gly Gln Thr Thr Phe
 50 55 60
 Lys Gln Asn Trp Ile Ser Arg Ile Ser Cys Leu Leu Asn
 65 70 75

55 <210> 902
 <211> 221
 <212> PRT
 <213> Homo sapiens

60 <400> 902
 Gln Asn Asp Asp Ala Glu Val Ser Leu Met Glu Val Arg Phe Tyr Val
 1 5 10 15

Pro Pro Thr Gln Glu Asp Gly Val Asp Pro Val Glu Ala Phe Ala Gln
 20 25 30
 Asn Val Leu Ser Lys Ala Asp Val Ile Gln Ala Thr Gly Asp Ala Ile
 35 40 45
 5 Cys Ile Phe Arg Glu Leu Gln Cys Leu Thr Pro Arg Gly Arg Tyr Asp
 50 55 60
 Ile Arg Ile Tyr Pro Thr Phe Leu His Leu His Gly Lys Thr Phe Asp
 65 70 75 80
 Tyr Lys Ile Pro Tyr Thr Thr Val Leu Arg Leu Phe Leu Leu Pro His
 85 90 95
 10 Lys Asp Gln Arg Gln Met Phe Phe Val Ile Ser Leu Asp Pro Pro Ile
 100 105 110
 Lys Gln Gly Gln Thr Arg Tyr His Phe Leu Ile Leu Leu Phe Ser Lys
 115 120 125
 15 Asp Glu Asp Ile Ser Leu Thr Leu Asn Met Asn Glu Glu Val Glu
 130 135 140
 Lys Arg Phe Glu Gly Arg Leu Thr Lys Asn Met Ser Gly Ser Leu Tyr
 145 150 155 160
 Glu Met Val Ser Arg Val Met Lys Ala Leu Val Asn Arg Lys Ile Thr
 165 170 175
 20 Val Pro Gly Asn Phe Gln Gly His Ser Gly Ala Gln Cys Ile Thr Cys
 180 185 190
 Ser Tyr Lys Ala Lys Leu Xaa Thr Ala Leu Pro Ala Gly Ala Gly Leu
 195 200 205
 25 His Leu Arg Xaa Gln Ala Thr Cys Ala His Xaa Leu Arg
 210 215 220

<210> 903

<211> 170

30 <212> PRT

<213> Homo sapiens

<400> 903

Gly Arg Glu Ser Xaa Met Arg Ile Trp Ile Leu His Cys Pro Ala Ser
 1 5 10 15
 His Pro Xaa Xaa Pro Gln Ile Ile Asn Ser His Pro Trp Glu Ala Ala
 20 25 30
 Lys Leu Xaa Arg Leu Pro Thr Ala Leu Gly Thr Tyr Xaa Pro Thr Gly
 35 40 45
 40 Xaa His Val Xaa Met Ala Xaa Asn Pro Gly Thr Ala Phe His Glu Xaa
 50 55 60
 Lys Leu Val Gln Asn Met Gly Gly Glu Ser Gly Gly Val Lys Arg Gln
 65 70 75 80
 Ala Gln Xaa Glu Pro Ser Ser Val Ser Thr His Arg Ile Leu Thr Leu
 85 90 95
 45 Lys Pro Xaa Ser Trp Gly Glu Tyr Trp Leu Val Leu Leu Leu Xaa Xaa
 100 105 110
 Pro Arg Ser Ser Ser Xaa Xaa Xaa Cys Ser Xaa Ser Leu Pro Glu Lys
 115 120 125
 50 Xaa Xaa Ser Leu Xaa Thr Asn Xaa Leu Leu Phe Glu Ala Leu Ala Leu
 130 135 140
 Thr Ala Leu Xaa Gly Arg Leu Xaa Ile Xaa Glu Pro Pro Xaa Xaa Gly
 145 150 155 160
 Xaa Gly Phe Leu Phe Pro Phe Xaa Thr Leu
 165 170

<210> 904

<211> 266

60 <212> PRT

<213> Homo sapiens

<400> 904

Gln Ser Thr Val Ala Ser Gly Thr Val Ala Arg Val Glu Pro Asn Ile

1 5 10 15
 Lys Trp Phe Gly Asn Thr Arg Val Ile Lys Gln Ser Ser Leu Gln Lys
 20 25 30
 Phe Gln Glu Glu Met Asp Thr Val Met Lys Asp Pro Tyr Lys Val Val
 35 40 45
 5 Met Lys Gln Ser Lys Leu Pro Met Ser Leu Leu His Asp Arg Ile Arg
 50 55 60
 Pro His Asn Leu Lys Val His Ile Leu Asp Thr Glu Ser Phe Glu Thr
 65 70 75 80
 10 Thr Phe Gly Pro Lys Ser Gln Arg Lys Arg Pro Asn Leu Phe Ala Ser
 85 90 95
 Asp Met Gln Ser Leu Ile Glu Asn Ala Glu Met Ser Thr Glu Ser Tyr
 100 105 110
 Asp Gln Gly Lys Asp Arg Asp Leu Val Thr Glu Asp Thr Gly Val Arg
 115 120 125
 15 Asn Glu Ala Gln Glu Glu Ile Tyr Lys Lys Gly Gln Ser Lys Arg Ile
 130 135 140
 Trp Gly Glu Leu Tyr Lys Val Ile Asp Ser Ser Asp Val Val Val Gln
 145 150 155 160
 20 Val Leu Asp Ala Arg Asp Pro Met Gly Thr Arg Ser Pro His Ile Glu
 165 170 175
 Thr Tyr Leu Lys Lys Glu Lys Pro Trp Lys His Leu Ile Phe Val Leu
 180 185 190
 Asn Lys Cys Asp Leu Val Pro Thr Trp Ala Thr Lys Arg Xaa Val Ala
 195 200 205
 25 Val Leu Phe Gln Asp Tyr Pro Thr Leu Ala Xaa His Ala Ser Leu Thr
 210 215 220
 Xaa Pro Phe Gly Lys Gly Ala Phe Ile His Xaa Cys Gly Ser Phe Gly
 225 230 235 240
 30 Lys Leu Pro Thr Xaa Gln Glu Asn Arg Ser Xaa Val Gly Ser Leu Ala
 245 250 255
 Phe Pro Lys Val Gly Lys Glu Xaa Leu Gly
 260 265
 35 <210> 905
 <211> 257
 <212> PRT
 <213> Homo sapiens
 40 <400> 905
 Gly Ser Xaa Ser Xaa Lys Thr Gln Pro Arg Pro Xaa Pro Gly Gly Glu
 1 5 10 15
 Ser Pro Xaa Xaa Leu Gln Gly Xaa Gly Ser Arg Phe Xaa Pro Xaa Xaa
 20 25 30
 45 Arg Xaa Xaa Lys Gly Pro Val Pro Cys Val Cys Leu Pro Gln Arg Cys
 35 40 45
 Ser Xaa Xaa Xaa Xaa Glu Xaa Xaa Arg Thr Leu Val Lys Ser Thr Trp
 50 55 60
 Xaa Leu Ser Phe Leu Gly Met Xaa Trp Phe Xaa Trp Arg Cys Gln Xaa
 65 70 75 80
 50 Phe Glu Glu Glu Leu Glu Ser Phe Phe Asp Glu Glu Glu Glu Glu
 85 90 95
 Glu Xaa Gln Arg Asp Xaa Ala Glu Glu Xaa Ser Ser Glu Pro Glu Glu
 100 105 110
 55 Glu Asn Val Gly Asn Asp Xaa Lys Ala Val Ile Lys Xaa Leu Asp Glu
 115 120 125
 Lys Ile Ala Lys Tyr Gln Lys Phe Leu Asp Lys Ala Lys Ala Lys Lys
 130 135 140
 Phe Ser Ala Val Arg Ile Ser Lys Gly Leu Ser Glu Lys Ile Phe Ala
 145 150 155 160
 60 Lys Pro Glu Glu Gln Xaa Xaa Xaa Leu Glu Glu Asp Val Asp Xaa Arg
 165 170 175
 Ala Pro Ser Lys Lys Gly Lys Lys Arg Lys Xaa Gln Arg Glu Glu Glu

180 185 190
 Gln Glu His Ser Asn Lys Ala Pro Arg Xaa Leu Thr Ser Lys Glu Arg
 195 200 205
 5 Arg Arg Ala Val Arg Gln Gln Arg Pro Lys Lys Val Gly Val Arg Xaa
 210 215 220
 Tyr Glu Xaa Pro Asn Val Lys Asn Arg Asn Arg Asn Lys Lys Lys Thr
 225 230 235 240
 Asn Asp Ser Glu Gly Gln Lys Xaa Xaa Arg Lys Lys Phe Arg Gln Lys
 245 250 255
 10 Gln

<210> 906
 <211> 242
 15 <212> PRT
 <213> Homo sapiens

<400> 906
 20 Ala Glu Lys Leu Arg Ser Val Val Met Pro Met Glu Lys Glu Ile Ala
 1 5 10 15
 Ala Leu Lys Asp Lys Leu Thr Glu Ala Glu Asp Lys Ile Lys Glu Leu
 20 25 30
 Glu Ala Ser Lys Val Lys Glu Leu Asn His Tyr Leu Glu Ala Glu Lys
 35 40 45
 25 Ser Cys Arg Thr Asp Leu Glu Met Tyr Val Ala Val Leu Asn Thr Gln
 50 55 60
 Lys Ser Val Leu Gln Glu Asp Ala Glu Lys Leu Arg Lys Glu Leu His
 65 70 75 80
 Glu Val Cys His Leu Leu Glu Gln Glu Arg Gln Gln His Asn Gln Leu
 85 90 95
 30 Lys His Thr Trp Gln Lys Ala Asn Asp Gln Phe Leu Glu Ser Gln Arg
 100 105 110
 Leu Leu Met Arg Asp Met Gln Arg Met Glu Ile Val Leu Thr Ser Glu
 115 120 125
 35 Gln Leu Arg Gln Val Glu Glu Leu Lys Lys Lys Asp Gln Glu Asp Asp
 130 135 140
 Glu Gln Gln Arg Leu Asn Lys Arg Lys Asp His Lys Lys Ala Asp Val
 145 150 155 160
 Glu Glu Glu Ile Lys Ile Pro Val Val Cys Ala Leu Thr Gln Glu Glu
 165 170 175
 40 Ser Ser Ala Gln Leu Ser Asn Glu Glu Glu His Leu Asp Ser Thr Arg
 180 185 190
 Gly Ser Val His Ser Leu Xaa Ala Gly Leu Leu Leu Pro Ser Gly Asp
 195 200 205
 45 Pro Phe Ser Lys Ser Asp Asn Asp Met Phe Lys Asp Gly Leu Arg Arg
 210 215 220
 Ala Gln Ser Ser Arg Gln Leu Trp Asp Pro Arg Ala His Cys Asn Xaa
 225 230 235 240
 Lys Leu

<210> 907
 <211> 84
 <212> PRT
 55 <213> Homo sapiens

<400> 907
 Pro Ser Gln Ile Lys Val Phe Phe Xaa Xaa Xaa Gly Pro Pro Ser Lys
 1 5 10 15
 60 Lys Phe Phe Xaa Ser Xaa Lys Lys Gly Xaa Gly Xaa Lys Lys Phe Xaa
 20 25 30
 Pro Xaa Leu Gly Lys Gly Xaa Gly Val Ser Xaa Gly Ala Lys Ser Xaa
 35 40 45

Pro Xaa Gly Asn Phe Leu Phe Trp Xaa Lys Lys Pro Xaa Xaa Ser Xaa
 50 55 60
 Leu Ser Phe Val Xaa Pro Met Cys Phe Gly Tyr Lys Gln Xaa Xaa Val
 65 70 75 80
 5 Ser Leu Ser Arg

10 <210> 908
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 908
 15 Asn Pro Thr Glu Leu Phe Phe Cys Leu Lys Gly Leu Asn Xaa Ala Xaa
 1 5 10 15
 Tyr Ile Lys Xaa Pro Phe Met Leu Lys Thr Gln Leu Lys Glu Leu Val
 20 20 25 30
 Ser Thr Trp Thr Gly Thr Xaa Xaa Phe Val Tyr Thr Gln Asn Thr Leu
 35 40 45
 20 Xaa Xaa Gln Asn Leu Xaa Ser Ser Xaa Xaa Val Phe Xaa Thr Lys Lys
 50 55 60
 Gly Asn Ser His Xaa Xaa Gly Ile Leu Pro Gln Xaa Lys Pro Leu Xaa
 65 70 75 80
 25 Leu Ser Leu Asn Xaa Gly Xaa Ile Phe Leu Xaa Xaa Pro Leu Phe Phe
 85 90 95
 Xaa Xaa Lys Lys Ile Phe Trp Lys Gly Ala Gln Xaa
 100 105

30 <210> 909
 <211> 114
 <212> PRT
 <213> Homo sapiens

<400> 909
 35 Ala Phe Leu Leu Pro Lys Arg Ala Lys Xaa Cys Leu Xaa His Gln Xaa
 1 5 10 15
 Pro Ile Tyr Ala Glu Asn Pro Ile Glu Arg Ile Gly Phe Tyr Leu Asp
 20 25 30
 40 Arg Asp Thr Xaa Xaa Cys Leu Tyr Pro Lys His Ile Xaa Xaa Thr Lys
 35 40 45
 Leu Xaa Lys Leu Xaa Xaa Gly Phe Xaa Tyr Gln Lys Arg Lys Phe Pro
 50 55 60
 Xaa Gly Xaa Asp Phe Ala Pro Xaa Glu Thr Pro Xaa Pro Phe Pro Lys
 65 70 75 80
 45 Xaa Gly Xaa Asn Phe Phe Xaa Xaa Pro Pro Phe Phe Xaa Xaa Lys Lys
 85 90 95
 Asn Phe Leu Glu Gly Gly Pro Xaa Leu Xaa Lys Lys Thr Phe Ile Trp
 100 105 110
 Glu Gly

50 <210> 910
 <211> 164
 <212> PRT
 55 <213> Homo sapiens

<400> 910
 60 Lys Met Ala Ala Pro Glu Lys Met Thr Phe Pr Glu Lys Pro Ser His
 1 5 10 15
 Lys Lys Tyr Arg Ala Ala Leu Lys Lys Glu Lys Arg Lys Lys Arg Arg
 20 25 30
 Gln Glu Leu Ala Arg Leu Arg Asp Ser Gly Leu Ser Gln Lys Glu Glu
 35 40 45

Glu Glu Asp Thr Phe Ile Glu Glu Gln Gln Leu Glu Glu Glu Lys Leu
 50 55 60
 Leu Glu Arg Glu Arg Gln Arg Leu His Glu Glu Trp Leu Leu Arg Glu
 65 70 75 80
 5 Gln Lys Ala Gln Glu Glu Phe Arg Ile Lys Lys Glu Lys Glu Glu Ala
 85 90 95
 Ala Lys Lys Arg Gln Glu Glu Gln Glu Arg Lys Leu Lys Glu Gln Trp
 100 105 110
 10 Glu Glu Gln Gln Arg Lys Glu Arg Glu Glu Glu Gln Lys Arg Gln
 115 120 125
 Glu Lys Lys Glu Lys Glu Glu Ala Leu Gln Lys Met Leu Asp Gln Ala
 130 135 140
 Glu Asn Glu Leu Glu Asn Gly Thr Thr Trp Gln Asn Pro Glu Pro Pro
 145 150 155 160
 15 Trp Ile Ser Glu

<210> 911
 <211> 141
 20 <212> PRT
 <213> Homo sapiens

<400> 911
 25 Ser Ser Ile Phe Cys Lys Ala Ser Ser Phe Ser Phe Phe Ser Cys Arg
 1 5 10 15
 Phe Cys Ser Ser Ser Ser Leu Ser Phe Leu Cys Cys Ser Ser His Cys
 20 25 30
 Ser Phe Asn Phe Leu Ser Cys Ser Ser Cys Arg Phe Leu Ala Ala Ser
 35 40 45
 30 Ser Phe Ser Phe Phe Ile Leu Asn Ser Ser Cys Ala Phe Cys Ser Leu
 50 55 60
 Ser Asn His Ser Ser Cys Asn Leu Cys Leu Ser Leu Ser Asn Ser Phe
 65 70 75 80
 35 Ser Ser Ser Ser Cys Cys Ser Ser Ile Lys Val Ser Ser Ser Ser Ser
 85 90 95
 Phe Cys Glu Ser Pro Glu Ser Leu Ser Arg Ala Ser Ser Cys Arg Arg
 100 105 110
 Phe Phe Arg Phe Ser Phe Phe Arg Ala Ala Leu Tyr Phe Leu Trp Leu
 115 120 125
 40 Gly Phe Ser Gly Asn Val Ile Phe Ser Gly Ala Ala Ile
 130 135 140

<210> 912
 <211> 184
 45 <212> PRT
 <213> Homo sapiens

<400> 912
 50 Pro Gly Glu Lys Trp Arg Phe Gly Phe Phe Xaa Lys Pro Pro Asn Val
 1 5 10 15
 Gln Xaa Glu Xaa Pro Ala Xaa Phe Phe Met Gly Ser Glu Ile Xaa Xaa
 20 25 30
 Ile Ile Phe Gly Xaa Val Ile Xaa Thr Phe Xaa Cys Phe Xaa Ile Gly
 35 40 45
 55 Leu Xaa Xaa Pro Leu Gly Xaa Thr Pro Lys Xaa Gly Lys Gly Trp Ala
 50 55 60
 Pro Pro Xaa Ile Phe Xaa Xaa Gly Xaa Gly Glu Xaa Lys Xaa Leu Val
 65 70 75 80
 60 Gln Xaa Xaa Pro Xaa Lys Lys Met Gly Asn Pro Lys Gly Lys Xaa Xaa
 85 90 95
 Val Pro Gly Gly Xaa Xaa Phe Xaa Asn Ala Xaa Gln Lys Xaa Gly Xaa
 100 105 110
 Gly Pro Ile Xaa Glu Ala Lys Glu Lys Ile Gly Pro Pro Xaa Gly Pro

115 120 125
 Pro Pro Gly Ala Gly Ala Pro Gly Xaa Gly Xaa Gly Xaa Gly Xaa Pro
 130 135 140
 Gly Xaa Pro Pro Xaa Gly Ala Lys Val Pro Xaa Gly Pro Xaa Xaa Xaa
 5 145 150 155 160
 Ala Xaa Gly Gly Xaa Val Xaa Xaa Xaa Xaa Xaa Xaa Val Xaa Asn
 165 170 175
 Pro Xaa Lys Leu Val Xaa Phe Phe
 180
 10
 <210> 913
 <211> 181
 <212> PRT
 <213> Homo sapiens
 15
 <400> 913
 Lys Met Ala Ile Trp Val Phe Xaa Lys Thr Pro Gln Cys Pro Xaa Gly
 1 5 10 15
 Xaa Pro Cys Xaa Phe Phe His Gly Phe Arg Asn Pro Xaa Asn Tyr Phe
 20 20 25 30
 Trp Xaa Gly Asn Xaa Xaa Ile Xaa Leu Phe Pro Xaa Arg Thr Gly Xaa
 35 40 45
 Xaa Phe Gly Xaa Asn Ser Gln Xaa Arg Glu Arg Met Gly Pro Pro Xaa
 50 55 60
 25 Asp Phe Xaa Xaa Arg Leu Xaa Gly Xaa Lys Xaa Pro Ser Pro Xaa Xaa
 65 70 75 80
 Ser Xaa Lys Lys Asn Gly Glu Ser Gln Arg Lys Ser Xaa Xaa Pro Arg
 85 90 95
 Gly Xaa Xaa Phe Pro Xaa Arg Xaa Ser Lys Ser Xaa Xaa Xaa Pro Asn
 100 105 110
 30 Xaa Arg Ser Lys Gly Lys Asn Arg Ala Pro Xaa Arg Ala Pro Thr Arg
 115 120 125
 Gly Arg Gly Thr Arg Xaa Arg Xaa Arg Xaa Arg Xaa Pro Arg Xaa Pro
 130 135 140
 35 Pro Xaa Arg Ser Gln Ser Ser Phe Xaa Ser Xaa Xaa Xaa Gly Xaa Arg
 145 150 155 160
 Arg Xaa Gly Xaa Lys Xaa Xaa Thr Xaa Xaa Ser Pro Xaa Ser Lys Xaa
 165 170 175
 Thr Ser Phe Xaa Phe
 180
 40
 <210> 914
 <211> 114
 <212> PRT
 <213> Homo sapiens
 45
 <400> 914
 Lys Xaa Lys Leu Val Xaa Leu Asp Xaa Gly Xaa Xaa Xaa Val Xaa Xaa
 1 5 10 15
 50 Xaa Leu Pro Xaa Leu Xaa Leu Xaa Xaa Xaa Xaa Asp Xaa Lys Glu Leu
 20 25 30
 Trp Leu Arg Xaa Gly Gly Xaa Leu Gly Xaa Arg Xaa Arg Xaa Arg Xaa
 35 40 45
 Arg Val Pro Arg Pro Arg Val Gly Ala Leu Xaa Gly Ala Leu Phe Phe
 50 55 60
 55 Pro Leu Leu Arg Xaa Leu Gly Xaa Ser Xaa Leu Phe Xaa Gly Arg Xaa
 65 70 75 80
 Gly Xaa Xaa Phe Pro Leu Gly Xaa Xaa Leu Phe Leu Trp Asp Ser Pro
 85 90 95
 60 Phe Phe Xaa Xaa Xaa Gly Xaa Gly Leu Gly Xaa Xaa Leu Pro Xaa Asn
 100 105 110
 Leu Xaa

<210> 915
 <211> 202
 <212> PRT
 5 <213> Homo sapiens

<400> 915
 Pro Asn Leu His Xaa Trp Glu Ser Ala Leu Met Ile Trp Gly Ser Ile
 1 5 10 15
 10 Glu Lys Glu His Asp Lys Leu His Glu Glu Ile Gln Asn Leu Ile Lys
 20 25 30
 Ile Gln Ala Ile Ala Val Cys Met Glu Asn Gly Asn Phe Lys Glu Ala
 35 40 45
 15 Glu Glu Val Phe Glu Arg Ile Phe Gly Asp Pro Asn Ser His Met Pro
 50 55 60
 Phe Lys Ser Lys Leu Leu Met Ile Ile Ser Gln Lys Asp Thr Phe His
 65 70 75 80
 Ser Phe Phe Gln His Phe Ser Tyr Asn His Met Met Glu Lys Ile Lys
 85 90 95
 20 Ser Tyr Val Asn Tyr Val Leu Ser Glu Lys Ser Ser Thr Phe Leu Met
 100 105 110
 Lys Ala Ala Lys Val Val Glu Ser Lys Arg Thr Arg Thr Ile Thr
 115 120 125
 25 Ser Gln Asp Lys Pro Ser Gly Asn Asp Val Glu Met Glu Thr Glu Ala
 130 135 140
 Asn Leu Asp Thr Arg Lys Ser Val Ser Asp Lys Gln Ser Ala Val Thr
 145 150 155 160
 Glu Ser Ser Glu Gly Thr Val Ser Leu Leu Arg Ser His Lys Asn Leu
 165 170 175
 30 Phe Leu Ser Lys Leu Gln His Gly Thr Gln Gln Gln Asp Leu Asn Lys
 180 185 190
 Lys Glu Arg Arg Val Gly Thr Pro Gln Ser
 195 200

35 <210> 916
 <211> 217
 <212> PRT
 <213> Homo sapiens

40 <400> 916
 Leu Arg Lys Glu Leu Glu Arg Gln Ala Glu Arg Leu Glu Lys Glu Leu
 1 5 10 15
 Ala Ser Gln Gln Glu Lys Arg Ala Ile Glu Lys Asp Met Met Lys Lys
 20 25 30
 45 Glu Ile Thr Lys Glu Arg Glu Tyr Met Gly Ser Lys Met Leu Ile Leu
 35 40 45
 Ser Gln Asn Ile Ala Gln Leu Glu Ala Gln Val Glu Lys Val Thr Lys
 50 55 60
 Glu Lys Ile Ser Ala Ile Asn Gln Leu Glu Glu Ile Gln Ser Gln Leu
 65 70 75 80
 Ala Ser Arg Glu Met Asp Val Thr Lys Val Cys Gly Glu Met Arg Tyr
 85 90 95
 Gln Leu Asn Lys Thr Asn Met Glu Lys Asp Glu Ala Glu Lys Glu His
 100 105 110
 55 Arg Glu Phe Arg Ala Lys Thr Asn Arg Asp Leu Glu Ile Lys Asp Gln
 115 120 125
 Glu Ile Glu Lys Leu Arg Ile Glu Leu Asp Glu Ser Lys Gln His Leu
 130 135 140
 60 Glu Gln Glu Gln Gln Lys Ala Ala Leu Ala Arg Glu Glu Cys Leu Arg
 145 150 155 160
 Leu Thr Glu Leu Leu Gly Glu Ser Glu His Gln Leu His Leu Thr Arg
 165 170 175
 Gln Glu Lys Asp Ser Ile Gln Gln Ser Phe Ser Lys Glu Ala Lys Ala

180 185 190
 Gln Ala Leu Gln Pro Ser Lys Glu Ser Arg Ser Leu Pro Gln Lys Ile
 195 200 205
 Ser Lys Trp Asn Pro Pro Cys Lys Thr
 5 210 215

 <210> 917
 <211> 107
 <212> PRT
 10 <213> Homo sapiens

 <400> 917
 Pro Lys Lys Leu Asp Gln Xaa Ser Gln Lys Pro Arg Ser Glu Ile Ala
 1 5 10 15
 15 Gln Leu Ser Gln Glu Lys Arg Tyr Thr Tyr Asp Lys Leu Gly Lys Xaa
 20 25 30
 Gln Arg Arg Asn Glu Glu Leu Glu Glu Gln Cys Val Gln His Gly Arg
 35 40 45
 Val His Glu Xaa Met Lys Gln Arg Leu Arg Gln Leu Asp Lys His Ser
 20 50 55 60
 Gln Ala Thr Ala Gln Gln Leu Val Gln Leu Leu Ser Lys Gln Asn Gln
 65 70 75 80
 Leu Leu Leu Glu Arg Gln Ser Leu Ser Glu Glu Val Asp Arg Leu Arg
 85 90 95
 25 Thr Gln Leu Pro Ser Met Pro Gln Xaa Asp Cys
 100 105

 <210> 918
 <211> 98
 30 <212> PRT
 <213> Homo sapiens

 <400> 918
 Pro Leu Leu His Xaa Leu Met Tyr Ser Pro Met Leu Asp Thr Leu Phe
 1 5 10 15
 Leu Gln Phe Phe Ile Ser Ser Leu Xaa Leu Ser Gln Phe Ile Ile Cys
 20 25 30
 Ile Pro Phe Phe Leu Thr Glu Leu Ser Tyr Phe Arg Ser Gly Phe Leu
 35 40 45
 40 Arg Xaa Leu Val Gln Phe Leu Gly Leu Met Xaa Asn Ile Leu Pro Leu
 50 55 60
 Thr Phe Val Lys Asn Val Phe Leu Gly Xaa Gln Gln Gln Asn Thr Gly
 65 70 75 80
 His Phe Gln Xaa Trp His Ala Gly Leu Ser Phe Ala Gly Ile Phe Trp
 45 85 90 95
 Xaa Thr

 <210> 919
 50 <211> 98
 <212> PRT
 <213> Homo sapiens

 <400> 919
 55 Ile Ile Tyr Phe Thr Leu Phe His Pro Gly Gln Gln Ser Xaa Cys Gly
 1 5 10 15
 Met Leu Gly Asn Trp Val Arg Ser Arg Ser Thr Ser Ser Asp Arg Leu
 20 25 30
 Cys Leu Ser Arg Arg Ser Trp Phe Cys Leu Leu Arg Ser Cys Thr Ser
 35 40 45
 60 Cys Trp Ala Val Ala Trp Leu Cys Leu Ser Ser Cys Leu Ser Leu Cys
 50 55 60
 Phe Ile Xaa Ser Cys Thr Leu Pro Cys Trp Thr His Cys Ser Ser Asn
 343

	65					70					75					80
	Ser	Ser	Phe	Leu	Leu	Xaa	Asn	Phe	Pro	Asn	Leu	Ser	Tyr	Val	Tyr	Leu
					85					90					95	
5	Phe	Ser														
			<210>	920												
			<211>	236												
			<212>	PRT												
10			<213>	Homo sapiens												
			<400>	920												
	Gln	Thr	His	Thr	Asn	Val	His	Met	Gln	Thr	Ile	Glu	Arg	Leu	Val	Lys
	1				5					10					15	
15	Glu	Arg	Asp	Asp	Leu	Met	Ser	Ala	Leu	Val	Ser	Val	Arg	Ser	Ser	Leu
				20					25					30		
	Ala	Asp	Thr	Gln	Gln	Arg	Glu	Ala	Ser	Ala	Tyr	Glu	Gln	Val	Lys	Gln
			35					40					45			
	Val	Leu	Gln	Ile	Ser	Glu	Glu	Ala	Asn	Phe	Glu	Lys	Thr	Lys	Ala	Leu
20		50					55					60				
	Ile	Gln	Cys	Asp	Gln	Leu	Arg	Lys	Glu	Leu	Glu	Arg	Gln	Ala	Glu	Arg
	65					70					75					80
	Leu	Glu	Lys	Glu	Leu	Ala	Ser	Gln	Gln	Glu	Lys	Arg	Ala	Ile	Glu	Lys
					85					90					95	
25	Asp	Met	Met	Lys	Lys	Glu	Ile	Thr	Lys	Glu	Arg	Glu	Tyr	Met	Gly	Ser
				100					105					110		
	Lys	Met	Leu	Ile	Leu	Ser	Gln	Asn	Ile	Ala	Gln	Leu	Glu	Ala	Gln	Val
			115					120					125			
	Glu	Lys	Val	Thr	Lys	Glu	Lys	Ile	Ser	Ala	Ile	Asn	Gln	Leu	Glu	Glu
30		130					135					140				
	Ile	Gln	Ser	Gln	Leu	Ala	Ser	Arg	Glu	Met	Asp	Val	Thr	Lys	Val	Cys
	145					150					155					160
	Gly	Glu	Met	Arg	Tyr	Gln	Leu	Asn	Lys	Thr	Asn	Met	Glu	Lys	Asp	Glu
				165					170						175	
35	Ala	Glu	Lys	Glu	His	Arg	Glu	Phe	Arg	Ala	Lys	Thr	Asn	Arg	Asp	Leu
			180						185					190		
	Glu	Ile	Lys	Asp	Gln	Glu	Ile	Glu	Lys	Leu	Arg	Ile	Glu	Leu	Asp	Glu
			195					200					205			
	Ser	Lys	His	Thr	Trp	Asn	Arg	Ser	Ser	Xaa	Arg	His	Pro	Gly	Gln	Lys
40		210					215					220				
	Xaa	Val	Pro	Glu	Thr	Asn	Xaa	Thr	Ala	Gly	Arg	Ile				
	225					230					235					
			<210>	921												
45			<211>	112												
			<212>	PRT												
			<213>	Homo sapiens												
			<400>													

<210> 922
 <211> 186
 <212> PRT
 5 <213> Homo sapiens

<400> 922
 Leu Xaa Gly Asp Phe Glu Xaa Gln Xaa Xaa Xaa Pro Gln Gln Glu Lys
 1 5 10 15
 10 Val Ser Phe Xaa Gln Xaa Phe Xaa Lys Glu Glu Arg Pro Lys Pro Xaa
 20 25 30
 Arg Pro Arg Lys Xaa Ser Arg Ser Cys Xaa Arg Asn Xaa Ala Asn Gly
 35 40 45
 Ser Pro Ala Cys Gln Asn Xaa Lys Met Thr Ser Phe Xaa Cys Cys Xaa
 50 55 60
 15 Pro Arg Ile His Phe Cys Lys Val Lys Glu Arg Met Leu Tyr Ile Ser
 65 70 75 80
 Gln Glu Thr Gly Pro Xaa Ser Gln Lys Thr Arg Phe Glu Ile Ala Gln
 85 90 95
 20 Leu Ser Gln Glu Lys Arg Tyr Thr Tyr Asp Lys Leu Gly Lys Xaa Gln
 100 105 110
 Arg Arg Asn Glu Glu Leu Glu Glu Gln Cys Val Gln His Gly Arg Val
 115 120 125
 His Glu Thr Met Lys Gln Arg Leu Arg Gln Leu Asp Lys His Ser Gln
 130 135 140
 25 Ala Thr Ala Gln Gln Leu Val Gln Leu Leu Ser Lys Gln Asn Gln Leu
 145 150 155 160
 Leu Leu Glu Arg Gln Ser Leu Ser Glu Glu Val Asp Arg Leu Arg Thr
 165 170 175
 30 Gln Leu Pro Ser Met Pro Gln Ser Asp Cys
 180 185

<210> 923
 <211> 135
 35 <212> PRT
 <213> Homo sapiens

<400> 923
 Pro Leu Leu His Arg Leu Met Tyr Ser Pro Met Leu Asp Thr Leu Phe
 1 5 10 15
 Leu Gln Phe Phe Ile Ser Ser Leu Xaa Leu Ser Gln Phe Ile Ile Cys
 20 25 30
 Ile Pro Phe Phe Leu Thr Glu Leu Ser Tyr Phe Lys Ser Gly Phe Leu
 35 40 45
 45 Arg Xaa Trp Ser Ser Phe Leu Ala Asn Val Gln His Ser Phe Phe Asn
 50 55 60
 Phe Ala Lys Met Tyr Ser Gly Xaa Ala Thr Xaa Lys Thr Gly His Phe
 65 70 75 80
 Xaa Val Leu Ala Cys Trp Ala Ser Ile Cys Xaa Ile Ser Xaa Ala Thr
 85 90 95
 50 Pro Ala Xaa Phe Ser Trp Pro Xaa Arg Leu Gly Pro Phe Phe Leu Xaa
 100 105 110
 Lys Xaa Leu Xaa Lys Ala Asn Phe Phe Leu Leu Gly Xaa Xaa Xaa Leu
 115 120 125
 55 Xaa Leu Lys Ile Pro Xaa Gln
 130 135

<210> 924
 <211> 159
 60 <212> PRT
 <213> Homo sapiens

<400> 924

Ala Asp Arg Glu Gly Gly Cys Ala Ala Gly Arg Gly Arg Glu Leu Glu
 1 5 10 15
 Pro Glu Leu Glu Pro Gly Pro Gly Pro Gly Ser Ala Leu Glu Xaa Gly
 20 25 30
 5 Glu Glu Phe Glu Ile Val Asp Arg Ser Gln Leu Pro Gly Pro Gly Asp
 35 40 45
 Leu Arg Ser Ala Thr Arg Pro Arg Ala Ala Glu Gly Trp Ser Ala Pro
 50 55 60
 Ile Leu Thr Leu Ala Arg Arg Ala Thr Gly Asn Leu Ser Ala Ser Cys
 65 70 75 80
 10 Gly Ser Ala Leu Arg Ala Ala Ala Gly Leu Gly Gly Gly Asp Ser Gly
 85 90 95
 Asp Gly Thr Ala Arg Ala Ala Ser Lys Cys Gln Met Met Glu Glu Arg
 100 105 110
 15 Ala Asn Leu Met His Met Met Lys Leu Ser Ile Lys Val Leu Leu Gln
 115 120 125
 Ser Ala Leu Ser Leu Gly Arg Ser Leu Asp Ala Asp His Ala Pro Leu
 130 135 140
 Gln Gln Phe Phe Cys Ser Asp Gly Ala Leu Pro Gln Thr Trp Ala
 145 150 155
 20

<210> 925

<211> 154

<212> PRT

25 <213> Homo sapiens

<400> 925

Gly Ser Ala Pro Ser Leu Gln Lys Asn Cys Cys Lys Gly Ala Trp Ser
 1 5 10 15
 30 Ala Ser Arg Leu Arg Pro Arg Leu Arg Ala Asp Trp Ser Asn Thr Leu
 20 25 30
 Met Leu Ser Phe Ile Met Cys Ile Arg Leu Ala Arg Ser Ser Ile Ile
 35 35 40 45
 Trp His Leu Glu Ala Ala Arg Ala Val Pro Ser Pro Leu Ser Pro Pro
 50 55 60
 35 Pro Ser Pro Ala Ala Ala Arg Ser Ala Leu Pro Gln Leu Ala Asp Arg
 65 70 75 80
 Phe Pro Val Ala Leu Arg Ala Arg Val Arg Met Gly Ala Asp Gln Pro
 85 90 95
 40 Ser Ala Ala Arg Gly Leu Val Ala Leu Arg Arg Ser Pro Gly Pro Gly
 100 105 110
 Ser Trp Leu Arg Ser Thr Ile Ser Asn Ser Ser Xaa Gly Ser Ser Ala
 115 120 125
 Asp Pro Gly Pro Gly Pro Gly Ser Ser Ser Gly Ser Ser Arg Pro
 130 135 140
 45 Arg Pro Ala Ala Gln Pro Pro Ser Arg Ser
 145 150

<210> 926

50 <211> 134

<212> PRT

<213> Homo sapiens

<400> 926

Leu Ser Ser Pro Cys Leu Arg Gln Cys Ser Ile Thr Thr Lys Glu Leu
 1 5 10 15
 Leu Gln Gly Gly Met Val Arg Ile Gln Ala Ala Ala Gln Ala Gln Ser
 20 25 30
 Arg Leu Glu Gln His Leu Asp Ala Glu Phe His His Val His Gln Val
 35 40 45
 60 Gly Thr Leu Leu His His Leu Ala Leu Arg Ser Cys Ala Arg Arg Ala
 50 55 60
 Val Pro Ala Val Pro Ala Ala Gln Pro Arg Gly Arg Ala Gln Arg Ala

	65	70	75	80
	Pr Ala Ala Arg Arg Gln Val Pro Gly Gly Pro Ala Cys Gln Gly Gln	85	90	95
5	Asp Gly Arg Arg Pro Ala Leu Gly Arg Pro Arg Pro Arg Cys Ala Pro	100	105	110
	Gln Val Ala Trp Ala Gly Gln Leu Ala Ser Val His Asp Leu Lys Leu	115	120	125
	Phe Ser Xaa Leu Lys Arg			
	130			
10	<210> 927			
	<211> 424			
	<212> PRT			
	<213> Homo sapiens			
15	<400> 927			
	Ile Arg Tyr Leu Glu Val Leu Cys Thr Lys Lys Val Ser Glu Lys Met	5	10	15
20	Glu Phe Phe Asn Ile Ser Val Asp Asn Thr Cys Ser Leu Phe Arg Gly	20	25	30
	Leu Gln Lys Glu Glu Val Val Leu Leu Thr His Gly Asp Ser Val Asp	35	40	45
	Lys Val Ala Asp Gly Phe Lys Val Val Ala Arg Ser Gly Asn Ile Val	50	55	60
25	Ala Gly Ile Ala Asn Glu Ser Lys Lys Leu Tyr Gly Ala Gln Phe His	65	70	75
	Pro Glu Val Gly Leu Thr Glu Asn Gly Lys Val Ile Leu Lys Asn Phe	85	90	95
30	Leu Tyr Asp Ile Thr Gly Cys Ser Gly Thr Phe Thr Val Gln Asn Arg	100	105	110
	Glu Leu Glu Cys Ile Arg Glu Ile Lys Glu Arg Val Gly Thr Ser Lys	115	120	125
	Val Leu Val Leu Leu Ser Gly Gly Val Asp Ser Thr Val Cys Thr Ala	130	135	140
35	Leu Leu Asn Arg Ala Leu Asn Gln Glu Gln Val Ile Ala Val His Ile	145	150	155
	Asp Asn Gly Phe Met Arg Lys Arg Glu Ser Gln Ser Val Glu Glu Ala	165	170	175
40	Leu Lys Lys Leu Gly Ile Gln Val Lys Val Ile Asn Ala Ala His Ser	180	185	190
	Phe Tyr Asn Gly Thr Thr Thr Leu Pro Ile Ser Asp Glu Asp Arg Thr	195	200	205
	Pro Arg Lys Arg Ile Ser Lys Thr Leu Asn Met Thr Thr Ser Pro Glu	210	215	220
45	Glu Lys Arg Lys Ile Ile Gly Asp Thr Phe Val Lys Ile Ala Asn Glu	225	230	235
	Val Ile Gly Glu Met Asn Leu Lys Pro Glu Glu Val Phe Leu Ala Gln	245	250	255
50	Gly Thr Leu Arg Pro Asp Leu Ile Glu Ser Ala Ser Leu Val Ala Ser	260	265	270
	Gly Lys Ala Glu Leu Ile Lys Thr His His Asn Asp Thr Glu Leu Ile	275	280	285
	Lys Lys Leu Arg Glu Glu Gly Lys Val Ile Glu Pro Leu Lys Asp Phe	290	295	300
55	His Lys Asp Glu Val Arg Ile Leu Gly Arg Glu Leu Gly Leu Pro Glu	305	310	315
	Glu Leu Val Ser Arg His Pro Phe Pro Gly Pro Gly Leu Ala Ile Arg	325	330	335
60	Val Ile Cys Ala Glu Glu Pro Tyr Ile Cys Lys Asp Phe Pro Glu Thr	340	345	350
	Asn Asn Ile Leu Lys Ile Val Ala Asp Phe Ser Ala Ser Val Lys Lys	355	360	365
	Pro His Thr Leu Leu Gln Arg Val Lys Ala Cys Thr Thr Glu Glu Asp			

370 375 380
 Gln Glu Lys Leu Met Gln Ile Thr Ser Leu His Ser Leu Asn Ala Phe
 385 390 395 400
 Leu Leu Pro Ile Lys Thr Val Xaa Val Gln Gly Asp Cys Arg Ser Tyr
 405 410 415
 5 Ser Tyr Arg Val Trp Asn Xaa Gln
 420

 <210> 928
 10 <211> 191
 <212> PRT
 <213> Homo sapiens

 <400> 928
 15 Pro Arg Ser Ala Ala Val Ala Pro Phe Gly Ala Phe Leu Ala Ala Gly
 1 5 10 15
 Ser Ser Pro Leu Pro Ala Ala Pro Arg Pro Gly Leu Leu Leu Asn Leu
 20 20 25 30
 Ser Pro Arg Arg Arg Pro Phe Arg His Pro Pro Ala Pro Ser Arg Thr
 35 40 45
 20 Val Ala Val Thr Ala Ala Ala Pro Ala Leu Ala Pro Met Ala Leu Cys
 50 55 60
 Asn Gly Asp Ser Lys Leu Glu Asn Ala Gly Gly Asp Leu Lys Asp Gly
 65 70 75 80
 25 His His His Tyr Glu Gly Ala Val Val Ile Leu Asp Ala Gly Ala Gln
 85 90 95
 Tyr Gly Lys Val Ile Asp Arg Arg Val Arg Glu Leu Phe Val Gln Ser
 100 105 110
 Glu Ile Phe Pro Leu Glu Thr Pro Ala Phe Ala Ile Lys Glu Gln Gly
 115 120 125
 30 Phe Arg Ala Ile Ile Ile Ser Gly Gly Pro Asn Ser Val Tyr Ala Glu
 130 135 140
 Asp Ala Pro Trp Phe Asp Pro Thr Ile Phe Thr Ile Gly Lys Pro Val
 145 150 155 160
 35 Leu Gly Ile Cys Tyr Gly Met Gln Met Met Asn Lys Val Phe Gly Gly
 165 170 175
 Thr Val His Lys Lys Ser Val Arg Lys Asp Gly Val Phe Gln His
 180 185 190

 40 <210> 929
 <211> 203
 <212> PRT
 <213> Homo sapiens

 45 <400> 929
 Arg Pro Leu Asn Asn Glu His Val Leu Ser Thr Leu Met Leu Lys Asn
 1 5 10 15
 Ser Ile Phe Ser Asp Thr Phe Phe Val His Ser Thr Ser Lys Tyr Leu
 20 25 30
 50 Ile His His Leu His Thr Ile Ala Asn Ser Lys Asn Arg Leu Ala Asn
 35 40 45
 Ser Glu Tyr Cys Trp Ile Lys Pro Gly Ser Ile Phe Ser Ile His Arg
 50 55 60
 Ile Arg Ser Ser Arg Asp Asp Asn Ser Thr Glu Ser Leu Phe Leu Tyr
 65 70 75 80
 55 Ser Lys Cys Trp Cys Phe Gln Gly Glu Asn Phe Arg Leu His Glu Gln
 85 90 95
 Phe Pro His Ser Ser Val Tyr Asp Phe Pro Val Leu S r Thr Ser Ile
 100 105 110
 60 Gln Asn Asp Asn Ser Ser Phe Ile Val Val Val Ala Ile Leu Lys Val
 115 120 125
 Ser Ser Ser Ile Leu Gln Leu Gly Val Ser Val Ala Gln Ser His Arg
 130 135 140

Gly Gln Gly Arg Ser Arg Gly Gly Asp Gly Asp Ser Thr Arg Arg Gly
 145 150 155 160
 Gly Arg Val Pro Glu Gly Ser Ala Pro Arg Ala Glu Val Glu Lys Glu
 165 170 175
 5 Ala Trp Ser Arg Ser Ser Arg Gln Arg Arg Gly Ala Ser Arg Gln Lys
 180 185 190
 Ser Ala Glu Trp Ser Asn Ser Ser Gly Ala Arg
 195 200

10 <210> 930
 <211> 236
 <212> PRT
 <213> Homo sapiens

15 <400> 930
 Pro Arg Ser Ala Ala Val Ala Pro Phe Gly Ala Phe Leu Ala Ala Gly
 1 5 10 15
 Ser Ser Pro Leu Pro Ala Ala Pro Arg Pro Gly Leu Leu Leu Asn Leu
 20 25 30
 Ser Pro Arg Arg Arg Pro Phe Arg His Pro Pro Ala Pro Ser Arg Thr
 35 40 45
 Val Ala Val Thr Ala Ala Ala Pro Ala Leu Ala Pro Met Ala Leu Cys
 50 55 60
 Asn Gly Asp Ser Lys Leu Glu Asn Ala Gly Gly Asp Leu Lys Asp Gly
 65 70 75 80
 25 His His His Tyr Glu Gly Ala Val Val Ile Leu Asp Ala Gly Ala Gln
 85 90 95
 Tyr Gly Lys Val Ile Asp Arg Arg Val Arg Glu Leu Phe Val Gln Ser
 100 105 110
 30 Glu Ile Phe Pro Leu Glu Thr Pro Ala Phe Ala Ile Lys Glu Gln Gly
 115 120 125
 Phe Arg Ala Ile Ile Ile Ser Gly Gly Pro Asn Ser Val Tyr Ala Glu
 130 135 140
 Asp Ala Pro Trp Phe Asp Pro Thr Ile Phe Thr Ile Gly Lys Pro Val
 145 150 155 160
 35 Leu Gly Ile Cys Tyr Gly Met Xaa Met Met Asn Xaa Val Phe Gly Gly
 165 170 175
 Thr Val His Lys Lys Lys Cys Gln Lys Arg Trp Ser Phe Ser Thr Leu
 180 185 190
 40 Val Xaa Ile Ile His Val His Tyr Ser Xaa Ala Phe Xaa Lys Glu Lys
 195 200 205
 Leu Val Leu Ala Tyr Thr Trp Glu Asn Ser Val Lys Gln Ser Asn Leu
 210 215 220
 Met Glu Xaa Lys Val Gly Ala Pro Phe Trp Xaa Lys
 225 230 235

<210> 931
 <211> 189
 <212> PRT
 50 <213> Homo sapiens

<400> 931
 Lys Thr Pro Ser Phe Leu Thr Leu Phe Phe Val His Ser Thr Ser Lys
 1 5 10 15
 55 Tyr Xaa Ile His His Xaa His Thr Ile Ala Asn Ser Lys Asn Arg Leu
 20 25 30
 Ala Asn Ser Glu Tyr Cys Trp Ile Lys Pro Gly Ser Ile Phe Ser Ile
 35 40 45
 His Arg Ile Arg S r Ser Arg Asp Asp Asn Ser Thr Glu Ser Leu Phe
 50 55 60
 60 Leu Tyr Ser Lys Cys Trp Cys Phe Gln Gly Glu Asn Phe Arg Leu His
 65 70 75 80
 Glu Gln Phe Pro His Ser Ser Val Tyr Asp Phe Pro Val Leu Ser Thr

85 90 95
 Ser Ile Gln Asn Asp Asn Ser Ser Phe Ile Val Val Val Ala Ile Leu
 100 105 110
 5 Lys Val Ser Ser Ser Ile Leu Gln Leu Gly Val Ser Val Ala Gln Ser
 115 120 125
 His Arg Gly Gln Gly Arg Ser Arg Gly Gly Asp Gly Asp Ser Thr Arg
 130 135 140
 Arg Gly Gly Arg Val Pro Glu Gly Ser Ala Pro Arg Ala Glu Val Glu
 145 150 155 160
 10 Lys Glu Ala Trp Ser Arg Ser Ser Arg Gln Arg Arg Gly Ala Ser Arg
 165 170 175
 Gln Lys Ser Ala Glu Trp Ser Asn Ser Ser Gly Ala Arg
 180 185
 15 <210> 932
 <211> 175
 <212> PRT
 <213> Homo sapiens
 20 <400> 932
 Val Cys Arg Gly Leu Trp Phe Pro Gln Leu Gly Gly Xaa Xaa Ser Ser
 1 5 10 15
 Lys Asn Asp Pro Xaa Trp Glu Xaa Leu Xaa Phe Xaa Xaa Arg Leu Xaa
 20 25 30
 25 Pro Gly Met Cys His Asn Val Asn Xaa Val Val Tyr Ile Phe Gly Xaa
 35 40 45
 Pro Val Lys Xaa Pro Xaa Thr Xaa Val Thr Pro Pro Phe Leu Thr Thr
 50 55 60
 Gly Xaa Val Ser Thr Leu Arg Gln Xaa Asp Phe Xaa Ala His Asn Ile
 65 70 75 80
 30 Phe Arg Glu Phe Gly Tyr Xaa Gly Lys Ile Xaa Gln Xaa Pro Xaa Ile
 85 90 95
 Leu Xaa Pro Leu His Phe Asp Xaa Xaa Xaa Leu Gln Xaa Gln Pro Xaa
 100 105 110
 35 Cys Xaa Arg Phe Xaa Val Ile Arg Xaa Phe Ile Xaa Xaa Asp Phe Met
 115 120 125
 Thr Xaa Xaa Pro Ala Xaa Pro Gly Asn Glu Ile Pro Val Lys Xaa Val
 130 135 140
 Leu Xaa Met Val Xaa Xaa Ile Xaa Xaa Ile Pro Xaa Ile Xaa Arg Ile
 145 150 155 160
 40 Met Tyr Asp Leu Thr Ser Lys Pro Pro Gly Thr Xaa Glu Xaa Xaa
 165 170 175
 45 <210> 933
 <211> 202
 <212> PRT
 <213> Homo sapiens
 50 <400> 933
 Gly Asn Ile Val Ala Gly Ile Ala Asn Glu Ser Lys Lys Leu Tyr Gly
 1 5 10 15
 Ala Gln Phe His Pro Glu Val Gly Leu Thr Glu Asn Gly Lys Val Ile
 20 25 30
 Leu Lys Asn Phe Leu Tyr Asp Ile Ala Gly Cys Ser Gly Thr Phe Thr
 35 40 45
 55 Val Gln Asn Arg Glu Leu Glu Cys Ile Arg Glu Ile Lys Glu Arg Val
 50 55 60
 Gly Thr Ser Lys Val Leu Val Leu Leu Ser Gly Gly Val Asp Ser Thr
 65 70 75 80
 60 Val Cys Thr Ala Leu Leu Asn Arg Ala Leu Asn Gln Glu Gln Val Ile
 85 90 95
 Ala Val His Ile Asp Asn Gly Phe Met Arg Lys Arg Glu Ser Gln Ser
 100 105 110

Val Glu Glu Ala Leu Lys Lys Leu Gly Ile Gln Val Lys Val Ile Asn
 115 120 125
 Ala Ala His Ser Phe Tyr Asn Gly Thr Thr Thr Leu Pro Ile Ser Asp
 130 135 140
 5 Glu Asp Arg Thr Pro Arg Lys Arg Ile Ser Lys Thr Leu Asn Met Thr
 145 150 155 160
 Thr Ser Pro Glu Glu Lys Arg Lys Ile Ile Gly Asp Thr Phe Val Lys
 165 170 175
 10 Ile Ala Asn Glu Val Ile Gly Glu Met Asn Leu Lys Pro Xaa Glu Val
 180 185 190
 Phe Leu Ala Gln Gly Leu Tyr Xaa Leu Ile
 195 200

15 <210> 934
 <211> 152
 <212> PRT
 <213> Homo sapiens

20 <400> 934
 Pro Ala Xaa Tyr Phe Xaa Lys Lys Met Val Gly Phe Lys Lys Xaa Pro
 1 5 10 15
 Xaa Pro Lys Lys Lys Val Phe Ser Ser Thr Tyr Tyr Phe Xaa Ile Ala
 20 25 30
 25 Gln Ala Gln Xaa Pro Gly Lys Trp Lys Ala Trp Lys Thr Asn Xaa Xaa
 35 40 45
 Trp Lys Val Gln Val Xaa Trp Pro Lys Asn Ser His Phe Ile Phe Asn
 50 55 60
 Glu Ile Phe Pro Xaa Val Leu Ile Thr Phe Pro Xaa Xaa Ser Gln Leu
 65 70 75 80
 30 Phe Asp Glu Leu Xaa Val Ile Val Met Gly Phe Asp Glu Ser Ser Phe
 85 90 95
 Ala Thr Cys Asn Lys Xaa Trp His Phe Gln Leu Asp Gln Xaa Val Lys
 100 105 110
 Thr Leu Gly Lys Glu Asn Leu Xaa Trp Phe Gln Val His Phe Ser Asn
 115 120 125
 35 Tyr Phe Ile Gly Asn Leu Asn Lys Ser Ile Pro Asn Asp Phe Ser Phe
 130 135 140
 Leu Phe Arg Thr Cys Gly His Ile
 145 150

40 <210> 935
 <211> 176
 <212> PRT
 <213> Homo sapiens

45 <400> 935
 Val Cys Arg Val Thr Val Val Pro Thr Val Thr Cys Val Glu Ser Pro
 1 5 10 15
 Val Lys Met Asn Leu Thr Gly Asn His Phe Ile Phe Leu Ala Arg Leu
 20 25 30
 50 Ile Pro Arg Met Cys His Asn Val Asn Arg Val Val Tyr Ile Phe Gly
 35 40 45
 Pro Pro Val Lys Glu Pro Pro Thr Asp Val Thr Pro Thr Phe Leu Thr
 50 55 60
 55 Thr Gly Val Leu Ser Thr Leu Arg Gln Ala Asp Phe Glu Ala His Asn
 65 70 75 80
 Ile Leu Arg Glu Ser Gly Tyr Ala Gly Lys Ile Ser Gln Met Pro Val
 85 90 95
 Ile Leu Thr Pro Leu His Phe Asp Arg Asp Pro Leu Gln Lys Gln Pro
 100 105 110
 60 Ser Cys Gln Arg Ser Val Val Ile Arg Thr Phe Ile Thr Ser Asp Phe
 115 120 125
 Met Thr Gly Ile Pro Ala Thr Pro Gly Asn Glu Ile Pro Val Glu Val

130 135 140
 Val Leu Lys Met Val Thr Glu Ile Lys Lys Ile Pro Gly Ile Ser Arg
 145 150 155 160
 Ile Met Tyr Asp Leu Thr Ser Lys Pro Pro Gly Thr Thr Glu Trp Glu
 5 165 170 175

<210> 936
 <211> 218
 <212> PRT
 10 <213> Homo sapiens

<400> 936
 Arg Thr Pro Arg Lys Arg Ile Ser Lys Thr Leu Asn Met Thr Thr Ser
 1 5 10 15
 15 Pro Glu Glu Lys Arg Lys Ile Ile Gly Asp Thr Phe Val Lys Ile Ala
 20 20 25 30
 Asn Glu Val Ile Gly Glu Met Asn Leu Lys Pro Glu Glu Val Phe Leu
 35 40 45
 Ala Gln Gly Thr Leu Arg Pro Asp Leu Ile Glu Ser Ala Ser Leu Val
 50 55 60
 20 Ala Ser Gly Lys Ala Glu Leu Ile Lys Thr His Asn Asp Thr Glu
 65 70 75 80
 Leu Ile Arg Lys Leu Arg Glu Glu Gly Lys Val Ile Glu Pro Leu Lys
 85 90 95
 25 Asp Phe His Lys Asp Glu Val Arg Ile Leu Gly Arg Glu Leu Gly Leu
 100 105 110
 Pro Glu Glu Leu Val Ser Arg His Pro Phe Pro Gly Pro Gly Leu Ala
 115 120 125
 30 Ile Arg Val Ile Cys Ala Glu Glu Pro Tyr Ile Cys Lys Asp Phe Pro
 130 135 140
 Glu Thr Asn Asn Ile Leu Lys Ile Val Ala Asp Phe Ser Ala Ser Val
 145 150 155 160
 Lys Lys Pro His Thr Leu Leu Gln Arg Val Lys Ala Cys Thr Thr Glu
 165 170 175
 35 Glu Asp Gln Glu Lys Leu Met Gln Ile Thr Ser Leu His Ser Leu Asn
 180 185 190
 Ala Phe Leu Leu Pro Ile Lys Thr Val Xaa Val Gln Gly Asp Cys Arg
 195 200 205
 Ser Tyr Ser Tyr Arg Val Trp Asn Xaa Gln
 40 210 215

<210> 937
 <211> 246
 <212> PRT
 45 <213> Homo sapiens

<400> 937
 Ala Ala Ala Pro Ala Leu Ala Pro Met Ala Leu Cys Asn Gly Asp Ser
 1 5 10 15
 50 Lys Leu Glu Asn Ala Gly Gly Asp Leu Lys Asp Gly His His His Tyr
 20 25 30
 Glu Gly Ala Val Val Ile Leu Asp Ala Gly Ala Gln Tyr Gly Lys Val
 35 40 45
 Ile Asp Arg Arg Val Arg Glu Leu Phe Val Gln Ser Glu Ile Phe Pro
 50 55 60
 55 Leu Glu Thr Pro Ala Phe Ala Ile Lys Glu Gln Gly Phe Arg Ala Ile
 65 70 75 80
 Ile Ile Ser Gly Gly Pro Asn Ser Val Tyr Ala Glu Asp Ala Pro Trp
 85 90 95
 60 Phe Asp Pro Ala Ile Phe Thr Ile Gly Lys Pro Val Leu Gly Ile Cys
 100 105 110
 Tyr Gly Met Gln Met Met Asn Lys Val Phe Gly Gly Thr Val His Lys
 115 120 125

Lys Ser Val Arg Glu Asp Gly Val Phe Asn Ile Ser Val Asp Asn Thr
 130 135 140
 Cys Ser Leu Phe Arg Gly Leu Gln Lys Glu Glu Val Val Leu Leu Thr
 145 150 155 160
 5 His Gly Asp Ser Val Asp Lys Val Ala Asp Gly Phe Lys Val Val Ala
 165 170 175
 Arg Ser Gly Asn Ile Val Ala Gly Ile Ala Asn Glu Ser Lys Lys Leu
 180 185 190
 Tyr Gly Ala Gln Phe His Pro Glu Val Gly Leu Thr Glu Asn Gly Lys
 195 200 205
 10 Val Ile Leu Lys Asn Phe Leu Tyr Asp Ile Thr Trp Met Gln Trp Asn
 210 215 220
 Leu His Arg Ala Xaa Thr Glu Lys Leu Glu Cys Xaa Xaa Glu Ile Lys
 225 230 235 240
 15 Arg Glu Ser Xaa Ala Arg
 245

<210> 938
 <211> 145
 20 <212> PRT
 <213> Homo sapiens

<400> 938
 Thr Cys Ile Ile His Thr Asn Val Glu Asn Ser Ile Phe Ser Asp Thr
 1 5 10 15
 Phe Phe Val His Ser Thr Ser Lys Tyr Leu Ile His His Leu His Thr
 20 25 30
 Ile Ala Asn Ser Lys Asn Arg Leu Ala Asn Ser Glu Tyr Cys Trp Ile
 35 40 45
 30 Lys Pro Gly Ser Ile Phe Ser Ile His Arg Ile Arg Ser Ser Arg Asp
 50 55 60
 Asp Asn Ser Thr Glu Ser Leu Phe Leu Tyr Ser Lys Cys Trp Cys Phe
 65 70 75 80
 Gln Gly Glu Asn Phe Arg Leu His Glu Gln Phe Pro His Ser Ser Val
 85 90 95
 35 Tyr Asp Phe Pro Val Leu Ser Thr Ser Ile Gln Asn Asp Asn Ser Ser
 100 105 110
 Phe Ile Val Val Val Ala Ile Leu Lys Val Ser Ser Ser Ile Leu Gln
 115 120 125
 40 Leu Gly Val Ser Val Ala Gln Ser His Arg Gly Gln Gly Arg Ser Arg
 130 135 140
 Gly
 145

45 <210> 939
 <211> 220
 <212> PRT
 <213> Homo sapiens

<400> 939
 Thr Met Glu Ala Lys Asp Gln Lys Lys His Arg Lys Lys Asn Ser Gly
 1 5 10 15
 Pro Lys Ala Ala Lys Lys Lys Lys Arg Leu Leu Gln Asp Leu Gln Leu
 20 25 30
 55 Gly Asp Glu Glu Asp Ala Arg Lys Arg Asn Pro Lys Ala Phe Ala Val
 35 40 45
 Gln Ser Ala Val Arg Met Ala Arg Ser Phe His Arg Thr Gln Asp Leu
 50 55 60
 Lys Thr Lys Lys His His Ile Pro Val Val Asp Arg Thr Pro Leu Glu
 65 70 75 80
 60 Pro Pro Pro Ile Val Val Val Met Gly Pro Pro Lys Val Gly Lys
 85 90 95
 Ser Thr Leu Ile Gln Cys Leu Ile Arg Asn Phe Thr Arg Gln Lys Leu

[illegible]

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45      <210> 941
        <211> 132
        <212> PRT
        <213> Homo sapiens

        <400> 941
50  Gly Gln Lys Glu Xaa Phe Leu Ile Ser Xaa Ala Xaa Ser Gln Asn Xaa
    1      5      10      15
    Leu Pro Xaa Gly Xaa Ser Xaa Phe Lys Xaa Gln Ala Gln Ala Pro Asn
        20      25      30
    Gln Lys Ala Gly Lys Val Pro Lys Gly Gln Ala Glu Pro Gly Xaa His
    35      40      45
55  Thr Arg Ala Phe Met Lys Xaa Arg Ser Leu Ala Leu Leu Asp Ala Leu
    50      55      60
    Ser Thr Val His Ser Gln Lys Met Lys Lys Ala Lys Glu Gln Arg Xaa
    65      70      75      80
60  Leu Xaa Asn Lys Glu Pro Phe Arg Ala Lys Gln Lys Glu Glu Glu Glu
    85      90      95
    Lys Leu Lys Arg Gln Lys Asp Leu Arg Lys Lys Leu Phe Arg Ile Gln
    100      105      110

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Gly Gln Lys Glu Arg Arg Asn Gln Lys Ser Ser Leu Lys Gly Ala Glu
 115 120 125
 Gly Gln Xaa Gln
 130

5

<210> 942
 <211> 142
 <212> PRT
 <213> Homo sapiens

10

<400> 942
 Asn Cys Leu Pro Pro Xaa Ile Gln Gly Gln Ser Leu Gln Ser Lys Gly
 1 5 10 15
 Ser Leu Xaa Leu Ala Leu Ser Pro Leu Gln Thr Gly Leu Leu Val Ser
 15 20 25 30
 Ser Phe Leu Leu Pro Leu Asn Ser Glu Glu Leu Leu Pro Glu Val Leu
 35 40 45
 Leu Pro Leu Gln Leu Leu Leu Leu Leu Leu Leu Gly Ser Glu Gly
 50 55 60
 Leu Phe Ile Xaa Gln Xaa Pro Leu Leu Leu Gly Leu Leu His Leu Leu
 20 65 70 75 80
 Thr Met His Arg Thr Gln Ser Ile Gln Gln Cys Lys Gly Ser Xaa Phe
 85 90 95
 His Glu Gly Ser Arg Met Xaa Ala Gly Leu Arg Leu Ser Phe Trp His
 100 105 110
 Leu Ala Cys Leu Leu Val Trp Gly Leu Gly Leu Xaa Leu Lys Xaa Gly
 115 120 125
 Xaa Ala Xaa Trp Gln Xaa Val Leu Gly Xaa Gly Xaa Gly Asn
 130 135 140

25

<210> 943
 <211> 127
 <212> PRT
 <213> Homo sapiens

30

<400> 943
 Ala Lys Arg Asn Leu Phe Asn Ser Leu Xaa His Ser Gln Xaa Xaa Cys
 1 5 10 15
 Xaa Arg Xaa Xaa His Xaa Arg Pro Ser Pro Ser Pro Ser Lys Gly Arg
 35 20 25 30
 Gln Gly Ala Lys Asp Arg Arg Arg Pro Ala Val Ile Arg Glu Pro His
 35 40 45
 Glu Arg Lys Ile Leu Ala Leu Leu Asp Ala Leu Ser Thr Val His Ser
 50 55 60
 Gln Lys Met Lys Lys Ala Lys Glu Gln Arg His Leu His Asn Lys Glu
 45 65 70 75 80
 His Phe Arg Ala Lys Gln Lys Glu Glu Glu Glu Lys Leu Lys Arg Gln
 85 90 95
 Lys Asp Leu Arg Lys Lys Leu Phe Arg Ile Gln Gly Gln Lys Glu Arg
 100 105 110
 Arg Asn Gln Lys Ser Ser Leu Lys Gly Ala Glu Gly Gln Leu Gln
 115 120 125

50

<210> 944
 <211> 159
 <212> PRT
 <213> Homo sapiens

55

<400> 944
 Asn Cys Leu Pro Pro Gln Ile Gln Gly Gln Ser Leu Gln Ser Lys Gly
 1 5 10 15
 Ser Leu Gln Leu Ala Leu Ser Pro Leu Gln Thr Gly Leu Leu Val Ser
 20 25 30

60

20 <210> 945
 <211> 250
 <212> PRT
 <213> Homo sapiens

60 <210> 946
 <211> 128
 <212> PRT
 <213> Homo sapiens

<400> 946
Arg Ala Ser Asn Ser Ser Thr Ser Cys Arg Arg Trp Ser Gly Thr Ala
356

1 5 10 15
 Asn Gly Pro Ala Xaa Ser Glu Phe Arg Leu Leu Trp Ser Ser Leu Glu
 20 25 30
 Val Met Ile Ser Leu Phe Glu Val Thr Glu Val Val Pro Asp Pro Thr
 5 35 40 45
 Asn Ile Gly Phe Glu Ser Phe Gly Phe Phe Phe Leu Leu Xaa Phe
 50 55 60
 Thr Leu Val Glu Leu Asn Gly Ala Ser Pro Leu Ser Cys Phe Leu Asn
 65 70 75 80
 10 Thr Val Gln Ala Gly Val His Tyr Ile Lys Arg Ile His Leu Lys His
 85 90 95
 Tyr Ala Met Leu Gly Asn Leu Gly Phe Trp Gly Leu Leu Xaa Xaa Xaa
 100 105 110
 15 Ile Leu Asn Lys Pro Gly Leu Ser Phe Lys Xaa Lys Pro Gly Leu Pro
 115 120 125

 <210> 947
 <211> 127
 <212> PRT
 20 <213> Homo sapiens

 <400> 947
 Ala Val Met Gln Pro Ser Ser Val Gln Tyr Ser Cys Gln Ser Gln Gln
 1 5 10 15
 25 Asn Glu Gly Ile Pro Arg Glu Lys Val Leu Asn Leu Leu Leu Phe Leu
 20 25 30
 Val Ser Val Glu Phe Leu Leu Gly Lys Thr His Ile Leu Gln Arg Thr
 35 40 45
 Ser Cys Tyr Ser Cys Pro Arg Asp His Val Pro Pro Lys Thr Glu Arg
 30 50 55 60
 Ser Asn His Ile Glu Leu Asn Ile Phe Val Leu Gly Ser Cys Pro Ile
 65 70 75 80
 Ala Ser Tyr Cys Gly Gln His Ile Arg Tyr Cys Val Gly His Arg Glu
 85 90 95
 35 Leu Arg Ile Leu Leu His Leu Ala Glu Asp Gly Gln Ala Leu Gln Met
 100 105 110
 Gly Leu Xaa Asn Leu Asn Phe Asp Cys Tyr Gly Leu His Leu Lys
 115 120 125

 40 <210> 948
 <211> 183
 <212> PRT
 <213> Homo sapiens

 45 <400> 948
 Trp Thr Pro Ala Cys Thr Val Leu Arg Lys Gln Asp Ser Gly Glu Ala
 1 5 10 15
 Pro Phe Ser Ser Thr Lys Val Lys Xaa Lys Ser Lys Lys Lys Lys Pro
 20 25 30
 50 Lys Asp Ser Lys Pro Met Leu Val Gly Ser Gly Thr Thr Ser Val Thr
 35 40 45
 Ser Asn Asn Glu Ile Ile Thr Ser Ser Glu Asp His Ser Asn Arg Asn
 50 55 60
 Ser Asp Xaa Ala Gly Pro Phe Ala Val Pro Asp His Leu Arg Gln Asp
 55 65 70 75 80
 Val Glu Glu Phe Glu Ala Leu Tyr Asp Gln His Ser Asn Glu Tyr Val
 85 90 95
 Val Arg Asn Lys Lys Leu Trp Asp Met Asn Pro Lys Gln Lys Cys Ser
 100 105 110
 60 Thr Leu Tyr Asp Tyr Phe Ser Gln Phe Leu Glu Glu His Gly Pro Leu
 115 120 125
 Asp Met Ser Asn Lys Met Phe Ser Ala Glu Tyr Glu Phe Phe Pro Glu
 130 135 140

Glu Thr Arg Gln Ile Leu Glu Lys Ala Gly Gly Leu Lys Pro Phe Leu
 145 150 155 160
 Leu Gly Cys Pro Arg Phe Val Val Il Asp Asn Cys Ile Ala Leu Lys
 165 170 175
 5 Lys Val Ala Ser Arg Leu Lys
 180
 <210> 949
 <211> 219
 10 <212> PRT
 <213> Homo sapiens
 <400> 949
 15 Leu Leu Asn Gly Leu Asp Pro Gln Lys Ile Lys Gln Leu Asn Leu Ala
 1 5 10 15
 Met Ile Asn Tyr Val Leu Val Val Tyr Gly Leu Ala Ile Ser Leu Leu
 20 20 25 30
 Gly Ile Gly Gln Pro Glu Glu Leu Ser Glu Ala Glu Asn Gln Phe Lys
 35 40 45
 20 Arg Ile Ile Glu His Tyr Pro Ser Glu Gly Leu Asp Cys Leu Ala Tyr
 50 55 60
 Cys Gly Ile Gly Lys Val Tyr Leu Lys Lys Asn Arg Phe Leu Glu Ala
 65 70 75 80
 Leu Asn His Phe Glu Lys Ala Arg Thr Leu Ile Tyr Arg Leu Pro Gly
 25 85 90 95
 Val Leu Thr Trp Pro Thr Ser Asn Val Ile Ile Glu Glu Ser Gln Pro
 100 105 110
 Gln Lys Ile Lys Met Leu Leu Glu Lys Phe Val Glu Glu Cys Lys Phe
 115 120 125
 30 Pro Pro Val Pro Asp Ala Ile Cys Cys Tyr Gln Lys Cys His Gly Tyr
 130 135 140
 Ser Lys Ile Gln Ile Tyr Ile Thr Asp Pro Asp Phe Lys Gly Phe Ile
 145 150 155 160
 Arg Ile Ser Cys Cys Gln Tyr Cys Lys Ile Glu Phe His Met Asn Cys
 35 165 170 175
 Trp Lys Lys Leu Lys Thr Thr Thr Phe Asn Asp Lys Ile Asp Lys Gly
 180 185 190
 Phe Ser Thr Arg Glu Tyr Val Leu Pro Leu Thr Val Xaa Gly Ser Phe
 195 200 205
 40 Leu Xaa Ile Ile Ile Phe Ser Ser Gly Trp Val
 210 215
 <210> 950
 <211> 116
 45 <212> PRT
 <213> Homo sapiens
 <400> 950
 50 Arg Ala Ser Asn Ser Ser Thr Ser Cys Arg Arg Trp Ser Gly Thr Ala
 1 5 10 15
 Asn Gly Pro Ala Glu Ser Glu Phe Arg Leu Leu Trp Ser Ser Leu Glu
 20 25 30
 Val Met Ile Ser Leu Phe Glu Val Thr Glu Val Val Pro Asp Pro Thr
 35 40 45
 55 Asn Ile Gly Phe Glu Ser Phe Gly Phe Phe Phe Leu Leu Phe Phe
 50 55 60
 Thr Leu Val Glu Leu Asn Xaa Ala Ser Pro Leu Ser Cys Phe Leu Asn
 65 70 75 80
 Thr Val Gln Arg Val Pro Leu Tyr Gln Arg Ile His Leu Lys His Tyr
 85 90 95
 60 Ala Met Leu Gly Asn Leu Ala Leu Gly Ser Ser Ser Thr Ile Leu Asn
 100 105 110
 Asn Gly Phe Leu

115

<210> 951

<211> 127

5 <212> PRT

<213> Homo sapiens

<400> 951

10 Ala Val Met Gln Pro Ser Ser Val Gln Tyr Ser Cys Gln Ser Gln Gln
 1 5 10 15
 Asn Glu Gly Ile Pro Arg Glu Lys Val Leu Asn Leu Leu Leu Phe Leu
 20 25 30
 Val Ser Val Glu Phe Leu Leu Gly Lys Thr His Ile Leu Gln Arg Thr
 35 40 45
 15 Ser Cys Tyr Ser Cys Pro Arg Asp His Val Pro Pro Lys Thr Glu Arg
 50 55 60
 Ser Asn His Ile Glu Leu Asn Ile Phe Val Leu Gly Ser Cys Pro Ile
 65 70 75 80
 20 Ala Ser Tyr Cys Gly Gln His Ile Arg Tyr Cys Val Gly His Arg Glu
 85 90 95
 Leu Arg Ile Leu Leu His Leu Ala Glu Asp Gly Gln Ala Leu Gln Met
 100 105 110
 Gly Leu Gln Asn Leu Asn Phe Asp Cys Tyr Gly Leu His Leu Lys
 115 120 125

25

<210> 952

<211> 184

<212> PRT

<213> Homo sapiens

30

<400> 952

Tyr Asn Gly Thr Arg Cys Thr Val Leu Arg Lys Gln Asp Ser Gly Glu
 1 5 10 15
 35 Xaa Pro Phe Ser Ser Thr Lys Val Lys Asn Lys Ser Lys Lys Lys Lys
 20 25 30
 Pro Lys Asp Ser Lys Pro Met Leu Val Gly Ser Gly Thr Thr Ser Val
 35 40 45
 Thr Ser Asn Asn Glu Ile Ile Thr Ser Ser Glu Asp His Ser Asn Arg
 50 55 60
 40 Asn Ser Asp Ser Ala Gly Pro Phe Ala Val Pro Asp His Leu Arg Gln
 65 70 75 80
 Asp Val Glu Glu Phe Glu Ala Leu Tyr Asp Gln His Ser Asn Glu Tyr
 85 90 95
 45 Val Val Arg Asn Lys Lys Leu Trp Asp Met Asn Pro Lys Gln Lys Cys
 100 105 110
 Ser Thr Leu Tyr Asp Tyr Phe Ser Gln Phe Leu Glu Glu His Gly Pro
 115 120 125
 Leu Asp Met Ser Asn Lys Met Phe Ser Ala Glu Tyr Glu Phe Phe Pro
 130 135 140
 50 Glu Glu Thr Arg Gln Ile Leu Glu Lys Ala Gly Gly Leu Lys Pro Phe
 145 150 155 160
 Leu Leu Gly Cys Pro Arg Phe Val Val Ile Asp Asn Cys Ile Ala Leu
 165 170 175
 55 Lys Lys Val Ala Ser Arg Leu Lys
 180

<210> 953

<211> 185

<212> PRT

60 <213> Homo sapiens

<400> 953

Tyr Asn Xaa Xaa Pro Leu Val Leu Val Leu Arg Lys Gln Asp Ser Gly

1 5 10 15
 Glu Xaa Pro Phe Ser Ser Thr Lys Val Lys Asn Lys Ser Lys Lys Lys
 20 25 30
 5 Lys Pro Lys Asp Ser Lys Pro Met Leu Val Gly Ser Gly Thr Thr Ser
 35 40 45
 Val Thr Ser Asn Asn Glu Ile Thr Ser Ser Glu Asp His Ser Asn
 50 55 60
 Arg Asn Ser Asp Ser Ala Gly Pro Phe Ala Val Pro Asp His Leu Arg
 65 70 75 80
 10 Gln Asp Val Glu Glu Phe Glu Ala Leu Tyr Asp Gln His Ser Asn Glu
 85 90 95
 Tyr Val Val Arg Asn Lys Lys Leu Trp Asp Met Asn Pro Lys Gln Lys
 100 105 110
 15 Cys Ser Thr Leu Tyr Asp Tyr Phe Ser Gln Phe Leu Glu His Gly
 115 120 125
 Pro Leu Asp Met Ser Asn Lys Met Phe Ser Ala Glu Tyr Glu Phe Phe
 130 135 140
 Pro Glu Glu Thr Arg Gln Ile Leu Glu Lys Ala Gly Gly Leu Lys Pro
 145 150 155 160
 20 Phe Leu Leu Gly Cys Pro Arg Phe Val Val Ile Asp Asn Cys Ile Ala
 165 170 175
 Leu Lys Lys Val Ala Ser Arg Leu Lys
 180 185

 25 <210> 954
 <211> 125
 <212> PRT
 <213> Homo sapiens

 30 <400> 954
 Met Gln Pro Ser Ser Val Gln Tyr Ser Cys Gln Ser Gln Gln Asn Glu
 1 5 10 15
 Gly Ile Pro Arg Glu Lys Val Leu Asn Leu Leu Leu Phe Leu Val Ser
 20 25 30
 35 Val Glu Phe Leu Leu Gly Lys Thr His Ile Leu Gln Arg Thr Ser Cys
 35 40 45
 Tyr Ser Cys Pro Arg Asp His Val Pro Pro Lys Thr Glu Arg Ser Asn
 50 55 60
 His Ile Glu Leu Asn Ile Phe Val Leu Gly Ser Cys Pro Ile Ala Ser
 65 70 75 80
 40 Tyr Cys Gly Gln His Ile Arg Tyr Cys Val Gly His Arg Glu Leu Arg
 85 90 95
 Ile Leu Leu His Leu Ala Glu Asp Gly Gln Ala Leu Gln Met Gly Leu
 100 105 110
 45 Gln Asn Leu Asn Phe Asp Cys Tyr Gly Leu His Leu Lys
 115 120 125

 <210> 955
 <211> 212
 50 <212> PRT
 <213> Homo sapiens

 <400> 955
 Glu Asp Glu Lys Arg Arg Arg Lys Glu Glu Glu Glu Arg Arg Met Lys
 1 5 10 15
 Leu Glu Met Glu Ala Lys Arg Lys Gln Glu Glu Glu Glu Arg Lys Lys
 20 25 30
 Arg Glu Asp Asp Glu Lys Arg Ile Gln Ala Glu Val Glu Ala Gln Leu
 35 40 45
 60 Ala Arg Gln Lys Glu Glu Glu Ser Gln Gln Gln Ala Val Leu Glu Gln
 50 55 60
 Glu Arg Arg Asp Arg Glu Leu Ala Leu Arg Ile Ala Gln Ser Glu Ala
 65 70 75 80

Glu Leu Ile Ser Asp Glu Ala Gln Ala Asp Leu Ala Leu Arg Ser Leu
 85 90 95
 Asp Ser Tyr Pro Val Thr Ser Lys Asn Asp Gly Thr Arg Pro Lys Met
 100 105 110
 5 Thr Pro Glu Gln Met Ala Lys Glu Met Ser Glu Phe Leu Ser Arg Gly
 115 120 125
 Pro Ala Val Leu Ala Thr Lys Ala Ala Ala Gly Thr Lys Lys Tyr Asp
 130 135 140
 10 Leu Ser Lys Trp Lys Tyr Ala Glu Leu Arg Asp Thr Ile Asn Thr Ser
 145 150 155 160
 Cys Asp Ile Glu Leu Leu Ala Ala Cys Arg Glu Glu Phe His Arg Arg
 165 170 175
 Leu Lys Val Tyr His Ala Trp Lys Ser Lys Asn Lys Lys Arg Asn Leu
 180 185 190
 15 Glu Gln Ser Asn Val Leu Gln Ser Leu Leu Leu Ile Met Leu Ser Lys
 195 200 205
 Thr Gln Gln Leu
 210

 20 <210> 956
 <211> 121
 <212> PRT
 <213> Homo sapiens

 25 <400> 956
 His Phe Phe Gly His Leu Phe Arg Cys His Phe Gly Ser Cys Ser Ile
 1 5 10 15
 Ile Phe Arg Ser Tyr Arg Ile Gly Ile Gln Ala Pro Gln Arg Gln Val
 20 25 30
 30 Gly Leu Gly Leu Ile Thr Asp Glu Leu Gly Phe Thr Leu Gly Asn Pro
 35 40 45
 Gln Gly Gln Leu Pro Val Pro Ala Leu Leu Leu Gln Asn Cys Leu Leu
 50 55 60
 35 Leu Gly Phe Leu Leu Leu Leu Ser Gly Gln Leu Cys Leu His Phe Ser
 65 70 75 80
 Leu Asn Ala Phe Phe Ile Ile Phe Pro Phe Leu Ser Leu Phe Phe Phe
 85 90 95
 Leu Phe Ser Leu Cys Phe His Leu Lys Phe His Pro Pro Phe Leu Leu
 100 105 110
 40 Phe Leu Ser Ser Thr Phe Phe Val Phe
 115 120

 <210> 957
 <211> 221
 45 <212> PRT
 <213> Homo sapiens

 <400> 957
 Glu Arg Lys Arg Arg Glu Glu Asp Glu Lys Arg Arg Arg Lys Glu Glu
 1 5 10 15
 Glu Glu Arg Arg Met Lys Leu Glu Met Glu Ala Lys Arg Lys Gln Glu
 20 25 30
 Glu Glu Glu Arg Lys Lys Arg Glu Asp Asp Glu Lys Arg Ile Gln Ala
 35 40 45
 55 Glu Val Glu Ala Gln Leu Ala Arg Gln Lys Glu Glu Glu Ser Gln Gln
 50 55 60
 Gln Ala Val Leu Glu Gln Glu Arg Arg Asp Arg Glu Leu Ala Leu Arg
 65 70 75 80
 Ile Ala Gln Ser Glu Ala Glu Leu Ile Ser Asp Glu Ala Gln Ala Asp
 85 90 95
 60 Leu Ala Leu Arg Arg Gly Pro Ala Val Leu Ala Thr Lys Ala Ala Ala
 100 105 110
 Gly Thr Lys Lys Tyr Asp Leu Ser Lys Trp Lys Tyr Ala Glu Leu Arg

115 120 125
 Asp Thr Ile Asn Thr Ser Cys Asp Ile Glu Leu Leu Ala Ala Cys Arg
 130 135 140
 5 Glu Glu Phe His Arg Arg Leu Lys Val Tyr His Ala Trp Lys Ser Lys
 145 150 155 160
 Asn Lys Lys Arg Asn Thr Glu Thr Glu Gln Arg Ala Pro Lys Ser Val
 165 170 175
 Thr Asp Tyr Ala Gln Gln Asn Pro Ala Ala Gln Ile Pro Ala Arg Gln
 180 185 190
 10 Arg Glu Ile Glu Met Asn Pro Thr Ala Thr Leu Leu Ser His Xaa Ile
 195 200 205
 His Ser Ala Leu Pro Asp Gln Tyr Lys Arg Pro Ser Glu
 210 215 220
 15 <210> 958
 <211> 93
 <212> PRT
 <213> Homo sapiens
 20 <400> 958
 Phe Ser Lys Cys Ser Ala Ser Asn Ile Phe Leu Phe Lys Lys Phe Leu
 1 5 10 15
 Val Ser Phe Leu Ala Phe Glu Val Leu Val Ile Val Asp Leu Phe His
 20 25 30
 25 Lys Leu Cys Asn Ser Glu Ile Leu Val Phe Ser Lys Cys Leu Phe Tyr
 35 40 45
 Ile Thr Asp Asn Phe Lys Met Phe Ser Leu Cys Ala Val Ser Ile Asp
 50 55 60
 Ser Asn Val Ser Ser Phe Lys Pro Asn Ile Tyr Asp Phe His Ile Trp
 30 65 70 75 80
 Asn Leu Lys Thr Lys Ile His Gln Gly Val Met Leu Thr
 85 90
 35 <210> 959
 <211> 93
 <212> PRT
 <213> Homo sapiens
 40 <400> 959
 Phe Ser Lys Cys Ser Ala Ser Asn Ile Phe Leu Phe Lys Lys Phe Leu
 1 5 10 15
 Val Ser Phe Leu Ala Phe Glu Val Leu Val Ile Val Asp Leu Phe His
 20 25 30
 45 Lys Leu Cys Asn Ser Glu Ile Leu Val Phe Ser Lys Cys Leu Phe Tyr
 35 40 45
 Ile Thr Asp Asn Phe Lys Met Phe Ser Leu Cys Ala Val Ser Ile Asp
 50 55 60
 Ser Asn Val Ser Ser Phe Lys Pro Asn Ile Tyr Asp Phe His Ile Trp
 65 70 75 80
 50 Asn Leu Lys Thr Lys Ile His Gln Gly Val Met Leu Thr
 85 90
 55 <210> 960
 <211> 193
 <212> PRT
 <213> Homo sapiens
 60 <400> 960
 Trp Trp Asn His Phe Arg Ser Lys Asn Val Arg Arg Ile Asn Leu Gln
 1 5 10 15
 Lys Asn Ile Ile Gly Ser Ser Pro Val Ala Asp Phe Ser Ala Ile Lys
 20 25 30
 Glu Leu Asp Thr Leu Asn Asn Glu Ile Val Asp Leu Gln Arg Glu Lys
 362

35 40 45
 Asn Asn Val Glu Gln Asp Leu Lys Glu Lys Glu Asp Thr Ile Lys Gln
 50 55 60
 5 Arg Thr Ser Glu Val Gln Asp Leu Gln Asp Glu Val Gln Arg Glu Asn
 65 70 75 80
 Thr Asn Leu Gln Lys Leu Gln Ala Gln Lys Gln Gln Val Gln Glu Leu
 85 90 95
 Leu Asp Glu Leu Asp Glu Gln Lys Ala Gln Leu Glu Glu Gln Leu Lys
 100 105 110
 10 Glu Val Arg Lys Lys Cys Ala Glu Glu Ala Gln Leu Ile Ser Ser Leu
 115 120 125
 Lys Ala Glu Leu Thr Ser Gln Glu Ser Gln Ile Ser Thr Tyr Glu Glu
 130 135 140
 Glu Leu Ala Lys Ala Arg Glu Glu Leu Ser Arg Leu Gln Gln Glu Thr
 15 145 150 155 160
 Gln Asn Trp Arg Xaa Ser Val Lys Ser Gly Lys Ala Gln Phe Xaa Thr
 165 170 175
 Xaa Leu Ala Ala Pro Thr Arg Phe Thr Thr Xaa Lys Leu Val Gln Cys
 180 185 190
 20 Gln

25 <210> 961
 <211> 82
 <212> PRT
 <213> Homo sapiens

<400> 961
 30 Leu Thr Tyr Arg Gly Lys Arg Ile Met Trp Asn Arg Thr Leu Arg Arg
 1 5 10 15
 Arg Lys Ile Leu Leu Asn Arg Gly Gln Val Arg Phe Arg Ile Phe Lys
 20 25 30
 Met Lys Phe Lys Gly Arg Ile Leu Ile Cys Lys Asn Tyr Arg Pro Arg
 35 35 40 45
 Asn Ser Arg Tyr Arg Asn Ser Leu Met Asn Trp Met Ser Arg Lys Pro
 50 55 60
 Ser Trp Arg Ser Asn Ser Arg Lys Ser Glu Arg Asn Val Leu Arg Arg
 65 70 75 80
 40 Pro Asn

45 <210> 962
 <211> 219
 <212> PRT
 <213> Homo sapiens

<400> 962
 50 Ala Ala Gln Leu Ser Leu Thr Gln Leu Ser Ser Gly Asn Pro Val Tyr
 1 5 10 15
 Glu Lys Tyr Tyr Arg Gln Val Asp Thr Gly Asn Thr Gly Arg Val Leu
 20 25 30
 Ala Ser Asp Ala Ala Ala Phe Leu Lys Lys Ser Gly Leu Pro Asp Leu
 35 40 45
 55 Ile Leu Gly Lys Ile Trp Asp Leu Ala Asp Thr Asp Gly Lys Gly Ile
 50 55 60
 Leu Asn Lys Gln Glu Phe Phe Val Ala Leu Arg Leu Val Ala Cys Ala
 65 70 75 80
 Gln Asn Gly Leu Glu Val Ser Leu Ser Ser Leu Asn Leu Ala Val Pro
 85 90 95
 60 Pro Pro Arg Phe His Asp Thr Ser Ser Pro Leu Leu Ile Ser Gly Thr
 100 105 110
 Ser Ala Ala Glu Leu Pro Trp Ala Val Lys Pro Glu Asp Lys Ala Lys
 115 120 125

Tyr Asp Ala Ile Phe Asp Ser Leu Ser Pro Val Asn Gly Phe Leu Ser
 130 135 140
 Gly Asp Lys Val Lys Pro Val Leu Leu Asn Ser Lys Leu Pro Val Asp
 145 150 155 160
 5 Ile Leu Gly Arg Val Trp Glu Leu Ser Asp Ile Asp His Asp Gly Met
 165 170 175
 Leu Asp Arg Xaa Xaa Phe Ala Val Ala Met Phe Leu Val Tyr Xaa Ala
 180 185 190
 10 Thr Gly Lys Lys Asn Leu Cys Gln Cys Pro Cys Xaa Gln Pro Trp Val
 195 200 205
 Pro Pro Ile Leu Arg Lys Lys Thr Xaa Val Gly
 210 215

 <210> 963
 15 <211> 109
 <212> PRT
 <213> Homo sapiens

 <400> 963
 20 Leu Ala Lys Asp Tyr Trp Tyr His Glu Ile Leu Val Glu Glu Gln Pro
 1 5 10 15
 Gly Ser Asn Tyr Leu Val Lys Leu Pro Ile His Ser Gly His Met Pro
 20 25 30
 25 Gln Asp Ala Lys Gln Gln Arg Ile Leu Val Cys Ser Gly Tyr Leu Cys
 35 40 45
 His Leu Cys Arg Leu Asn Pro Lys Ser Phe Gln Val Ser Ser Leu Glu
 50 55 60
 Ala Leu Ile Phe Ser Gly Lys Gln Gln His Gln Lys Pro Thr Pro Phe
 65 70 75 80
 30 Gln Tyr Cys Leu Tyr Gln Pro Val Tyr Ser Ile Phe His Ile Gln Asp
 85 90 95
 Ser His Leu Ile Thr Val Ser Glu Arg Ala Gly Pro Pro
 100 105

 35 <210> 964
 <211> 118
 <212> PRT
 <213> Homo sapiens

 <400> 964
 40 Pro Thr Xaa Val Phe Phe Leu Lys Met Gly Gly Thr Gln Gly Xaa Arg
 1 5 10 15
 Gln Gly His Trp His Arg Phe Phe Phe Pro Val Xaa Gln Tyr Thr Lys
 20 25 30
 45 Asn Met Ala Thr Ala Xaa Ser Xaa Leu Ser Ser Ile Pro Ser Trp Ser
 35 40 45
 Ile Ser Leu Asn Ser Gln Thr Leu Pro Arg Ile Ser Thr Gly Asn Leu
 50 55 60
 Glu Leu Ser Asn Thr Gly Phe Thr Leu Ser Pro Asp Arg Asn Pro Phe
 65 70 75 80
 50 Thr Gly Leu Lys Leu Ser Asn Ile Ala Ser Tyr Leu Ala Leu Ser Ser
 85 90 95
 Gly Phe Thr Ala His Gly Ser Ser Ala Ala Glu Val Pro Leu Ile Ser
 100 105 110
 55 Lys Gly Leu Leu Val Ser
 115

 <210> 965
 <211> 78
 60 <212> PRT
 <213> Homo sapiens

 <400> 965

Thr Gly Gln Gly Pro Xaa Lys Xaa Arg Met Ala Ala Met Leu Xaa Leu
 1 5 10 15
 Leu Leu Ala Leu Tyr Leu Met Xaa Ile Phe Xaa Gly Xaa Lys Phe Xaa
 20 25 30
 5 Pro Xaa Leu Ser Leu Lys Arg Asn Ile Xaa Phe Xaa Thr Xaa Phe Val
 35 40 45
 Arg Asn Arg Xaa Xaa Phe Ile Ser Gln Pro Pro Trp Xaa Gly Phe Gly
 50 55 60
 Gly Pro Lys Asn Xaa Xaa Lys Xaa Lys Xaa Xaa Phe Phe Lys
 10 65 70 75

<210> 966

<211> 181

<212> PRT

15 <213> Homo sapiens

<400> 966

Glu Leu Thr Val Phe Gln Ser Lys Asp Val Pro Glu Lys Thr Ser Ser
 1 5 10 15
 20 Pro Glu Glu Ser Ile Arg Met Thr Lys Gly Ile Thr Met Ala Thr Ala
 20 25 30
 Lys Ala Val Ala Ala Gly Asn Ser Cys Arg Gln Glu Asp Val Ile Ala
 35 40 45
 Thr Ala Asn Leu Ser Arg Lys Ala Val Ser Asp Met Leu Thr Ala Cys
 25 50 55 60
 Lys Gln Ala Ser Phe His Pro Asp Val Ser Asp Glu Val Arg Thr Arg
 65 70 75 80
 Ala Leu Arg Phe Gly Thr Glu Cys Thr Leu Gly Tyr Leu Asp Leu Leu
 85 90 95
 30 Glu His Val Leu Val Ile Leu Gln Lys Pro Thr Pro Glu Phe Lys Gln
 100 105 110
 Gln Leu Ala Ala Phe Ser Lys Arg Val Ala Gly Ala Val Thr Glu Leu
 115 120 125
 Ile Gln Ala Ala Glu Ala Met Lys Gly Thr Glu Trp Val Asp Pro Glu
 35 130 135 140
 Asp Pro Thr Val Ile Ala Glu Thr Glu Leu Leu Gly Ala Ala Ala Ser
 145 150 155 160
 Ile Glu Ala Ala Ala Lys Lys Leu Glu Gln Leu Lys Pro Arg Ala Lys
 165 170 175
 40 Pro Lys Gln Ala Gly
 180

<210> 967

<211> 90

45 <212> PRT

<213> Homo sapiens

<400> 967

Leu Ser Thr Gly Ser Arg Gly Phe Val Trp Met Thr Leu Cys Glu Leu
 1 5 10 15
 Lys Gln Pro Leu Gln Gly Lys Glu Pro Thr Asp Cys Ile Thr Ala Pro
 20 25 30
 Ala His Gln Ala Pro Thr Ala Phe Arg Asn Xaa Ala Leu Trp Thr Thr
 35 40 45
 55 Glu Glu Gln Asn Asn Arg Ser Val Phe Trp Ala Thr Lys Tyr Xaa Met
 50 55 60
 Gly Leu Gly Cys Thr Arg Ser Leu His Thr Glu Ala Xaa Lys Arg Ala
 65 70 75 80
 Asn Arg Gly Gly Asn Phe Ser Pro Pro Gly
 85 90

<210> 968

<211> 100

<212> PRT

<213> Homo sapiens

<400> 968

5 Asn Ser Leu Cys Arg Val Arg Ser Pro Gln Thr Val Leu Gln Pro Leu
 1 5 10 15
 Leu Thr Lys Pro Arg Arg Pro Ser Ala Thr Xaa Pro Phe Gly Leu Arg
 20 25 30
 Arg Asn Lys Ile Ile Val Gln Phe Ser Gly Pro Gln Asn Thr Xaa Trp
 10 35 40 45
 Val Trp Val Val Gln Gly Ala Tyr Thr Arg Arg Gln Xaa Ser Val Gln
 50 55 60
 Thr Gly Ala Gly Ile Phe His Pro Leu Gly Glu Pro Val Leu Lys Thr
 65 70 75 80
 15 Trp Lys Glu Asp Leu Ser His Pro Pro Gly Val His Thr Gly Leu Cys
 85 90 95
 Phe Trp Leu Leu
 100

20 <210> 969

<211> 125

<212> PRT

<213> Homo sapiens

25 <400> 969

Gly Leu Lys Xaa Xaa Ala Lys Met Arg Pro Xaa Gly Asn Ala Xaa Gly
 1 5 10 15
 Xaa Ile Gly Gln Thr Val Phe Xaa Lys Xaa Trp Ala Xaa Ser Glu Thr
 20 25 30
 30 Xaa Pro Xaa Xaa Pro Gly Xaa Ser Xaa Lys Xaa Xaa Gly Val Val Phe
 35 40 45
 Thr Phe Leu Ser Arg Gly His Xaa Trp Asn Val Arg Met Ser Xaa Val
 50 55 60
 Lys Cys Xaa Thr Gln Asn Ser Phe Ala Xaa Ser Xaa His Ala Ser Xaa
 35 65 70 75 80
 Cys Xaa Arg Lys Xaa Gly Cys Thr Phe His Gly Leu Val Thr Asn Lys
 85 90 95
 Glu Lys Ser Val Leu Cys Cys Xaa Gln Thr Leu Trp Leu Leu Leu Val
 100 105 110
 40 Leu Leu Leu Gly Leu Leu Leu Asp Leu Phe Met Ile Leu
 115 120 125

<210> 970

<211> 122

45 <212> PRT

<213> Homo sapiens

<400> 970

Asn Xaa Pro Xaa Xaa Ser Arg Xaa Lys Xaa Glu Xaa Xaa Gly Gly Cys
 1 5 10 15
 Phe His Ile Phe Val Pro Trp Ala Xaa Val Glu Cys Ser Tyr Val Xaa
 20 25 30
 Gly Lys Met Xaa Tyr Pro Lys Phe Cys Arg Xaa Xaa Ser Cys Leu
 35 40 45
 55 Xaa Val Xaa Gln Lys Xaa Gly Val His Val Ser Trp Thr Cys Tyr Gln
 50 55 60
 Gln Arg Lys Val Ser Ile Met Leu Xaa Ser Asp Thr Leu Ala Phe Val
 65 70 75 80
 Gly Pro Ser Leu Arg Pro Ala Pro Gly Pro Leu Tyr Asp Ile Val Ile
 60 85 90 95
 Gly Lys Lys Ile Ile Asp Val Ile Glu Tyr Ser Ser Ser Ser Gln Glu
 100 105 110
 Lys Thr Glu Ala Gly Val Gly His Gly Ser

115 120

<210> 971
 <211> 169
 5 <212> PRT
 <213> Homo sapiens

<400> 971

10 Cys Ile Lys Gln Glu Leu Thr Val Phe Gln Ser Lys Asp Val Pro Glu
 1 5 10 15
 Lys Thr Ser Ser Pro Glu Glu Ser Ile Xaa Met Thr Lys Gly Ile Thr
 20 25 30
 Met Ala Thr Ala Lys Ala Val Ala Ala Gly Asn Ser Cys Xaa Gln Glu
 35 40 45
 15 Asp Val Ile Ala Thr Ala Asn Leu Ser Arg Lys Ala Val Ser Asp Met
 50 55 60
 Leu Thr Ala Cys Lys Gln Ala Ser Phe His Pro Asp Val Ser Asp Glu
 65 70 75 80
 Val Arg Thr Xaa Ala Leu Arg Phe Gly Thr Glu Cys Thr Leu Gly Tyr
 85 90 95
 20 Leu Asp Leu Leu Glu His Val Leu Val Ile Leu Gln Lys Pro Thr Pro
 100 105 110
 Glu Phe Lys Gln Gln Leu Ala Ala Phe Ser Lys Arg Val Ala Gly Ala
 115 120 125
 25 Val Thr Glu Leu Ile Gln Ala Ala Glu Ala Met Lys Gly Thr Glu Trp
 130 135 140
 Val Asp Pro Glu Asp Pro Thr Val Ile Ala Glu Thr Glu Leu Leu Gly
 145 150 155 160
 Ala Ala Ala Ser Ile Glu Ala Ala Cys
 165

<210> 972
 <211> 112
 35 <212> PRT
 <213> Homo sapiens

<400> 972

40 Arg Gly Glu Asn Xaa Ser Leu Ala Phe Arg Asp Gly Val His Pro Trp
 1 5 10 15
 Leu Leu Gly Pro Pro Gly Ala Arg Leu Gly Asp Ser Ser Glu Thr Asn
 20 25 30
 Pro Arg Ile Gln Ala Ala Ala Gly Arg Phe Leu Gln Ala Ser Arg Arg
 35 40 45
 Arg Cys Asp Arg Ala His Pro Gly Gly Gly Ser His Glu Arg Asn Arg
 50 55 60
 45 Val Gly Gly Ser Arg Arg Pro Asn Cys His Cys Arg Asn Arg Val Thr
 65 70 75 80
 Gly Gly Cys Ser Ile His Arg Ser Cys Leu Leu Lys Lys Leu Glu Gln
 85 90 95
 50 Leu Lys Pro Arg Ala Lys Pro Lys Gln Ala Asp Glu Thr Leu Gly Leu
 100 105 110

<210> 973
 <211> 95
 55 <212> PRT
 <213> Homo sapiens

<400> 973

60 Leu Cys Phe Cys Asn Asp Ser Trp Val Phe Trp Ile His Pro Leu Cys
 1 5 10 15
 Ser Phe His Gly Phe Arg Arg Leu Asp Glu Leu Cys His Ser Ala Gly
 20 25 30
 Asp Ser Leu Gly Glu Ser Gly Gln Leu Leu Leu Glu Phe Trp Gly Trp

35 40 45
 Phe Leu Lys Asn His Gln Asp Val Leu Gln Glu Val Gln Val Ala Lys
 50 55 60
 Gly Ala Leu Arg Pro Glu Thr Gln Gly Xaa Gly Ser His Leu Val Thr
 5 65 70 75 80
 Asp Ile Gly Val Glu Gly Cys Leu Leu Ala Ser Arg Gln His Ile
 85 90 95

 <210> 974
 10 <211> 95
 <212> PRT
 <213> Homo sapiens

 <400> 974
 15 Pro Arg Val His Ser Val Pro Lys Arg Lys Ala Xaa Val Leu Thr Ser
 1 5 10 15
 Ser Leu Thr Ser Gly Trp Lys Asp Ala Cys Leu Gln Ala Val Asn Ile
 20 20 25 30
 Ser Asp Thr Ala Phe Arg Leu Arg Leu Ala Val Ala Ile Thr Ser Ser
 35 40 45
 Cys Xaa His Glu Phe Pro Ala Thr Ala Leu Ala Val Ala Met Val
 50 55 60
 Met Pro Phe Val Ile Xaa Met Asp Ser Ser Gly Asp Asp Val Phe Ser
 65 70 75 80
 25 Gly Thr Ser Phe Asp Trp Asn Thr Val Ser Ser Cys Phe Met His
 85 90 95

 <210> 975
 <211> 159
 30 <212> PRT
 <213> Homo sapiens

 <400> 975
 35 Arg Xaa Xaa Gly Gly Thr Gln Lys Gly Xaa Pro Gln Xaa Met Ala Pro
 1 5 10 15
 Xaa Xaa Asn Trp Thr Asn Lys Phe Ser Xaa Lys Val Gly Pro Leu Ser
 20 25 30
 Trp Lys Xaa Ala Pro Xaa Xaa Pro Gly Xaa Ser Leu Glu Xaa Leu Xaa
 35 40 45
 Xaa Leu Phe Ser His Phe Leu Ser Pro Trp Ala Xaa Gly Gly Met Phe
 50 55 60
 Xaa Met Ser His Gly Tyr Asn Cys Leu Thr His Lys Phe Phe Cys Arg
 65 70 75 80
 Xaa Pro Ser Cys Xaa Xaa Val Xaa Gln Xaa Xaa Gly Val His Val Ser
 45 85 90 95
 Trp Thr Cys Tyr Gln Gln Arg Lys Val Ser Ile Met Leu Phe Ser Asp
 100 105 110
 Thr Leu Ala Phe Val Gly Pro Ser Leu Arg Pro Ala Pro Gly Pro Leu
 115 120 125
 50 Tyr Asp Ile Val Ile Gly Lys Lys Ile Ile Asp Val Ile Glu Tyr Ser
 130 135 140
 Ser Ser Ser Gln Glu Lys Thr Glu Ala Gly Val Gly His Gly Ser
 145 150 155

 55 <210> 976
 <211> 118
 <212> PRT
 <213> Homo sapiens

 60 <400> 976
 Xaa Trp Asn Pro Lys Gly Glu Xaa Pro Gly Xaa Gly Pro Trp Xaa Xaa
 1 5 10 15
 Leu Asp Lys Gln Val Phe Xaa Lys Gly Trp Ala Ile Lys Leu Glu Thr

20 25 30
 Xaa Pro Xaa Xaa Ser Arg Val Xaa Pro Gly Xaa Pro Xaa Xaa Phe Val
 35 40 45
 Phe Thr Phe Phe Val Pro Val Gly His Xaa Trp Asn Val Arg Xaa Val
 5 50 55 60
 Thr Arg Val Gln Leu Ser Tyr Pro Gln Ile Leu Leu Pro Xaa Pro Phe
 65 70 75 80
 Met Xaa His Xaa Xaa Ser Glu Xaa Arg Gly Ala Arg Phe Met Asp Leu
 85 90 95
 10 Leu Pro Thr Lys Lys Ser Gln Tyr Tyr Val Val Leu Arg His Phe Gly
 100 105 110
 Phe Cys Trp Ser Phe Ser
 115
 15 <210> 977
 <211> 141
 <212> PRT
 <213> Homo sapiens
 20 <400> 977
 Trp Leu Xaa Ala Ser Xaa Cys Ser Val Leu Met Cys Val Ser Trp Lys
 1 5 10 15
 Xaa Ala Arg Leu Ala Ala Gln Arg Gly Gln Ser Val Arg Leu Trp Leu
 20 25 30
 25 Xaa Arg Gly Cys Arg Arg Xaa Leu Trp Gly Xaa Arg Leu Xaa Leu Arg
 35 40 45
 Gly Arg Leu Arg Gly Arg Arg Gly Leu Trp Gly Leu Leu Arg Gly Trp
 50 55 60
 Arg Arg Arg Leu Leu Leu Gly His Pro His Val Ala Arg Ala Arg Arg
 65 70 75 80
 30 Gly Gly Arg Gly Ala Ala Asp Ala Val Ala Arg Val Gly Asp Leu
 85 90 95
 Ala Val Arg Gly Arg His Pro Arg Val Ala Val Gly Arg Gln Val Leu
 100 105 110
 35 Val Lys Leu Val Asp Ile Glu Gly Leu Asp Val Gly Asp Asp Val Ala
 115 120 125
 Ala Gln Leu Ala Asp Val His Val Ala Glu Val Asp Arg
 130 135 140
 40 <210> 978
 <211> 72
 <212> PRT
 <213> Homo sapiens
 45 <400> 978
 Leu Glu Xaa Gly Pro Ala Ser Cys Ser Ala Trp Ser Glu Cys Ala Pro
 1 5 10 15
 Val Ala Ala Xaa Gly Val Pro Pro Xaa Ala Val Gly Xaa Pro Pro Thr
 20 25 30
 50 Xaa Ala Gly Ala Pro Ala Gly Pro Ala Gly Pro Val Gly Ala Ala Ala
 35 40 45
 Gly Val Ala Ala Ala Pro Ala Ala Trp Thr Ser Thr Arg Gly Pro Arg
 50 55 60
 Ser Pro Gly Trp Pro Arg Cys Cys
 55 65 70
 <210> 979
 <211> 96
 <212> PRT
 60 <213> Homo sapiens
 <400> 979
 Pro Ile Asp Phe Arg Asp Val Asp Ile Gly Glu Leu Ser Ser Asp Val
 369

1 5 10 15
 Ile Ser Asn Ile Glu Thr Phe Asp Val Asn Glu Phe Asp Gln Tyr Leu
 20 25 30
 5 Pro Pro Asn Gly His Pro Gly Val Pro Ala Thr His Gly Gln Val Thr
 35 40 45
 Tyr Thr Gly Ser Tyr Gly Ile Ser Ser Thr Ala Ala Thr Pro Ala Ser
 50 55 60
 Ala Gly His Val Trp Met Ser Lys Gln Gln Ala Pro Pro Pro Pro
 65 70 75 80
 10 Gln Gln Pro Pro Gln Ala Pro Pro Ala Pro Gln Ala Pro Pro Gln Xaa
 85 90 95

 <210> 980
 <211> 103
 15 <212> PRT
 <213> Homo sapiens

 <400> 980
 20 Ala Ala Thr Ser Ser Pro Thr Ser Arg Pro Ser Met Ser Thr Ser Leu
 1 5 10 15
 Thr Ser Thr Cys Arg Pro Thr Ala Thr Arg Gly Cys Arg Pro Arg Thr
 20 25 30
 Ala Arg Ser Pro Thr Arg Ala Ala Thr Ala Ser Ala Ala Pro Arg Pro
 35 40 45
 25 Pro Arg Arg Ala Arg Ala Thr Cys Gly Cys Pro Ser Ser Arg Arg Arg
 50 55 60
 Arg His Pro Arg Ser Ser Pro His Arg Pro Arg Arg Pro Arg Arg Arg
 65 70 75 80
 30 Pro Arg Xaa Arg Arg Arg Xaa Pro His Ser Xaa Arg Arg His Pro Xaa
 85 90 95
 Ser Ser His Arg Arg Thr Leu
 100

 <210> 981
 35 <211> 164
 <212> PRT
 <213> Homo sapiens

 <400> 981
 40 Asp Ala Gly Ala His Ala Gly Ala Arg Gln Arg Leu Gln Gln Glu Gln
 1 5 10 15
 Ala Ala Arg Gln Ala Ala His Glu Arg Leu His Gly Val Gly Ala Gly
 20 25 30
 Gly Ala Gln Glu Ala Arg Gly Pro Val Pro Ala Leu Ala Gln Arg Arg
 35 40 45
 45 Ala Gln Gln Asp Ala Gly Gln Ala Leu Glu Thr Ser Glu Arg Glu Arg
 50 55 60
 Glu Ala Ala Leu Arg Gly Gly Gly Gly Ala Ala Ala Arg Ala Ala Gln
 65 70 75 80
 50 Glu Gly Pro Pro Gly Leu Gln Val Pro Ala Ala Ala Glu Glu Val Gly
 85 90 95
 Glu Glu Arg Ala Gly Gly Gly Arg Gly Gly His Gly Ala Asp Ala His
 100 105 110
 Leu Pro Gln Arg His Leu Gln Gly Ala Ala Gly Arg Leu Ala Thr Leu
 115 120 125
 55 Leu Xaa Arg His Glu Arg Gly Ala Leu Pro Arg Arg Ala Leu Gly Ala
 130 135 140
 Ile Pro Gly Pro Thr Asp Pro Thr His His Pro Gln Asn Arg Arg Ala
 145 150 155 160
 60 Ala Gly Gln Gly

<210> 982

<211> 192
 <212> PRT
 <213> Homo sapiens

5 <400> 982
 Thr Leu Val Pro Met Pro Val Arg Val Asn Gly Ser Ser Lys Asn Lys
 1 5 10 15
 Pro His Val Lys Arg Pro Met Asn Ala Phe Met Val Trp Ala Gln Ala
 20 25 30
 10 Ala Arg Arg Lys Leu Ala Asp Gln Tyr Pro His Leu His Asn Ala Glu
 35 40 45
 Leu Ser Lys Thr Leu Gly Lys Leu Trp Arg Leu Leu Asn Glu Ser Glu
 50 55 60
 Lys Arg Pro Phe Val Glu Glu Ala Glu Arg Leu Arg Val Gln His Lys
 15 65 70 75 80
 Lys Asp His Pro Asp Tyr Lys Tyr Gln Pro Arg Arg Arg Lys Ser Val
 85 90 95
 Lys Asn Gly Gln Ala Glu Ala Glu Glu Ala Thr Glu Gln Thr His Ile
 100 105 110
 20 Ser Pro Asn Ala Ile Phe Lys Ala Leu Gln Ala Asp Ser Pro His Ser
 115 120 125
 Ser Xaa Gly Met Ser Glu Val His Ser Pro Gly Glu His Ser Gly Gln
 130 135 140
 Ser Gln Gly Pro Pro Thr Pro Thr Thr Pro Lys Thr Asp Val Gln
 25 145 150 155 160
 Pro Gly Lys Ala Asp Leu Lys Arg Glu Gly Arg Pro Leu Pro Glu Gly
 165 170 175
 Gly Arg Gln Ala Pro Tyr Arg Leu Ser Arg Arg Gly His Xaa Ala Ser
 180 185 190

<210> 983
 <211> 196
 <212> PRT
 <213> Homo sapiens

35 <400> 983
 Arg Arg Cys Ser Ala Arg Xaa Met Ser Thr Ser Arg Lys Ser Ile Gly
 1 5 10 15
 Gly Leu Ser Ala Pro Leu Trp Gln Gly Ala Pro Leu Ser Leu Gln Val
 20 25 30
 40 Ser Leu Ala Arg Leu His Val Gly Phe Gly Gly Gly Gly Trp Gly Arg
 35 40 45
 Trp Ala Leu Gly Leu Pro Arg Val Leu Ala Gly Gly Val His Leu Ala
 50 55 60
 45 His Ala Xaa Gly Gly Val Trp Arg Val Gly Leu Gln Arg Leu Glu Asp
 65 70 75 80
 Gly Val Gly Gly Asp Val Arg Leu Leu Arg Gly Leu Leu Cys Leu Arg
 85 90 95
 Leu Pro Val Leu His Arg Leu Pro Pro Pro Arg Leu Val Leu Val Ile
 100 105 110
 50 Arg Val Val Leu Leu Val Leu His Ala Gln Pro Leu Arg Leu Leu His
 115 120 125
 Glu Gly Pro Leu Leu Ala Leu Val Gln Lys Ser Pro Glu Leu Ala Gln
 130 135 140
 55 Arg Leu Ala Glu Leu Gly Val Val Gln Val Arg Val Leu Val Arg Glu
 145 150 155 160
 Leu Pro Ala Arg Arg Leu Arg Pro His His Glu Gly Val His Gly Pro
 165 170 175
 Leu Asp Val Arg Leu Val Leu Ala Gly Ala Val Asp Ala His Arg His
 180 185 190
 60 Gly His Gln Arg
 195

<210> 984
 <211> 99
 <212> PRT
 <213> Homo sapiens

5

<400> 984

Met Ser Leu Arg Lys Lys Lys Lys Lys Lys Lys Gln Xaa Gln Asn Lys
 1 5 10 15
 Lys Xaa Lys Lys Thr Pro Met Ser Lys Gly Glu Phe Trp Val Xaa Ser
 10 20 25 30
 Phe Ser Phe Phe Gly Leu Phe Phe Arg Asp His Leu Xaa His Xaa Arg
 35 40 45
 Pro Leu Trp Gly Gly Pro Pro Gln Xaa Ser Xaa Trp Lys Leu Gly Xaa
 50 55 60
 Xaa Thr Gly Phe Val Xaa Lys Xaa Leu Gly Gly Leu Gly Gly Xaa Xaa
 15 65 70 75 80
 Pro Gly Met Xaa Lys Gly Asp Pro His Xaa Gly Val Arg Ala Xaa Xaa
 85 90 95
 Gly Gly Trp

20

<210> 985
 <211> 96
 <212> PRT
 <213> Homo sapiens

25

<400> 985

Gly Arg Arg Arg Arg Arg Lys Asn Lys Xaa Lys Ile Lys Lys Xaa Lys
 1 5 10 15
 Lys His Gln Cys Pro Lys Gly Asn Ser Gly Xaa Gly Pro Ser Leu Ser
 30 20 25 30
 Ser Gly Tyr Phe Leu Gly Ile Ile Xaa Ala Xaa Xaa Ala Leu Cys Gly
 35 35 40 45
 Glu Ala Leu Leu Xaa Gly Pro Xaa Gly Asn Leu Gly Xaa Xaa Pro Gly
 50 55 60
 Leu Xaa Pro Asn Xaa Trp Gly Gly Leu Val Gly Xaa Xaa Arg Gly Xaa
 65 70 75 80
 Gly Lys Gly Thr Pro Ile Xaa Val Phe Gly Pro Xaa Xaa Gly Gly Gly
 85 90 95

40

<210> 986
 <211> 133
 <212> PRT
 <213> Homo sapiens

45

<400> 986

Gly His Pro Glu Gly Pro Gly Ala His Leu Asp Met Asn Ser Leu Asp
 1 5 10 15
 Arg Ala Gln Ala Ala Lys Asn Lys Gly Asn Lys Tyr Phe Lys Ala Gly
 50 20 25 30
 Lys Tyr Glu Gln Ala Ile Gln Cys Tyr Thr Glu Ala Ile Ser Leu Cys
 35 40 45
 Pro Thr Glu Lys Asn Val Asp Leu Ser Thr Phe Tyr Gln Asn Arg Ala
 50 55 60
 Ala Ala Phe Glu Gln Leu Gln Lys Trp Lys Glu Val Ala Gln Asp Cys
 55 65 70 75 80
 Thr Lys Ala Val Glu Leu Asn Pro Lys Tyr Val Lys Ala Leu Phe Arg
 85 90 95
 Arg Ala Lys Ala His Glu Lys Leu Asp Asn Lys Lys Glu Cys Leu Glu
 60 100 105 110
 Asp Val Thr Ala Val Cys Ile Leu Glu Gly Phe Gln Asn Gln Gln Ser
 115 120 125
 Met Leu Leu Ala Arg

130

5 <210> 987
 <211> 103
 <212> PRT
 <213> Homo sapiens

10 <400> 987
 Leu Leu Met Gly Phe Cys Thr Ser Lys Glu Ser Phe His Ile Phe Gly
 1 5 10 15
 Ile Lys Phe Asn Ser Phe Cys Thr Val Leu Cys His Phe Phe Pro Phe
 20 25 30
 Leu Gln Leu Phe Lys Gly Ser Ser Ser Val Leu Ile Lys Cys Arg Lys
 35 40 45
 15 Val Asn Ile Leu Leu Cys Arg Ala Gln Ala Asn Ser Leu Ser Ile Ala
 50 55 60
 Leu Asn Ser Leu Phe Ile Phe Ser Cys Phe Lys Ile Phe Ile Ala Phe
 65 70 75 80
 20 Ile Leu Gly Cys Leu Gly Ser Ile Lys Arg Val His Val Gln Val Ser
 85 90 95
 Thr Gly Thr Phe Arg Val Ser
 100

25 <210> 988
 <211> 64
 <212> PRT
 <213> Homo sapiens

30 <400> 988
 Asn Gly Thr Cys Phe Ser Phe Leu Cys Val Ser Leu Pro Asn Pro Lys
 1 5 10 15
 Met Lys Glu Gly Arg Arg Val Glu Glu Asn Val Ser Val Asn Val Asn
 20 25 30
 Thr Ala Met Gln Ile Lys Thr Phe Leu Lys Ser Glu Val Ile Gln Arg
 35 35 40 45
 Cys Arg Thr Phe Leu Tyr Leu Gly Val Ile Arg Arg Cys Ile Ile Ser
 50 55 60

40 <210> 989
 <211> 77
 <212> PRT
 <213> Homo sapiens

45 <400> 989
 Met Thr Ser Asp Phe Lys Lys Val Phe Ile Cys Met Ala Val Phe Thr
 1 5 10 15
 Leu Thr Leu Thr Phe Ser Ser Thr Leu Leu Pro Ser Phe Ile Leu Gly
 20 25 30
 Leu Gly Arg Glu Thr Gln Arg Lys Leu Lys His Val Pro Phe Tyr Thr
 35 40 45
 50 Val Ile Pro Asn Ser His Gly Leu Leu Pro Val Val Lys Met Phe Glu
 50 55 60
 Thr Ala Leu Lys Ala Ala Ser Val Cys Ile Phe Leu Leu
 65 70 75

55 <210> 990
 <211> 218
 <212> PRT
 <213> Homo sapiens

60 <400> 990
 Pro Gly Ser Gly His Pro Glu Gly Pro Gly Ala His Leu Asp Met Asn
 1 5 10 15

Ser Leu Asp Arg Ala Gln Ala Ala Lys Asn Lys Gly Asn Lys Tyr Phe
 20 25 30
 Lys Ala Gly Lys Tyr Glu Gln Ala Ile Gln Cys Tyr Thr Glu Ala Ile
 35 40 45
 5 Ser Leu Cys Pro Thr Glu Lys Asn Val Asp Leu Ser Thr Phe Tyr Gln
 50 55 60
 Asn Arg Ala Ala Ala Phe Glu Gln Leu Gln Lys Trp Lys Glu Val Ala
 65 70 75 80
 10 Gln Asp Cys Thr Lys Ala Val Glu Leu Asn Pro Lys Tyr Val Lys Ala
 85 90 95
 Leu Phe Arg Arg Ala Lys Ala His Glu Lys Leu Asp Asn Lys Lys Glu
 100 105 110
 Cys Leu Glu Asp Val Thr Ala Val Cys Ile Leu Glu Gly Phe Gln Asn
 115 120 125
 15 Gln Gln Ser Met Leu Leu Ala Asp Lys Val Leu Lys Leu Leu Gly Lys
 130 135 140
 Glu Lys Ala Lys Glu Lys Tyr Lys Asn Arg Glu Pro Leu Met Pro Ser
 145 150 155 160
 20 Pro Gln Phe Ile Lys Ser Tyr Phe Ser Ser Phe Thr Asp Asp Ile Ile
 165 170 175
 Ser Gln Pro Met Leu Lys Gly Glu Lys Ser Asp Glu Asp Lys Asp Lys
 180 185 190
 Glu Gly Xaa Ala Leu Glu Val Lys Arg Lys Phe Trp Ile Leu Lys Xaa
 195 200 205
 25 Pro Thr Val Tyr Xaa Arg Arg Lys Leu Arg
 210 215

<210> 991

<211> 268

30 <212> PRT

<213> Homo sapiens

<400> 991

Glu Asn Ile Met Val Phe Asn Trp Trp Ala Leu Phe Ser Glu Lys Ala
 1 5 10 15
 Val His Leu Gln Glu Glu Leu Ile Ala Ile Asn Ser Lys Lys Glu Glu
 20 25 30
 Leu Asn Gln Ser Val Asn Arg Val Lys Glu Leu Glu Leu Glu Glu
 35 40 45
 40 Ser Val Lys Ala Gln Ser Leu Ala Ile Thr Lys Gln Asn His Met Leu
 50 55 60
 Asn Glu Lys Val Lys Glu Met Ser Asp Tyr Ser Leu Leu Lys Glu Glu
 65 70 75 80
 45 Lys Leu Glu Leu Leu Ala Gln Asn Lys Leu Leu Lys Gln Gln Leu Glu
 85 90 95
 Glu Ser Arg Asn Glu Asn Leu Arg Leu Leu Asn Arg Leu Ala Gln Pro
 100 105 110
 Ala Pro Glu Leu Ala Val Phe Gln Lys Glu Leu Arg Lys Ala Glu Lys
 115 120 125
 50 Ala Ile Val Val Glu His Glu Glu Phe Glu Ser Cys Arg Gln Ala Leu
 130 135 140
 His Lys Gln Leu Gln Asp Glu Ile Glu His Ser Ala Gln Leu Lys Ala
 145 150 155 160
 Gln Ile Leu Gly Tyr Lys Ala Ser Val Lys Ser Leu Thr Thr Gln Val
 165 170 175
 55 Ala Asp Leu Lys Leu Gln Leu Lys Gln Thr Gln Thr Ala Leu Glu Asn
 180 185 190
 Glu Val Tyr Cys Asn Pro Lys Gln Ser Val Ile Asp Arg Ser Val Asn
 195 200 205
 60 Gly Leu Ile Asn Gly Asn Val Val Pro Cys Asn Gly Glu Ile Ser Gly
 210 215 220
 Asp Phe Leu Asn Asn Pro Phe Lys Gln Glu Asn Val Leu Ala Arg Met
 225 230 235 240

Gly Ala Ser Arg Il Thr Asn Tyr Pro Thr Ala Trp Val Glu Gly Ser
 245 250 255
 Ser Pro Asp Ser Asp Leu Glu Phe Val Ala Gln Tyr
 260 265

5

<210> 992
 <211> 219
 <212> PRT
 <213> Homo sapiens

10

<400> 992
 Val Lys Ala Gln Ser Leu Ala Ile Thr Lys Gln Asn His Met Leu Asn
 1 5 10 15
 Glu Lys Val Lys Glu Met Ser Asp Tyr Ser Leu Leu Lys Glu Glu Lys
 15 20 25 30
 Leu Glu Leu Leu Ala Gln Asn Lys Leu Leu Lys Gln Gln Leu Glu Glu
 35 40 45
 Ser Arg Asn Glu Asn Leu Arg Leu Leu Asn Arg Leu Ala Gln Pro Ala
 50 55 60
 20 Pro Glu Leu Ala Val Phe Gln Lys Glu Leu Arg Lys Ala Glu Lys Ala
 65 70 75 80
 Ile Val Val Glu His Glu Glu Phe Glu Ser Cys Arg Gln Ala Leu His
 85 90 95
 Lys Gln Leu Gln Asp Glu Ile Glu His Ser Ala Gln Leu Lys Ala Gln
 25 100 105 110
 Ile Leu Gly Tyr Lys Ala Ser Val Lys Ser Leu Thr Thr Gln Val Ala
 115 120 125
 Asp Leu Lys Leu Gln Leu Lys Gln Thr Gln Thr Ala Leu Glu Asn Glu
 130 135 140
 30 Val Tyr Cys Asn Pro Lys Gln Ser Val Ile Asp Arg Ser Val Asn Gly
 145 150 155 160
 Leu Ile Asn Gly Asn Val Val Pro Cys Asn Gly Glu Ile Ser Gly Asp
 165 170 175
 Phe Leu Asn Asn Pro Phe Lys Gln Glu Asn Val Leu Ala Arg Met Gly
 35 180 185 190
 Ala Ser Arg Ile Thr Asn Tyr Xaa Thr Ala Trp Val Xaa Gly Ser Ser
 195 200 205
 Pro Asp Ser Asp Leu Glu Phe Val Ala Gln Tyr
 210 215

40

<210> 993
 <211> 194
 <212> PRT
 <213> Homo sapiens

45

<400> 993
 Met Arg Ser Leu Asn His Leu Phe Gly Phe Cys Arg Glu His Ala Lys
 1 5 10 15
 Ala Ser Trp Xaa Met Gly Gly Leu Ser Pro Ala Gly Xaa Tyr Val Ser
 50 20 25 30
 Cys Gly Arg Cys Cys Ser Cys Leu Cys Pro Ser His Ile Ser Thr Gln
 35 40 45
 Gly Val Asp Gln Lys Gln Ile Glu Xaa Gln Lys Glu Glu Lys Ile
 50 55 60
 55 Arg Glu Gln Gln Val Lys Glu Arg Arg Gln Arg Glu Glu Arg Arg Gln
 65 70 75 80
 Ser Asn Leu Gln Glu Val Leu Glu Arg Glu Arg Arg Glu Leu Glu Lys
 85 90 95
 Leu Tyr Gln Glu Arg Lys Met Ile Glu Glu Ser Leu Lys Ile Lys Ile
 60 100 105 110
 Lys Lys Glu Leu Glu Met Glu Asn Glu Leu Glu Met Ser Asn Gln Glu
 115 120 125
 Ile Lys Asp Lys Ser Ala His Ser Glu Asn Pro Leu Glu Lys Tyr Met

130 135 140
 Lys Ile Ile Gln Gln Glu Gln Asp Gln Glu Ser Ala Asp Lys Ser Ser
 145 150 155 160
 Lys Lys Met Val Gln Glu Gly Ser Leu Val Asp Thr Leu Gln Ser Ser
 5 165 170 175
 Asp Lys Val Glu Ser Leu Thr Gly Phe Ser His Glu Glu Leu Asp Asp
 180 185 190
 Ser Trp

 10
 <210> 994
 <211> 189
 <212> PRT
 <213> Homo sapiens

 15
 <400> 994
 Glu Asn Ile Met Val Phe Asn Trp Trp Ala Leu Phe Ser Glu Lys Ala
 1 5 10 15
 Val His Leu Gln Glu Glu Leu Ile Ala Ile Asn Ser Lys Lys Glu Glu
 20 20 25 30
 Leu Asn Gln Ser Val Asn Arg Val Lys Glu Leu Glu Leu Glu Glu
 35 40 45
 Ser Val Lys Ala Gln Ser Leu Ala Ile Thr Lys Gln Asn His Met Leu
 50 55 60
 25 Asn Glu Lys Val Lys Glu Met Ser Asp Tyr Ser Leu Leu Lys Glu Glu
 65 70 75 80
 Lys Leu Glu Leu Leu Ala Gln Asn Lys Leu Leu Lys Gln Gln Leu Glu
 85 90 95
 Glu Ser Arg Asn Glu Asn Leu Arg Leu Leu Asn Arg Leu Ala Gln Pro
 30 100 105 110
 Ala Pro Glu Leu Ala Val Phe Gln Lys Glu Leu Arg Lys Ala Glu Lys
 115 120 125
 Ala Ile Val Val Glu His Glu Glu Phe Glu Ser Cys Arg Gln Ala Leu
 130 135 140
 35 His Lys Gln Leu Gln Asp Glu Ile Glu His Ser Ala Gln Leu Lys Ala
 145 150 155 160
 Gln Ile Leu Gly Tyr Lys Ala Ser Val Lys Ser Leu Thr Thr Xaa Val
 165 170 175
 Ala Asp Leu Lys Leu Gln Leu Lys Gln Thr Gln Thr Pro
 40 180 185

 <210> 995
 <211> 125
 <212> PRT
 45 <213> Homo sapiens

 <400> 995
 Lys Thr Glu Gly Arg Glu Lys Glu Arg Arg Gln Ser Asn Xaa Gln Glu
 1 5 10 15
 50 Val Leu Glu Arg Glu Arg Arg Glu Leu Glu Lys Leu Tyr Gln Glu Arg
 20 25 30
 Lys Met Ile Glu Glu Ser Leu Lys Ile Lys Ile Lys Lys Glu Leu Glu
 35 40 45
 Met Glu Asn Glu Leu Glu Met Ser Asn Gln Glu Ile Lys Asp Lys Ser
 50 55 60
 55 Ala His Ser Glu Asn Pro Leu Glu Lys Tyr Met Lys Ile Ile Gln Gln
 65 70 75 80
 Glu Gln Asp Gln Glu Ser Ala Asp Lys Ser Ser Lys Lys Met Val Gln
 85 90 95
 60 Glu Gly Ser Leu Val Asp Thr Leu Gln Ser Ser Asp Lys Val Glu Ser
 100 105 110
 Leu Thr Gly Phe Xaa His Glu Glu Leu Asp Asp Ser Trp
 115 120 125

<210> 996
 <211> 466
 <212> PRT
 5 <213> Homo sapiens

<400> 996
 Thr Ile His Gln Val Ser Leu Asp Leu Asp Ser Leu Ala Glu Ser Pro
 1 5 10 15
 10 Glu Ser Asp Phe Met Ser Ala Val Asn Glu Phe Val Ile Glu Glu Asn
 20 25 30
 Leu Ser Ser Pro Asn Pro Ile Ser Asp Pro Gln Ser Pro Glu Met Met
 35 40 45
 Val Glu Ser Leu Tyr Ser Ser Val Ile Asn Ala Ile Asp Ser Arg Arg
 50 55 60
 15 Met Gln Asp Thr Asn Val Cys Gly Lys Glu Asp Phe Gly Asp His Thr
 65 70 75 80
 Ser Leu Asn Val Gln Leu Glu Arg Cys Arg Val Val Ala Gln Asp Ser
 85 90 95
 20 His Phe Ser Ile Gln Thr Ile Lys Glu Asp Leu Cys His Phe Arg Thr
 100 105 110
 Phe Val Gln Lys Glu Gln Cys Asp Phe Ser Asn Ser Leu Lys Cys Thr
 115 120 125
 Ala Val Glu Ile Arg Asn Ile Ile Glu Lys Val Lys Cys Ser Leu Glu
 130 135 140
 25 Ile Thr Leu Lys Glu Lys His Gln Lys Glu Leu Leu Ser Leu Lys Asn
 145 150 155 160
 Glu Tyr Glu Gly Lys Leu Asp Gly Leu Ile Lys Glu Thr Glu Glu Asn
 165 170 175
 30 Glu Asn Lys Ile Lys Lys Leu Lys Gly Glu Leu Val Cys Leu Glu Glu
 180 185 190
 Val Leu Gln Asn Lys Asp Asn Glu Phe Ala Leu Val Lys His Glu Lys
 195 200 205
 Glu Ala Val Ile Cys Leu Gln Asn Glu Lys Asp Gln Lys Leu Xaa Glu
 210 215 220
 35 Met Glu Asn Ile Met His Ser Gln Asn Cys Glu Ile Lys Glu Leu Lys
 225 230 235 240
 Gln Ser Arg Glu Ile Val Leu Glu Asp Leu Lys Lys Leu His Val Glu
 245 250 255
 40 Asn Asp Glu Lys Leu Gln Leu Leu Arg Ala Glu Leu Gln Ser Leu Glu
 260 265 270
 Gln Ser His Leu Lys Glu Leu Glu Asp Thr Leu Gln Val Arg His Ile
 275 280 285
 Gln Glu Phe Glu Lys Val Met Thr Asp His Arg Val Ser Leu Glu Glu
 290 295 300
 45 Leu Lys Lys Glu Asn Gln Gln Ile Ile Asn Gln Ile Gln Glu Ser His
 305 310 315 320
 Ala Glu Ile Ile Gln Glu Lys Glu Lys Gln Leu Gln Glu Leu Lys Leu
 325 330 335
 50 Lys Val Ser Asp Leu Ser Asp Thr Arg Cys Lys Leu Glu Val Glu Leu
 340 345 350
 Ala Leu Lys Glu Ala Glu Thr Asp Glu Ile Lys Ile Leu Leu Glu Glu
 355 360 365
 Ser Arg Ala Gln Gln Lys Glu Thr Leu Lys Ser Leu Leu Glu Gln Glu
 370 375 380
 55 Thr Glu Asn Leu Arg Thr Glu Ile Ser Lys Leu Asn Gln Lys Ile Gln
 385 390 395 400
 Asp Asn Asn Glu Asn Tyr Gln Val Gly Leu Ala Glu Leu Arg Thr Leu
 405 410 415
 60 Met Thr Ile Glu Lys Asp Gln Cys Ile Ser Glu Leu Ile Ser Arg His
 420 425 430
 Glu Glu Glu Ser Asn Ile Leu Lys Ala Glu Leu Asn Lys Ser Tyr Ile
 435 440 445

Phe Cys Ile Thr Gln Pro Phe Xaa Ile Glu Lys Asn Leu Lys Glu Pro
 450 455 460
 Ile Xaa
 465

5

<210> 997
 <211> 237
 <212> PRT
 <213> Homo sapiens

10

<400> 997
 His Ser Gln Asn Cys Glu Ile Lys Glu Leu Lys Gln Ser Arg Glu Ile
 1 5 10 15
 Val Leu Glu Asp Leu Lys Lys Leu His Val Glu Asn Asp Glu Lys Leu
 20 25 30
 Gln Leu Leu Arg Ala Glu Leu Gln Ser Leu Glu Gln Ser His Leu Lys
 35 40 45
 Glu Leu Glu Asp Thr Leu Gln Val Arg His Ile Gln Glu Phe Glu Lys
 50 55 60
 Val Met Thr Asp His Arg Val Ser Leu Glu Glu Leu Lys Lys Glu Asn
 65 70 75 80
 Gln Gln Ile Ile Asn Gln Ile Gln Glu Ser His Ala Glu Ile Ile Gln
 85 90 95
 Glu Lys Glu Lys Gln Leu Gln Glu Leu Lys Leu Lys Val Ser Asp Leu
 100 105 110
 Ser Asp Thr Arg Cys Lys Leu Glu Val Glu Leu Ala Leu Lys Glu Ala
 115 120 125
 Glu Thr Asp Glu Ile Lys Ile Leu Leu Glu Glu Ser Arg Ala Gln Gln
 130 135 140
 Lys Glu Thr Leu Lys Ser Leu Leu Glu Gln Glu Thr Glu Asn Leu Arg
 145 150 155 160
 Thr Glu Ile Ser Lys Leu Asn Gln Lys Ile Gln Asp Asn Asn Glu Asn
 165 170 175
 Tyr Gln Val Gly Leu Ala Glu Leu Arg Thr Leu Met Thr Ile Glu Lys
 180 185 190
 Asp Gln Cys Ile Ser Glu Leu Ile Ser Xaa His Glu Glu Glu Ser Asn
 195 200 205
 Ile Leu Lys Ala Glu Xaa Asn Lys Ser Tyr Ile Phe Cys Ile Thr Gln
 210 215 220
 Pro Phe Xaa Ile Glu Lys Asn Leu Lys Glu Pro Ile Xaa
 225 230 235

<210> 998
 <211> 278
 <212> PRT
 <213> Homo sapiens

45

<400> 998
 Thr Ile His Gln Val Ser Leu Asp Leu Asp Ser Leu Ala Glu Ser Pro
 1 5 10 15
 Glu Ser Asp Phe Met Ser Ala Val Asn Glu Phe Val Ile Glu Glu Asn
 20 25 30
 Leu Ser Ser Pro Asn Pro Ile Ser Asp Pro Gln Ser Pro Glu Met Met
 35 40 45
 Val Glu Ser Leu Tyr Ser Ser Val Ile Asn Ala Ile Asp Ser Arg Arg
 50 55 60
 Met Gln Asp Thr Asn Val Cys Gly Lys Glu Asp Phe Gly Asp His Thr
 65 70 75 80
 Ser Leu Asn Val Gln Leu Glu Arg Cys Arg Val Val Ala Gln Asp Ser
 85 90 95
 His Phe Ser Ile Gln Thr Ile Lys Glu Asp Leu Cys His Phe Arg Thr
 100 105 110
 Phe Val Gln Lys Glu Gln Cys Asp Phe Ser Asn Ser Leu Lys Cys Thr

115 120 125
 Ala Val Glu Ile Arg Asn Ile Ile Glu Lys Val Lys Cys Ser Leu Glu
 130 135 140
 Ile Thr Leu Lys Glu Lys His Gln Lys Glu Leu Leu Ser Leu Lys Asn
 5 145 150 155 160
 Glu Tyr Glu Gly Lys Leu Asp Gly Leu Ile Lys Glu Thr Glu Glu Asn
 165 170 175
 Glu Asn Lys Ile Lys Lys Leu Lys Gly Glu Leu Val Cys Leu Glu Glu
 180 185 190
 10 Val Leu Gln Asn Lys Asp Asn Glu Phe Ala Leu Val Lys His Glu Lys
 195 200 205
 Glu Ala Val Ile Cys Leu Gln Asn Glu Lys Asp Gln Lys Leu Xaa Glu
 210 215 220
 Met Glu Asn Ile Met Pro Ser Gln Asn Trp Glu Ile Xaa Glu Leu Lys
 15 225 230 235 240
 Gln Ser Arg Glu Ile Gly Leu Glu Asp Leu Lys Lys Leu Met Trp Lys
 245 250 255
 Met Met Arg Ser Xaa Gly Phe Gly Gly Xaa Thr Xaa Val Leu Gly Pro
 260 265 270
 20 Lys Ser Xaa Xaa Gly Ile
 275

 <210> 999
 <211> 168
 25 <212> PRT
 <213> Homo sapiens

 <400> 999
 Xaa Xaa Xaa His Glu Glu Glu Xaa Asn Xaa Leu Lys Gly Glu Leu Asn
 1 5 10 15
 Lys Xaa Thr Ser Leu His Asn Gln Ala Phe Glu Ile Glu Lys Xaa Leu
 20 25 30
 Lys Xaa Gln Ile Ile Xaa Leu Xaa Ser Lys Xaa Asp Ser Xaa Leu Xaa
 35 35 40 45
 Ala Xaa Glu Ser Gln Lys Asp Glu Lys Ile Xaa Pro Gln Glu Glu Lys
 50 55 60
 Xaa Glu Xaa Xaa Xaa Gln Thr Leu Glu Lys Xaa Ser Gln Lys Leu Val
 65 70 75 80
 Xaa Ser Gln Glu Gln Xaa Xaa Xaa Gln Leu Ile Gln Lys Xaa Asn Cys
 40 85 90 95
 Glu Lys Xaa Glu Ala Ile Gln Xaa Ala Leu Lys Xaa Phe Lys Leu Xaa
 100 105 110
 Xaa Xaa Val Val Xaa Lys Xaa Xaa Leu Glu Lys Val Xaa Xaa Xaa Glu
 115 120 125
 45 Asn Gln Xaa Ala Lys Ser Pro Ala Xaa Asp Xaa Xaa Gly Asp Phe
 130 135 140
 Ser Ser Leu Xaa Xaa Glu Leu Gln Xaa Lys Leu Gln Glu Xaa Lys Xaa
 145 150 155 160
 Lys Phe Leu Xaa Xaa Leu Glu Glu
 50 165

 <210> 1000
 <211> 194
 55 <212> PRT
 <213> Homo sapiens

 <400> 1000
 Glu Gly Lys Leu Gln Lys Ala Leu Glu Asp Ala Phe Leu Ala Ile Asp
 1 5 10 15
 60 Ala Lys Leu Thr Thr Glu Glu Val Ile Lys Glu Leu Ala Gln Ile Ala
 20 25 30
 Gly Arg Pro Thr Glu Asp Glu Asp Glu Lys Glu Lys Val Ala Asp Glu
 35 40 45

Asp Asp Val Asp Asn Glu Glu Ala Ala Leu Leu His Glu Glu Ala Thr
 50 55 60
 Met Thr Ile Glu Glu Leu Leu Thr Arg Tyr Gly Gln Asn Cys His Lys
 65 70 75 80
 5 Gly Pro Pro His Ser Lys Ser Gly Gly Gly Thr Gly Glu Glu Pro Gly
 85 90 95
 Ser Gln Gly Leu Asn Gly Glu Ala Gly Pro Glu Asp Ser Thr Arg Glu
 100 105 110
 Thr Pro Ser Gln Glu Asn Gly Pro Thr Ala Lys Ala Tyr Thr Gly Phe
 115 120 125
 10 Ser Ser Asn Ser Glu Arg Gly Thr Glu Ala Gly Gln Val Gly Glu Pro
 130 135 140
 Gly Ile Pro Thr Gly Glu Ala Gly Pro Ser Cys Ser Ser Ala Ser Asp
 145 150 155 160
 15 Lys Leu Leu Glu Leu Leu Ser Pro Ser Ser Leu Arg Thr Val Arg Met
 165 170 175
 Ser Gln Met Lys Arg Arg Lys Lys Lys Lys Thr Val Arg Asn Ala Ala
 180 185 190
 Arg Lys

20

<210> 1001

<211> 73

<212> PRT

25

<213> Homo sapiens

<400> 1001

Arg Val Ser Ser Ser Ser Ile Val Met Val Ala Ser Ser Cys Ser Ser
 1 5 10 15
 30 Ala Ala Ser Ser Leu Ser Thr Ser Ser Ser Ala Thr Phe Ser Phe
 20 25 30
 Ser Ser Ser Ser Ser Val Gly Arg Pro Ala Ile Cys Ala Ser Ser Leu
 35 35 40 45
 Met Thr Ser Ser Val Val Asn Leu Ala Ser Ile Ala Lys Lys Ala Ser
 50 55 60
 35 Ser Lys Ala Phe Cys Ser Leu Pro Ser
 65 70

40

<210> 1002

<211> 121

<212> PRT

<213> Homo sapiens

<400> 1002

His Lys Xaa Val Xaa Phe Thr Glu Ala Xaa Asn Ser Trp Ser Leu Pro
 1 5 10 15
 Gly Gly Xaa Trp Asn Val Met Thr Thr Gln Lys Val Val Asp Phe Ile
 20 25 30
 Gln Ser Lys Ile Ser Gln Ala Xaa Glu Asn Gly Lys Phe Gly Ile Val
 35 40 45
 50 Ile His Cys Glu Xaa Leu Leu Asp Gln Cys Xaa Ala Pro Asp Thr Phe
 50 55 60
 Gly Asp Gly Thr Gly Cys Asp Asn Met Thr Cys Ile Ile Ile Xaa Phe
 65 70 75 80
 55 Lys Pro Arg Asn Thr Ala Glu Leu Gln Pro Glu Ser Gly Lys Arg Lys
 85 90 95
 Leu Glu Glu Val Leu Ser Thr Glu Gly Ala Glu Glu Asn Gly Asn Ser
 100 105 110
 Asp Lys Lys Lys Lys Ala Lys Arg Asp
 115 120

60

<210> 1003

<211> 122

<212> PRT

<213> Homo sapiens

<400> 1003

5 Arg Arg Cys Ser Leu Leu Arg Gly Leu Lys Lys Met Ala Thr Ala Thr
 1 5 10 15
 Arg Arg Arg Arg Pro Ser Glu Thr Ser Ser His Pro Asp Pro Cys Pro
 20 25 30
 Pro Arg Leu Phe Xaa Glu Pro Ser Gly Pro Glu Thr Glu Phe Cys Leu
 35 40 45
 10 Phe Pro Leu Ala Leu Ala Val Gly Xaa Arg Cys Ala Gly Gly Ala Gly
 50 55 60
 Trp Leu His Ser Ala His Ser Lys Glu Gly Ser Pro Ser Thr Leu Gln
 65 70 75 80
 15 Pro Gly Ala Xaa Ala Val Leu Pro Ser Arg Xaa Cys Ser Ser Gly Ser
 85 90 95
 Ser Pro Val Leu Cys Leu Cys Ser Val Val Leu Glu Gly Arg Thr Gly
 100 105 110
 Gly Ser Gly Phe Tyr Ser Val Asn Phe Ile
 115 120
 20

<210> 1004

<211> 176

<212> PRT

25 <213> Homo sapiens

<400> 1004

Ala Ala Gln Leu Arg Met Val Asp Asp Gly Ser Gly Lys Val Glu Val
 1 5 10 15
 30 Trp Cys Ile Gln Asp Leu His Arg Gln Pro Val Asp Pro Lys Arg His
 20 25 30
 Gly Gln Leu Cys Ala Gly Asn Cys Tyr Leu Val Leu Tyr Thr Tyr Gln
 35 35 40 45
 Arg Leu Gly Arg Val Gln Tyr Ile Leu Tyr Leu Trp Gln Gly His Gln
 50 55 60
 35 Ala Thr Ala Asp Xaa Ile Glu Ala Leu Asn Ser Asn Ala Glu Glu Leu
 65 70 75 80
 Asp Val Met Tyr Gly Gly Val Leu Val Gln Glu His Val Thr Met Gly
 85 90 95
 40 Ser Glu Pro Pro His Phe Leu Ala Ile Phe Gln Gly Gln Leu Val Ile
 100 105 110
 Phe Gln Glu Arg Ala Gly His His Gly Lys Gly Gln Ser Ala Ser Thr
 115 120 125
 Thr Arg Leu Phe Gln Val Gln Gly Thr Asp Ser His Asn Thr Arg Thr
 130 135 140
 45 Met Glu Val Pro Ala Arg Ala Ser Ser Leu Asn Ser Ser Asp Ile Phe
 145 150 155 160
 Leu Leu Val Thr Ser Gln Arg Leu Leu Pro Leu Val Trp Glu Gly Leu
 165 170 175
 50

<210> 1005

<211> 143

<212> PRT

55 <213> Homo sapiens

<400> 1005

Pro Pro Pro Val Pro Ser His Val Asp His His Tyr Ser Pro Ser Gln
 1 5 10 15
 Thr Arg Gly Ser Arg Arg Trp Leu Val Thr Ser Lys Lys Met Ser Leu
 20 25 30
 60 Glu Leu Arg Asp Glu Ala Arg Ala Gly Thr Ser Met Val Leu Val Leu
 35 40 45
 Trp Leu Ser Val Pro Cys Thr Trp Lys Ser Leu Val Val Asp Ala Asp

50 55 60
 Cys Pro Phe Pro Trp Cys Pro Ala Leu Ser Trp Lys Ile Thr Ser Trp
 65 70 75 80
 Pro Trp Lys Met Ala Arg Lys Trp Gly Gly Ser Leu Pro Met Val Thr
 85 90 95
 Cys Ser Cys Thr Arg Thr Pro Pro Tyr Met Thr Ser Ser Ser Ala
 100 105 110
 Leu Leu Phe Arg Ala Ser Xaa Ser Ala Val Ala Trp Trp Pro Cys
 115 120 125
 10 His Arg Tyr Arg Met Tyr Trp Thr Arg Pro Ser Leu Trp Tyr Val
 130 135 140

<210> 1006

<211> 145

<212> PRT

<213> Homo sapiens

<400> 1006

20 Pro Xaa Val Pro Gln Glu Ser Gly Glu Trp Gln Pro Gly Lys Gln His
 1 5 10 15
 Gln Pro Xaa Phe Glu Ile Thr Ala Glu Val Asn Asn Leu Gly Leu Ser
 20 25 30
 Xaa Trp Pro Gly Asn Gly Arg Ala Gly Ala Val Ala Leu Gln Ala Leu
 35 40 45
 25 Lys Gly Ser Gln Asp Ser Ser Xaa Asn Asp Leu Val Arg Ser Pro Lys
 50 55 60
 Ser Ala Gly Ser Arg Thr Ser Xaa Ser Val Ser Ser Thr Xaa Ala Thr
 65 70 75 80
 Ile Asn Gly Gly Leu Arg Arg Glu Gln Xaa Met His Gln Ala Val Glu
 85 90 95
 Asp Leu Pro Xaa Xaa Val Asp Pro Ala Arg Arg Glu Phe Tyr Xaa Ser
 100 105 110
 Asp Xaa Asp Phe Gln Asp Xaa Phe Gly Lys Ser Lys Glu Glu Phe Tyr
 115 120 125
 35 Ser Met Ala Thr Trp Arg Gln Arg Gln Glu Lys Lys Gln Leu Gly Phe
 130 135 140
 Phe
 145

<210> 1007

<211> 98

<212> PRT

<213> Homo sapiens

<400> 1007

45 Cys Thr Arg Leu Leu Arg Thr Cys Xaa Arg Xaa Trp Thr Leu Pro Ala
 1 5 10 15
 Gly Ser Ser Xaa Xaa Gln Thr Xaa Thr Ser Lys Ile Xaa Leu Gly Asn
 20 25 30
 50 Pro Arg Arg Asn Phe Thr Ala Trp Pro Arg Gly Gly Ser Gly Arg Arg
 35 40 45
 Lys Ser Ser Trp Ala Phe Phe Glu Pro Lys Pro Xaa Arg Leu Pro Leu
 50 55 60
 Ser Pro Gly Pro Gln His Thr Tyr Asn Ala Gly Glu Ala Leu Leu Pro
 65 70 75 80
 Leu Pro Ser Xaa Ala Phe Gly His Pro Leu Xaa Val Ser Lys Ser Arg
 85 90 95
 Gln Pro

<210> 1008

<211> 65

<212> PRT

<213> Homo sapiens

<400> 1008

5 Ser Thr Cys Arg Gly Pro Lys Val Xaa Asn His Pro Met Lys Gly Gly
 1 5 10 15
 Glu Ala Leu Trp Pro Cys Leu Xaa Xaa Thr Asn Xaa Cys Xaa Pro Gly
 20 25 30
 Phe Leu Pro Leu Xaa Gly Xaa Lys Ser Phe Lys Xaa Thr Ser Leu Xaa
 35 40 45
 10 Pro Lys Ala Asn Pro Pro Xaa Phe Pro Xaa Xaa Phe Cys Xaa Phe Ser
 50 55 60
 Pro
 65

15 <210> 1009
 <211> 193
 <212> PRT
 <213> Homo sapiens

<400> 1009

20 Tyr Leu Val Ala Leu Asp Lys Leu Asn Pro Tyr Thr Leu Tyr Thr Phe
 1 5 10 15
 Arg Ile Arg Cys Ser Thr Glu Thr Phe Trp Lys Trp Ser Lys Trp Ser
 20 25 30
 25 Asn Lys Lys Gln His Leu Thr Thr Glu Ala Ser Pro Ser Lys Gly Pro
 35 40 45
 Asp Thr Trp Arg Glu Trp Ser Ser Asp Gly Lys Asn Leu Ile Ile Tyr
 50 55 60
 Trp Lys Pro Leu Pro Ile Asn Glu Ala Asn Gly Lys Ile Leu Ser Tyr
 65 70 75 80
 30 Asn Val Ser Cys Ser Ser Asp Glu Glu Thr Gln Ser Leu Ser Glu Ile
 85 90 95
 Pro Asp Pro Gln His Lys Ala Glu Ile Arg Leu Asp Lys Asn Asp Tyr
 100 105 110
 35 Ile Ile Ser Val Val Ala Lys Asn Ser Val Gly Ser Ser Pro Pro Ser
 115 120 125
 Lys Ile Ala Ser Met Glu Ile Pro Asn Asp Asp Leu Lys Ile Glu Gln
 130 135 140
 Val Val Gly Met Gly Lys Gly Ile Leu Leu Thr Trp His Tyr Asp Pro
 145 150 155 160
 40 Asn Met Thr Cys Asp Tyr Val Ile Lys Trp Cys Asn Ser Ser Arg Ser
 165 170 175
 Glu Pro Cys Leu Met Asp Trp Arg Lys Val Pro Gln Thr Ala Leu Lys
 180 185 190
 45 Leu

50 <210> 1010
 <211> 135
 <212> PRT
 <213> Homo sapiens

<400> 1010

55 Xaa Phe Pro Arg Asn Val Phe Pro Phe Xaa Leu Xaa Ile Glu Ser Ala
 1 5 10 15
 Xaa Val Ser Phe Thr Ser Lys Phe Gly His Gln Trp Glu Pro Ile Xaa
 20 25 30
 Leu Tyr Ile Gln Ser Trp Ser Val Ile Ile Asp Ile Leu Asp Phe Cys
 35 40 45
 60 Ile His Thr Gly Lys Asn Tyr Ile Leu Tyr Leu Val Glu Thr His Gln
 50 55 60
 Ile Leu Leu Gln Phe Gln Cys Cys Leu Arg Asn Phe Ser Pro Val His
 65 70 75 80

Lys Ala Trp Phe Arg Pro Arg Arg Val Thr Pro Leu Asn Asp Val Val
 85 90 95
 Ala Ser His Val Gly Val Val Met Pro Gly Glu Glu Asn Pro Leu Ser
 100 105 110
 5 His Pro Asn Asn Leu Phe Tyr Phe Glu Ile Ile Ile Trp Asn Phe His
 115 120 125
 Thr Arg Tyr Phe Gly Arg Trp
 130 135

 10 <210> 1011
 <211> 80
 <212> PRT
 <213> Homo sapiens

 15 <400> 1011
 Xaa Asn His Xaa Thr Arg Gly Lys Arg Pro Lys Val Xaa Trp Ile Trp
 1 5 10 15
 Ser Pro Arg Gly Xaa Xaa Xaa Val Gly Cys Xaa Pro Ser Gln Gly Ile
 20 25 30
 20 Leu Pro Leu Trp Xaa Met Ser Xaa His Ser Glu Ser Phe Pro Gln Pro
 35 40 45
 Pro Xaa Leu Val Pro Ser Ser His Phe Lys Tyr Lys Thr Lys Xaa Arg
 50 55 60
 Met Leu Leu Thr Gly Pro Val Pro Lys Gly Cys Phe Leu Glu Leu Ser
 25 65 70 75 80

 <210> 1012
 <211> 77
 <212> PRT
 30 <213> Homo sapiens

 <400> 1012
 Xaa Leu Thr Ile Xaa Pro Gly Val Ser Gly Gln Lys Xaa Asp Gly Phe
 1 5 10 15
 35 Gly Pro Pro Glu Glu Xaa Xaa Pro Trp Val Xaa Pro Gln Ala Arg Val
 20 25 30
 Phe Cys Pro Phe Xaa Xaa Cys Xaa Pro Thr Gln Ser Leu Phe Leu Ser
 35 40 45
 Pro His Xaa Leu Ser Arg Pro His Ile Leu Asn Ile Lys Leu Xaa Arg
 50 55 60
 40 Glu Cys Phe Leu Gln Asp Gln Tyr Pro Arg Ala Val Ser
 65 70 75

 <210> 1013
 <211> 117
 <212> PRT
 45 <213> Homo sapiens

 <400> 1013
 50 Leu Ile His Tyr Leu Gln Ile His Tyr Arg Ile Ser Asp Asp Lys Lys
 1 5 10 15
 Gln Thr Thr Asn Gln Lys Lys Gln Thr Lys Lys Thr Tyr Leu Ile Arg
 20 25 30
 Thr Leu Lys Ile Phe Lys Tyr Phe Cys Leu Lys Tyr Glu Lys Val Lys
 35 40 45
 55 Tyr Ile Gly Asn Leu Arg Ala Gly Lys Ile Gln Asp His Phe Leu Val
 50 55 60
 Phe Pro Ser Ala Phe Pro Arg Thr Thr Ile Thr Pro Asp Ile Ala Tyr
 65 70 75 80
 60 Glu Lys Gln Gly Trp Ala Glu Asp Ala Val Leu Lys Ala Ile Asn Ser
 85 90 95
 Ala Gln Leu Thr Lys Gln Leu Leu Pro Cys Asn Thr Gly Cys Pro Trp
 100 105 110

Ile Gln Ile Ser Leu
115

5 <210> 1014
<211> 212
<212> PRT
<213> Homo sapiens

<400> 1014
10 Ile Ser Asp Asn Ser Lys Ile Asn Phe Arg Leu Lys Pro Leu Asp Val
1 5 10 15
Ala Phe Met Lys Ala Ile His Asn Lys Val Asn Ile Val Pro Val Ile
20 25 30
Ala Lys Ala Asp Thr Leu Thr Leu Lys Glu Arg Glu Arg Leu Lys Lys
15 35 40 45
Arg Ile Leu Asp Glu Ile Glu Glu His Asn Ile Lys Ile Tyr His Leu
50 55 60
Pro Asp Ala Glu Ser Asp Glu Asp Glu Asp Phe Lys Glu Gln Thr Arg
65 70 75 80
20 Leu Leu Lys Ala Ser Ile Pro Phe Ser Val Val Gly Ser Asn Gln Leu
85 90 95
Ile Glu Ala Lys Gly Lys Lys Val Arg Gly Arg Leu Tyr Pro Trp Gly
100 105 110
Val Val Glu Val Glu Asn Pro Glu His Asn Asp Phe Leu Lys Leu Arg
115 120 125
25 Thr Met Leu Ile Thr His Met Gln Asp Leu Gln Glu Val Thr Gln Asp
130 135 140
Leu His Tyr Glu Asn Phe Arg Ser Glu Arg Leu Lys Arg Gly Gly Arg
145 150 155 160
30 Lys Val Glu Asn Glu Asp Met Asn Lys Asp Gln Ile Leu Leu Glu Lys
165 170 175
Glu Ala Glu Leu Arg Arg Met Gln Xaa Met Ile Ala Arg Met Gln Ala
180 185 190
Pro Asn Ala Asp Ala Xaa Cys Xaa Ala Gly Asp Gly Xaa Gly Gly Ala
195 200 205
35 Phe Arg Ala Thr
210

40 <210> 1015
<211> 143
<212> PRT
<213> Homo sapiens

<400> 1015
45 Gly Gly Pro Lys Ser Pro Ala Xaa Ala Ile Pro Gly Xaa Ala Xaa Gly
1 5 10 15
Ile Cys Ile Trp Gly Leu His Pro Cys Asn His Xaa Leu His Ala Ala
20 25 30
Glu Leu Ser Phe Phe Phe Gln Gln Asp Leu Val Phe Ile His Val Leu
35 40 45
50 Ile Leu His Phe Pro Ala Ala Ser Leu Glu Ser Leu Arg Thr Glu Val
50 55 60
Phe Ile Met Lys Val Leu Gly His Leu Leu Glu Ile Leu His Val Gly
65 70 75 80
55 Asp Glu His Gly Ser Gln Leu Gln Lys Val Ile Val Leu Trp Val Leu
85 90 95
His Phe His Asn Thr Pro Gly Val Glu Ala Ala Ser Asp Leu Leu Ser
100 105 110
Phe Gly Phe Asn Gln Leu Ile Gly Ser Asn His Arg Glu Trp Asp Ala
115 120 125
60 Ser Leu Glu Lys Ser Ser Leu Leu Phe Lys Ile Phe Ile Phe Ile
130 135 140

<210> 1016
 <211> 120
 <212> PRT
 <213> Homo sapiens

5

<400> 1016
 His Thr Phe Ile Asn Tyr Tyr Tyr Leu Thr Ala Ser Phe Tyr Gly Phe
 1 5 10 15
 Ser Ser Pro His Lys Asn Glu Lys Thr Leu Ser His Pro Gln Ile Lys
 10 20 25 30
 His Phe Leu His Leu Pro Thr Gln Pro Leu Ala Pro Phe Ile Trp Gln
 35 40 45
 Phe Leu Gly Gly Glu Phe Pro Thr Ser Val Xaa Met Asp Xaa Lys Arg
 50 55 60
 His Pro Leu Glu Xaa Ser Leu Arg Gly Pro Gln Xaa Lys Xaa Gly Thr
 15 65 70 75 80
 Leu Arg Xaa Pro Gly Xaa Xaa Lys Thr Lys Pro Gly Xaa Gly Xaa Asn
 85 90 95
 Gly Ala Asp Leu Ala Pro Tyr Pro Leu Leu Gln Asn Leu Lys Xaa Val
 100 105 110
 Phe Pro Phe Asp Leu Ala Xaa Arg
 115 120

<210> 1017
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 1017
 Val Phe Ser Lys Tyr Ile Ser Ile Gly Arg Asp Tyr Val Leu Val Lys
 1 5 10 15
 Glu Gln Leu Ser Ile Ile Lys Ser Ile Tyr Leu Asp Leu Gly Ser Lys
 20 25 30
 Thr Lys Gly Asp Gln Lys Cys Ser Ser Val Gly Pro Pro Ser Leu His
 35 35 40 45
 Ser Cys Tyr Gln Glu Ala Ala Cys Leu Lys Tyr Phe His Ser His Met
 50 55 60
 Arg Gly Leu Val Thr Ser Lys Leu Val Phe Leu Phe Tyr Arg Phe Ser
 65 70 75 80
 Ser Lys Val Ile Lys Cys Gln Thr Gln Ile Met Asp Ser Ala Trp Met
 85 90 95
 Tyr Ser Glu Val Met Glu His His Phe Leu Val Thr Phe Thr Gln
 100 105 110

<210> 1018
 <211> 219
 <212> PRT
 <213> Homo sapiens

<400> 1018
 Arg Glu Arg Val Thr Gln Ser Ala Leu Val Pro Val Leu Ala Met Ala
 1 5 10 15
 Ser Phe Val Thr Glu Val Leu Ala His Ser Gly Arg Leu Glu Lys Glu
 20 25 30
 Asp Leu Gly Thr Arg Ile Ser Arg Leu Thr Arg Arg Val Glu Glu Ile
 35 40 45
 Lys Gly Glu Val Cys Asn Met Ile Ser Lys Lys Tyr Ser Glu Phe Leu
 50 55 60
 Pro Ser Met Gln Ser Ala Gln Gly Leu Ile Thr Gln Val Asp Lys Leu
 65 70 75 80
 Ser Glu Asp Ile Asp Leu Leu Lys Ser Arg Ile Glu Ser Glu Val Arg
 85 90 95
 Arg Asp Leu His Val Ser Thr Gly Glu Phe Thr Asp Leu Lys Gln Gln

100 105 110
 Leu Glu Arg Asp Ser Val Val Leu Ser Leu Leu Lys Gln Leu Gln Glu
 115 120 125
 Phe Ser Thr Ala Ile Glu Glu Tyr Asn Cys Ala Leu Thr Glu Lys Lys
 130 135 140
 5 Tyr Val Thr Gly Ala Gln Arg Leu Glu Glu Ala Gln Lys Cys Leu Lys
 145 150 155 160
 Leu Leu Lys Ser Arg Lys Cys Phe Asp Leu Lys Ile Leu Lys Ser Leu
 165 170 175
 10 Ser Met Glu Leu Thr Ile Gln Glu Thr Glu His Thr Leu Ser Pro Trp
 180 185 190
 Arg Arg Val Ala Glu Ala Asp Cys Met Glu Val Pro Thr Ile Lys Arg
 195 200 205
 Tyr Gln Pro Val Trp Glu Ser Leu Pro Tyr Lys
 15 210 215

<210> 1019

<211> 99

<212> PRT

20 <213> Homo sapiens

<400> 1019

Arg Ser Arg Arg Thr Ser Leu Ser Ile Leu Asp Phe Ser Arg Ser Met
 1 5 10 15
 25 Ser Ser Asp Ser Leu Ser Thr Trp Val Ile Arg Pro Cys Ala Leu Cys
 20 25 30
 Met Leu Gly Arg Asn Ser Leu Tyr Phe Leu Leu Ile Ile Leu His Thr
 35 40 45
 Ser Pro Leu Ile Ser Ser Thr Arg Arg Val Arg Arg Leu Ile Arg Val
 50 55 60
 30 Pro Arg Ser Ser Phe Ser Ser Leu Pro Glu Cys Ala Lys Thr Ser Val
 65 70 75 80
 Thr Asn Glu Ala Met Ala Lys Thr Gly Thr Asn Ala Asp Trp Val Thr
 85 90 95
 35 Leu Ser Leu

<210> 1020

<211> 131

40 <212> PRT

<213> Homo sapiens

<400> 1020

Ser Gln Thr Ser Lys Met Tyr Trp Phe Thr Lys Thr Asn Gly Arg Phe
 1 5 10 15
 45 Lys Glu Val Phe Lys Gly Xaa Ile Met Pro Arg Glu Glu Ser Thr Tyr
 20 25 30
 Ser Arg His Ser Phe Leu Lys Lys Met Glu Leu Phe Asn Phe Ser Lys
 35 40 45
 50 Gly Ser Cys Ser Ser Phe Leu Cys Leu Lys Gln Gly Arg Ile Lys Ala
 50 55 60
 Leu Leu His Trp Lys Xaa Thr His Cys Gln Gly Xaa Phe Xaa Ile Trp
 65 70 75 80
 Pro Thr Asp Pro Asn Xaa Leu Pro Ser Trp Leu Trp Glu Pro Ser Ser
 85 90 95
 55 Ser Asn Ser Leu Glu Trp Leu Pro Phe Leu Ala His Xaa Thr Gly Asn
 100 105 110
 Leu Phe Leu Lys Phe Xaa Gly Ala Trp Leu Ser Ser Lys Xaa Lys Gly
 115 120 125
 60 Gln Xaa Pro
 130

<210> 1021

<211> 222
 <212> PRT
 <213> Homo sapiens

5 <400> 1021
 Pro Leu Glu Pro Ala Val Gly Pro Lys Ala Ala Cys Pro Leu Asp Ser
 1 5 10 15
 Glu Ser Ala Glu Gly Val Val Pro Pro Ala Ser Gly Gly Gly Arg Val
 20 25 30
 10 Gln Asn Ser Pro Pro Val Gly Arg Lys Thr Leu Pro Leu Thr Thr Ala
 35 40 45
 Pro Glu Ala Gly Glu Val Thr Pro Ser Asp Ser Gly Gly Gln Glu Asp
 50 55 60
 15 Ser Pro Ala Lys Gly Leu Ser Val Arg Leu Glu Phe Asp Tyr Ser Glu
 65 70 75 80
 Asp Lys Ser Ser Trp Asp Asn Gln Gln Glu Asn Pro Pro Pro Thr Lys
 85 90 95
 Lys Ile Gly Lys Lys Pro Val Ala Lys Met Pro Leu Arg Arg Pro Lys
 100 105 110
 20 Met Lys Lys Thr Pro Glu Lys Leu Asp Asn Thr Pro Ala Ser Pro Pro
 115 120 125
 Arg Ser Pro Ala Glu Pro Asn Asp Ile Pro Ile Ala Lys Gly Thr Tyr
 130 135 140
 25 Thr Phe Asp Ile Asp Lys Trp Asp Asp Pro Asn Phe Asn Pro Phe Ser
 145 150 155 160
 Ser Thr Ser Lys Met Gln Glu Ser Pro Lys Leu Pro Gln Gln Ser Tyr
 165 170 175
 Asn Phe Asp Pro Asp Thr Cys Asp Glu Ser Val Asp Pro Phe Lys Thr
 180 185 190
 30 Ser Ser Lys Pro Pro Ala His Leu Leu Asn Pro Gln Pro Ser Phe Glu
 195 200 205
 Ile Pro Ala Ser Ala Ile Gly Ser Gln Trp Ser Gly Pro Gly
 210 215 220

35 <210> 1022
 <211> 249
 <212> PRT
 <213> Homo sapiens

40 <400> 1022
 Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn Ile Xaa Xaa Ile
 1 5 10 15
 Cys Xaa Gly Xaa Gln Trp Xaa Xaa Arg Xaa Asn Xaa Xaa Xaa Xaa Xaa
 20 25 30
 45 His Xaa Xaa Leu Xaa Xaa Xaa Ile Xaa Xaa Xaa Gly Xaa Xaa Met Xaa
 35 40 45
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Met Xaa Xaa Cys Xaa Leu Xaa Xaa
 50 55 60
 Trp Gln Xaa Val Trp Xaa Arg Gln Ala Glu Ser Ala Cys Leu Leu Ile
 65 70 75 80
 50 His Xaa Cys Met Asn Xaa Pro Ala Leu Xaa Xaa Tyr Ser Xaa Arg Xaa
 85 90 95
 Cys Ser Phe Arg Asn Ala Gly Leu Val Gly Gly Leu Xaa Xaa Xaa Xaa
 100 105 110
 55 Xaa Ala Ser Asn Leu Xaa Asn Val Xaa Xaa Ala Pro Xaa Gln Xaa Xaa
 115 120 125
 Xaa Arg Val His Leu Xaa Gly Xaa Val Xaa Xaa Leu Leu Leu Leu Arg
 130 135 140
 60 Leu Gly Xaa Thr Xaa Xaa Cys Glu His Thr Phe Thr His Xaa Xaa Ile
 145 150 155 160
 Leu Ala Glu Xaa Leu Xaa Arg Thr Gly Pro Ile Xaa Xaa Ile Ser Ser
 165 170 175
 Ile Xaa Gly Xaa Pro Arg Xaa Leu Phe His Arg Xaa Leu Xaa Xaa Xaa

180 185 190
 Xaa Arg Leu Ala Xaa Phe Leu Xaa Lys Pro Ser Leu Val Xaa Xaa Pro
 195 200 205
 Leu Xaa Gly Xaa Xaa Xaa Leu Xaa Phe Leu Gly Asp Xaa Pro Leu Tyr
 5 210 215 220
 Xaa Xaa Xaa Xaa Gln Trp Xaa Leu Phe Xaa Xaa Phe Xaa Pro Ile Phe
 225 230 235 240
 Xaa Pro Xaa Ile Phe Xaa His Leu Tyr
 245
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 <212> PRT
 <213> Homo sapiens
 15
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 His Ile Met Lys Asn Ile Thr Ala Lys Arg Ser Arg Ala Arg Ile Val
 20 20 25 30
 Asp Lys Leu Leu Ala Leu Gly Leu Val Ala Glu Arg Arg Glu Leu Tyr
 35 40 45
 Lys Lys Arg Gln Lys Lys Leu Ala Ser Ser Ile Leu Pro Asn Gly Ala
 50 55 60
 25 Glu Ser Leu Lys Asp Phe Cys Gln Glu Asp Leu Glu Glu Glu Glu Asn
 65 70 75 80
 Leu Pro Glu Glu Asp Ser Glu Glu Glu Glu Glu Gly Gly Ser Glu Ala
 85 90 95
 Glu Gln Val Gln Gly Ser Leu Val Leu Ser Asn Glu Asn Leu Gly Gln
 30 100 105 110
 Ser Leu His Gln Glu Gly Phe Ser Ile Pro Leu Leu Trp Leu Gln Asn
 115 120 125
 Cys Leu Ile Arg Ala Ala Asp Asp Arg Glu Glu Asp Gly Cys Ser Gln
 130 135 140
 35 Ala Val Pro Leu Val Pro Leu Thr Glu Glu Asn Glu Glu Ala Met Glu
 145 150 155 160
 Asn Glu Gln Phe Gln Gln Leu Leu Arg Lys Leu Gly Val Arg Pro Pro
 165 170 175
 Ala Ser Gly Gln Glu Thr Phe Trp Arg Ile Pro Ala Lys Leu Ser Pro
 40 180 185 190
 Thr Gln Leu Arg Arg Ala Ala Ala Ser Phe Glu Ser Thr Arg Gly Gly
 195 200 205
 Thr Glu Thr Cys Ser Gln Asn Cys Ser Leu Lys Xaa Leu Glu Ser Lys
 210 215 220
 45 Ala Leu Met Lys Ser Thr Cys
 225 230
 <210> 1024
 <211> 116
 50 <212> PRT
 <213> Homo sapiens
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 Ile Arg Glu Xaa Ala Trp Asp Ser Thr Ala Leu Ser Ser Xaa Arg Ser
 55 1 5 10 15
 Phe Trp Val Leu Tyr Asp Pro Ser Asn Ser Asp Leu Asn Xaa Pro Xaa
 20 25 30
 Lys Asn Val Xaa Ile Ser Thr Pro Arg Ala Phe Leu Ala Phe Xaa Val
 35 40 45
 60 Ile Leu Asn Xaa Ser Leu Xaa Ser Gly Xaa Ser Val Leu Xaa Leu Gly
 50 55 60
 Phe Leu Gly Thr Ser Pro Thr Xaa Gly Gly Ser Cys Ser Leu Pro Leu
 65 70 75 80

Asn Xaa Xaa Xaa Leu Val Pro Arg Xaa Xaa Xaa Pro Thr Asn Leu Xaa
 85 90 95
 Val Phe Trp Xaa Gly Phe Pro Leu Xaa Gly Xaa Phe Tyr Xaa Thr Xaa
 100 105 110
 5 Gly Xaa Xaa Ser
 115
 <210> 1025
 <211> 110
 10 <212> PRT
 <213> Homo sapiens
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 15 Tyr Gln Thr Gln Ser Lys Xaa Ile His His Xaa Xaa Tyr Tyr Xaa Pro
 1 5 10 15
 Thr Leu Xaa Gln Met Gln Glu Trp Ala Xaa Ile Trp Xaa Leu Xaa Asp
 20 25 30
 Asp His Arg Lys Gln Asn Glu Asp Arg Gly Xaa Trp Xaa Xaa Xaa Lys
 35 40 45
 20 Xaa Val Gln Asn Ser Arg Leu Ser Cys His Lys Ala Pro His Xaa Xaa
 50 55 60
 Leu Arg Pro Thr Ser Xaa Xaa Lys Pro Lys Glu Gln Thr Asn Lys Arg
 65 70 75 80
 25 Gly Pro Gly Xaa Phe Xaa Tyr Phe Thr His Ser Xaa Tyr Leu Leu Arg
 85 90 95
 Ser Ser Asn Asn Gln Xaa Lys Trp Phe Leu Lys Lys Xaa Asn
 100 105 110
 <210> 1026
 30 <211> 93
 <212> PRT
 <213> Homo sapiens
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 35 Asn Xaa Glu Ser Xaa Pro Asp Pro Phe Tyr Trp Ser Val Pro Leu Ala
 1 5 10 15
 Xaa Xaa Trp Arg Trp Val Ala Xaa Pro Xaa Gly Glu Leu Tyr Asp Met
 20 25 30
 40 Thr Gly Gly Ser Phe Val Xaa Leu Xaa Xaa Thr Xaa Cys Leu Cys
 35 40 45
 Pro His Phe Val Ser Tyr Asp His Pro Xaa Xaa Thr Arg Xaa Arg Pro
 50 55 60
 Ile Pro Ala Phe Xaa Ile Gly Leu Glu Xaa Ser Thr Xaa Xaa Asp Glu
 65 70 75 80
 45 Xaa Val Cys Phe Val Phe Gly Ile Lys His Val Arg Leu
 85 90
 <210> 1027
 <211> 205
 50 <212> PRT
 <213> Homo sapiens
 <400> 1027
 55 Xaa Leu Xaa Ser Arg Ala Cys Arg Ser Thr Leu Val Asp Pro Lys Phe
 1 5 10 15
 Glu Thr Ile Val Glu Gln Ala Pro Leu Ala Ile Glu Asp Leu Leu Asn
 20 25 30
 Glu Leu Asp Thr Gln Asp Glu Glu Val Ala Ser Asp Ser Asp Glu Ser
 35 40 45
 60 Ser Glu Gly Gly Glu Arg Gly Asp Ala Leu Ser Gln Lys Arg Ser Glu
 50 55 60
 Lys Pro Pro Ala Gly Ser Ile Cys Arg Ala Glu Pro Glu Ala Gly Glu
 65 70 75 80

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20      <210> 1028
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        <212> PRT
        <213> Homo sapiens

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50 <210> 1029
 <211> 301
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 <213> Homo sapiens

391

85 90 95
 Ser Arg Ala Arg Ser Ala Val Pro Xaa Cys Ser Pro Ala Ser Ala Arg
 100 105 110
 5 Ala Ser Gly Ser Gly Pro Tyr Thr Pro Pro Pro Ala Pro Leu Pro Leu
 115 120 125
 His Ala Arg Ala Arg Gly Leu Leu Leu Thr Phe Pro Ser Leu Leu Leu
 130 135 140
 Gln Pro Glu Gln Thr Leu Leu Leu Arg Leu Leu Leu Pro Pro Pro
 145 150 155 160
 10 Phe Lys Gln Ala Pro Ala Gly Leu Leu Trp Asp Leu Ile Phe Arg Glu
 165 170 175
 Asn Ala Ser Cys Gln Val Leu Gln Leu Pro Asp His Phe Val Glu Thr
 180 185 190
 15 Leu Ser Val Leu Arg Arg Gly Ala Leu Ala Ala Gly His Phe Lys Gln
 195 200 205
 Ser Val Ser Asn Cys Leu Val Val Lys Leu Glu Asn Gly Ala Ala Thr
 210 215 220
 Val Pro Val Val Thr Cys Leu Leu Leu Thr Ser Leu Arg Phe Ser Pro
 225 230 235 240
 20 Ala Asp Gly Ala Cys Gly Arg Leu Leu Arg Pro Leu Leu Gly Gln Arg
 245 250 255
 Val Ser Thr Leu Thr Thr Leu Arg Gly Leu Ile Thr Val Arg Arg His
 260 265 270
 25 Leu Leu Ile Leu Cys Val Gln Phe Ile Gln Glu Val Phe Asn Gly Lys
 275 280 285
 Arg Gly Leu Leu His Asn Arg Leu Lys Leu Trp Ile His
 290 295 300

 30 <210> 1030
 <211> 216
 <212> PRT
 <213> Homo sapiens

 <400> 1030
 35 Pro Ser Gly Pro Arg Ser Ser Gln Pro Gln Ala Glu Ala Leu Gly Lys
 1 5 10 15
 Gly Pro Val Pro Gly Met Leu Ala Pro Asn Asp Gly Pro Ile Ser Pro
 20 25 30
 40 Val Pro Pro Phe Pro Pro Ala Trp His Arg Ser Ser Gly Ala Thr Xaa
 35 40 45
 Leu Ser Leu Xaa Asn Ser Pro Val Ser Leu Xaa Pro Arg Xaa Lys Arg
 50 55 60
 Gly Leu Ala Ser Leu Pro Ala Cys Pro Trp Pro Gly His Ile Thr Pro
 65 70 75 80
 45 Cys Val Ser Ser Ser Ser Pro Ala Pro Gly His Trp Pro Pro Leu Leu
 85 90 95
 Gly His Trp Ser Gly Ala Glu Gly Val Xaa Leu Xaa Trp Arg Ala Xaa
 100 105 110
 50 Phe Trp Pro Arg Ala Xaa Gly Leu Ile Ser Glu Ala Gly Pro Ala Gln
 115 120 125
 Leu Cys Leu Xaa Ala His Gln Pro Leu Pro Ala Pro Arg Gly Arg Ala
 130 135 140
 Pro Thr Pro Leu Leu Leu Leu Phe Leu Ser Met Pro Gly Leu Gly
 145 150 155 160
 55 Gly Ser Phe Ser Pro Phe Pro Leu Ser Cys Cys Asn Leu Ser Arg Arg
 165 170 175
 Phe Cys Phe Phe Val Phe Phe Cys Arg Leu Pro Ser Ser Arg Arg Leu
 180 185 190
 60 Gln Ala Phe Ser Gly Ile Ser Ser Ser Gly Lys Met Pro Pro Ala Arg
 195 200 205
 Ser Cys Ser Phe Arg Ile Thr Leu
 210 215

<210> 1031
 <211> 190
 <212> PRT
 <213> Homo sapiens

5

<400> 1031
 Phe Glu Thr Ile Val Glu Gln Ala Pro Leu Ala Ile Glu Asp Leu Leu
 1 5 10 15
 Asn Glu Leu Asp Thr Gln Asp Glu Glu Val Ala Ser Asp Ser Asp Glu
 20 25 30
 Ser Ser Glu Gly Gly Glu Arg Gly Asp Ala Leu Ser Gln Lys Arg Ser
 35 40 45
 Glu Lys Pro Pro Ala Gly Ser Ile Cys Arg Ala Glu Pro Glu Ala Gly
 50 55 60
 Glu Glu Gln Ala Gly Asp Asp Arg Asp Ser Gly Gly Pro Val Leu Gln
 65 70 75 80
 Phe Asp Tyr Glu Ala Val Ala Asn Arg Leu Phe Glu Met Ala Ser Arg
 85 90 95
 Gln Ser Thr Pro Ser Gln Asn Arg Lys Arg Leu Tyr Lys Val Ile Arg
 100 105 110
 Lys Leu Gln Asp Leu Ala Gly Gly Ile Phe Pro Glu Asp Glu Ile Pro
 115 120 125
 Glu Lys Ala Cys Arg Arg Leu Leu Glu Gly Arg Arg Gln Lys Lys Thr
 130 135 140
 Lys Lys Gln Lys Arg Leu Leu Arg Leu Gln Gln Glu Arg Gly Lys Gly
 145 150 155 160
 Glu Lys Glu Pro Pro Ser Pro Gly Met Glu Arg Lys Arg Ser Arg Arg
 165 170 175
 Arg Gly Val Gly Ala Arg Pro Arg Gly Ala Gly Arg Gly Trp
 180 185 190

<210> 1032
 <211> 124
 <212> PRT
 <213> Homo sapiens

35

<400> 1032
 Ala Phe Trp Leu Gly His Trp Ser Gly Ala Glu Gly Val Xaa Leu Xaa
 1 5 10 15
 Trp Arg Ala Xaa Phe Trp Pro Arg Ala Xaa Gly Leu Ile Ser Glu Ala
 20 25 30
 Gly Pro Ala Gln Leu Cys Leu Xaa Ala His Gln Pro Leu Pro Ala Pro
 35 40 45
 Arg Gly Arg Ala Pro Thr Pro Leu Leu Leu Leu Phe Leu Ser Met
 50 55 60
 Pro Gly Leu Gly Gly Ser Phe Ser Pro Phe Pro Leu Ser Cys Cys Asn
 65 70 75 80
 Leu Ser Arg Arg Phe Cys Phe Phe Val Phe Phe Cys Arg Leu Pro Ser
 85 90 95
 Ser Arg Arg Leu Gln Ala Phe Ser Gly Ile Ser Ser Ser Gly Lys Met
 100 105 110
 Pro Pro Ala Arg Ser Cys Ser Phe Arg Ile Thr Leu
 115 120

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<210> 1033
 <211> 231
 <212> PRT
 <213> Homo sapiens

60

<400> 1033
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 1 5 10 15
 Ala Ser Xaa Phe Leu Ala Thr Gly Xaa Trp Ala Asp Leu Gly Ser Arg

20 25 30
 Ala Arg Ser Ala Val Pro Xaa Cys Ser Pro Ala Ser Ala Arg Ala Ser
 35 40 45
 Gly Ser Gly Pro Tyr Thr Pro Pro Pro Ala Pro Leu Pro Leu His Ala
 5 50 55 60
 Arg Ala Arg Gly Leu Leu Thr Phe Pro Ser Leu Leu Leu Gln Pro
 65 70 75 80
 Glu Gln Thr Leu Leu Leu Leu Arg Leu Leu Leu Pro Pro Pro Phe Lys
 85 90 95
 10 Gln Ala Pro Ala Gly Leu Leu Trp Asp Leu Ile Phe Arg Glu Asn Ala
 100 105 110
 Ser Cys Gln Val Leu Gln Leu Pro Asp His Phe Val Glu Thr Leu Ser
 115 120 125
 Val Leu Arg Arg Gly Ala Leu Ala Ala Gly His Phe Lys Gln Ser Val
 15 130 135 140
 Ser Asn Cys Leu Val Val Lys Leu Glu Asn Gly Ala Ala Thr Val Pro
 145 150 155 160
 Val Val Thr Cys Leu Leu Leu Thr Ser Leu Arg Phe Ser Pro Ala Asp
 165 170 175
 20 Gly Ala Cys Gly Arg Leu Leu Arg Pro Leu Leu Gly Gln Arg Val Ser
 180 185 190
 Thr Leu Thr Thr Leu Arg Gly Leu Ile Thr Val Arg Arg His Leu Leu
 195 200 205
 Ile Leu Cys Val Gln Phe Ile Gln Glu Val Phe Asn Gly Lys Arg Gly
 25 210 215 220
 Leu Leu His Asn Arg Leu Lys
 225 230

30 <210> 1034
 <211> 149
 <212> PRT
 <213> Homo sapiens

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 35 Trp Ala His Leu Ser Ser Ala Ala Leu Pro Ser Arg Leu Ala Gln Glu
 1 5 10 15
 Phe Trp Ser His Xaa Pro Glu Ser Thr Xaa Gln Pro Gly Gln Pro Xaa
 20 25 30
 Pro Ala Xaa Gln Ala Arg Pro Gly Leu Pro Pro Cys Leu Ser Leu Ala
 40 35 40 45
 Arg Pro His His Ser Leu Arg Phe Phe Phe Phe Ser Gly Ser Trp Thr
 50 55 60
 Leu Ala Ala Phe Ala Arg Ala Leu Val Arg Gly Arg Gly Val Leu Leu
 65 70 75 80
 45 Leu Leu Ala Ser Pro Ser Leu Ala Thr Ala Pro Gly Leu Ile Ser Glu
 85 90 95
 Gln Gly Pro Leu Xaa Cys Ala Trp Leu Phe Thr Lys Pro Xaa Ala Arg
 100 105 110
 Ala Ser Gly Val Gly Pro Leu Thr Pro Leu Pro Pro Gly Tyr Xaa Phe
 50 115 120 125
 Pro Leu His Ala Pro Gly Leu Arg Gly Gly Xaa Leu Phe Xaa Pro Phe
 130 135 140
 Xaa Phe Phe Ser Leu
 145

55 <210> 1035
 <211> 126
 <212> PRT
 <213> Homo sapiens

60 <400> 1035
 Val Tyr Xaa Thr Ala Arg Ser Ala Xaa Ser Arg Xaa Ala Ser Glu Ala
 1 5 10 15

Trp Pro Pro Ser Leu Pro Val Leu Gly Pro Ala Thr Ser Leu Pro Ala
 20 25 30
 Phe Leu Leu Leu Leu Arg Leu Leu Asp Ile Gly Arg Leu Cys Ser Gly
 35 40 45
 5 Thr Gly Gln Gly Pro Arg Cys Pro Pro Ser Ser Gly Glu Pro Leu Phe
 50 55 60
 Gly His Gly Pro Trp Ala Asp Leu Gly Ala Gly Pro Ala Xaa Leu Cys
 65 70 75 80
 10 Leu Ala Val His Gln Thr Xaa Cys Pro Arg Leu Gly Gly Arg Ala Pro
 85 90 95
 Asn Thr Pro Ser Ser Trp Val Pro Xaa Ser Ser Ser Cys Pro Gly Ala
 100 105 110
 Ser Gly Gly Pro Xaa Phe Xaa Pro Phe Xaa Leu Phe Phe Pro
 115 120 125
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 <210> 1036
 <211> 179
 <212> PRT
 <213> Homo sapiens
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 Gly Pro Asp Pro Arg Gly Ala Gly Xaa Arg Phe Gly Glu Gln Pro Gly
 1 5 10 15
 25 Thr Xaa Glu Arg Ala Leu Leu Arg Asp Gln Pro Arg Gly Arg Gly Gln
 20 25 30
 Arg Gly Ala Arg Gln Lys Lys Glu Asp Thr Ser Ala Pro Asp Gln Cys
 35 40 45
 Pro Ser Lys Gly Gly Gln Cys Pro Gly Ala Gly Glu Glu Glu Thr
 50 55 60
 30 Gln Gly Val Met Trp Pro Gly Gln Gly Gln Ala Gly Arg Glu Ala Arg
 65 70 75 80
 Pro Arg Leu Xaa Arg Gly Xaa Arg Leu Thr Gly Leu Xaa Cys Arg Leu
 85 90 95
 35 Arg Xaa Val Ala Pro Glu Leu Leu Cys Gln Ala Gly Gly Lys Gly Gly
 100 105 110
 Thr Gly Glu Met Gly Pro Ser Leu Gly Ala Ser Ile Pro Gly Thr Gly
 115 120 125
 Pro Phe Pro Arg Ala Ser Ala Cys Gly Cys Asp Asp Leu Gly Pro Glu
 130 135 140
 40 Gly Gln Thr Pro Lys Thr Glu Thr Leu Pro Ala Ala Gly Leu Ala Ala
 145 150 155 160
 Pro Ala Val Gly Gly Ser Glu Asn Lys Met Pro Arg Ser Pro Cys Gln
 165 170 175
 Gly Ser Val
 45
 <210> 1037
 <211> 156
 <212> PRT
 50 <213> Homo sapiens
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 1 5 10 15
 55 Gly Pro Ser Ser Pro Ala Ser Val Thr Val Thr Val Gly Asp Glu Gly
 20 25 30
 Ala Asp Thr Pro Val Gly Ala Thr Pro Leu Ile Gly Asp Glu Ser Glu
 35 40 45
 60 Asn Leu Glu Gly Asp Gly Asp Leu Arg Gly Gly Arg Ile Leu Leu Gly
 50 55 60
 His Ala Thr Lys Ser Phe Pro Ser Ser Pro Ser Lys Gly Gly Ser Cys
 65 70 75 80
 Pro Ser Arg Ala Lys Met Ser Met Thr Gly Ala Gly Lys Ser Pro Pro
 85 90 95

85 90 95
 Ser Val Gln Ser Leu Ala Met Arg Leu Leu Ser Met Pro Gly Ala Gln
 100 105 110
 5 Gly Ala Ala Ala Ala Gly Ser Glu Pro Pro Pro Ala Thr Thr Ser Pro
 115 120 125
 Glu Gly Gln Pro Lys Val His Arg Ala Arg Lys Thr Met Ser Lys Pro
 130 135 140
 Gly Asn Gly Gln Val Ser Gly Met Gly Glu Met Gly
 145 150 155
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 <210> 1038
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 <212> PRT
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 20 Pro Ile Pro Leu Thr Cys Pro Phe Pro Gly Leu Asn Met Val Leu Arg
 20 25 30
 Ala Arg Trp Thr Leu Gly Cys Pro Ser Gly Leu Val Val Ala Gly Gly
 35 40 45
 Gly Ser Asp Pro Ala Ala Ala Pro Trp Ala Pro Gly Ile Leu Ser
 50 55 60
 25 Ser Leu Ile Ala Lys Leu Trp Thr Asp Gly Gly Asp Phe Pro Ala Pro
 65 70 75 80
 Val Ile Asp Ile Leu Ala Arg Leu Gly Gln Glu Pro Pro Leu Leu Gly
 85 90 95
 30 Glu Glu Gly Asn Asp Phe Val Ala Trp Pro Ser Arg Ile Arg Pro Pro
 100 105 110
 Arg Arg Ser Pro Ser Pro Ser Arg Phe Ser Asp Ser Ser Pro Met Ser
 115 120 125
 Gly Val Ala Pro Thr Gly Val Ser Ala Pro Ser Ser Pro Thr Val Thr
 130 135 140
 35 Val Thr Glu Ala Gly Asp Glu Gly Pro Ala Gly Ser Arg Glu Ser Gly
 145 150 155 160
 Leu Ala Leu Gly Arg Val Ser Ser Leu
 165
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 <210> 1039
 <211> 67
 <212> PRT
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 Gly Asn Gly Met Glu Lys Met Glu Tyr Pro Pro Xaa Asn Xaa Leu Xaa
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 Xaa Phe Phe Thr Val Xaa Leu Lys Gly Phe Tyr Ser Ile Tyr Ser Xaa
 20 25 30
 50 Pro Ile Phe Lys Xaa Arg Xaa Cys Cys Val Ser Lys Ile Xaa Leu Xaa
 35 40 45
 Leu Xaa Leu Glu Pro Thr Thr Gly Xaa Xaa Phe Leu Gln Val Tyr Ile
 50 55 60
 Xaa Gly Trp
 55 65
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 <211> 70
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 60 <213> Homo sapiens
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 Ala Cys Phe Phe Ser Ile Ser Ser Arg His Pro Ile Phe Phe Ser Phe
 20 25 30
 Lys Asn Leu Leu Val Gly Trp Leu Trp Trp Leu Ala Pro Val Ile Pro
 35 40 45
 5 Ala Leu Cys Glu Val Lys Ala Gly Arg Leu Leu Lys Pro Ser Ser Leu
 50 55 60
 Arg Pro Ala Trp Ala Thr
 65 70
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 <210> 1041
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 <212> PRT
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 1 5 10 15
 Pro Glu Pro Ser Ala Ser His Ala Leu Ser Asp Tyr Glu Thr Ser Glu
 20 20 25 30
 Lys Ser Phe Phe Ser Arg Asp Gln Lys Gln Asp Asn Glu Thr Glu Lys
 35 40 45
 Thr Ser
 50
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 <212> PRT
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 Val Met Val Asn Ser Phe Ser Gln Asp Leu Leu Met Glu His Ile Gln
 1 5 10 15
 Glu Ile Arg Thr Leu Arg Lys Arg Leu Glu Glu Ser Ile Lys Thr Asn
 35 20 25 30
 Glu Lys Leu Arg Lys Gln Leu Glu Arg Gln Gly Ser Glu Phe Val Gln
 35 40 45
 Gly Ser Thr Ser Ile Phe Ala Ser Gly Ser Glu Leu His Ser Ser Leu
 50 55 60
 40 Thr Ser Glu Ile His Phe Leu Arg Lys Gln Asn Gln Ala Leu Asn Ala
 65 70 75 80
 Met Leu Ile Lys Gly Ser Arg Asp Lys Gln Lys Glu Asn Asp Lys Leu
 85 90 95
 Arg Glu Ser Leu Ser Arg Lys Thr Val Ser Leu Glu His Leu Gln Arg
 45 100 105 110
 Glu Tyr Ala Ser Arg Glu Gly Arg Lys
 115 120
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 <213> Homo sapiens
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 Gln Arg Pro Leu Ser Xaa Xaa Gln Ala Gln Xaa Pro Gly Phe Pro Xaa
 20 25 30
 Gln Lys Ala Xaa Pro Gly Xaa Xaa Lys Asp Pro Ala Pro Phe Lys Pro
 35 40 45
 60 Xaa Ser Xaa Arg Xaa Phe Gln Val Ser Xaa Xaa Phe Xaa Pro Ser Phe
 50 55 60
 Ser Tyr Ala Phe Ser Ser Thr Xaa Lys Asp Cys Lys Ser Leu Ser Phe
 397

398

<210> 1046
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 <212> PRT
 5 <213> Homo sapiens

 <400> 1046
 Met Ser Phe Gln Gln Gly Ala Ser Ala Leu Ala Asp Leu Phe Glu Gln
 1 5 10 15
 10 Gly Leu Ile Val Leu Asn Xaa Ala Xaa Asp Met Ala Ala Phe Leu Leu
 20 25 30
 Ala His Arg Trp Trp Xaa Xaa Pro Gly Gly Thr His Thr Gly Val Leu
 35 40 45
 15 Ile Gly Arg Thr Ala Thr Val Xaa Glu Xaa Gly Val Arg Val Ile Pro
 50 55 60
 Lys Lys Trp Arg Ser Ser Glu Thr Xaa Phe Gly Val Xaa Gly Trp Xaa
 65 70 75 80
 Glu Xaa Asn Xaa Ile Lys Xaa Asn Xaa Leu Ser Met Gly Ile Phe Gly
 85 90 95
 20 Thr His Pro Val Cys Gln Gly
 100

<210> 1047
 <211> 178
 25 <212> PRT
 <213> Homo sapiens

 <400> 1047
 Glu Asn Leu Lys Gln Gln Leu Glu Glu Gln Glu Tyr Lys Leu Gln Lys
 1 5 10 15
 Glu Gln Asn Leu Asn Met Gln Leu Phe Ser Glu Ile His Asn Leu Gln
 20 25 30
 Asn Lys Phe Arg Asp Leu Ser Pro Pro Arg Tyr Asp Ser Leu Val Gln
 35 35 40 45
 Ser Gln Ala Arg Glu Leu Ser Leu Gln Arg Gln Gln Ile Lys Asp Gly
 50 55 60
 His Gly Ile Cys Val Ile Ser Arg Gln His Met Asn Thr Met Ile Lys
 65 70 75 80
 Ala Phe Glu Glu Leu Leu Gln Ala Ser Asp Val Asp Tyr Cys Val Ala
 85 90 95
 40 Glu Gly Phe Gln Glu Gln Leu Asn Gln Cys Ala Glu Leu Leu Glu Lys
 100 105 110
 Leu Glu Lys Leu Phe Leu Asn Gly Lys Ser Val Gly Val Glu Met Asn
 115 120 125
 45 Thr Gln Asn Glu Leu Met Glu Arg Ile Glu Glu Asp Asn Leu Thr Tyr
 130 135 140
 Gln His Leu Leu Pro Glu Ser Pro Glu Pro Ser Ala Ser His Ala Leu
 145 150 155 160
 Ser Asp Tyr Glu Thr Ser Glu Lys Ser Phe Phe Ser Arg Asp Gln Lys
 165 170 175
 50 Pro Arg

<210> 1048
 55 <211> 141
 <212> PRT
 <213> Homo sapiens

<400> 1048
 60 His Ser Asn Pro Arg Gly Ser Gln Leu His Lys Ser Arg Ala Gly Asn
 1 5 10 15
 Lys Gly Ser Thr Pro Ser Thr Ile Glu Gln Val Cys Glu Gln Cys Glu
 20 25 30

His Gly Gln Ala Asp Pro Gly Arg Gly Leu Gln Arg Leu Lys Leu Leu
 35 40 45
 Trp Arg Val Ser Leu Pro Glu Asp Gly Gln Cys Pro Leu His Cys Glu
 50 55 60
 5 Gln Ile Gly Glu Met Lys Ala Glu Val Thr Lys Leu His Lys Lys Leu
 65 70 75 80
 Phe Glu Gln Glu Lys Lys Leu Gln Asn Thr Met Lys Leu Leu Gln Leu
 85 90 95
 Ser Lys Arg Gln Glu Lys Val Ile Phe Asp Gln Leu Val Val Thr His
 10 100 105 110
 Lys Ile Leu Arg Lys Ala Arg Gly Asn Leu Glu Leu Arg Pro Gly Gly
 115 120 125
 Ala His Pro Gly Thr Cys Ser Pro Ser Arg Pro Gly Ser
 130 135 140
 15
 <210> 1049
 <211> 135
 <212> PRT
 <213> Homo sapiens
 20
 <400> 1049
 Ser Ser Ile Xaa Pro Lys Thr Trp Arg Pro Phe Leu Leu Ala His Lys
 1 5 10 15
 Val Val Ala Asn Asp Gln Xaa Gly His Thr Xaa Ser Ala Ser Cys Arg
 25 20 25 30
 Thr Ala Thr Val Xaa Arg Xaa Gly Asn Pro Cys His Phe Gln Lys Ser
 35 40 45
 Gly Gly Val Ser Glu Thr Glu Phe Xaa Xaa His Trp Pro Gly Arg Asn
 50 55 60
 30 Gln Xaa Asp Gln Met Xaa Tyr Pro Phe His Gly Xaa Ile Cys Xaa Ile
 65 70 75 80
 Xaa Phe Val Xaa Leu Lys Gly Xaa Leu Arg Asp Gly His Arg Leu Gly
 85 90 95
 Lys Pro Xaa Xaa Xaa Leu Xaa Leu Gly Leu Phe Xaa Pro Leu Ala Xaa
 35 100 105 110
 Val Leu Glu Pro Val Leu Lys Arg Xaa Xaa Phe Xaa Pro Xaa Leu Xaa
 115 120 125
 Ala Xaa Gln Thr Xaa Phe His
 130 135
 40
 <210> 1050
 <211> 218
 <212> PRT
 <213> Homo sapiens
 45
 <400> 1050
 Gly Val Pro Gly Trp Gln Ala Ala Leu Leu Ser Leu Pro Gly Ile Thr
 1 5 10 15
 Asn Arg Glu Ala Lys Lys Ser Arg Leu Pro Ile Leu Ile Lys Pro Ser
 50 20 25 30
 Arg Ser Leu Gly Asn Met Tyr Arg Leu Pro Ala Thr Gln Glu Val Val
 35 40 45
 Thr Gln Leu Gln Ser Gln Ile Leu Glu Leu Gln Gly Glu Leu Lys Glu
 50 55 60
 55 Phe Lys Thr Cys Asn Lys Gln Leu His Gln Lys Leu Ile Leu Ala Glu
 65 70 75 80
 Ala Val Met Glu Gly Arg Pro Thr Pro Asp Lys Thr Leu Leu Asn Ala
 85 90 95
 Gln Pro Pro Val Gly Ala Ala Tyr Gln Asp Ser Pro Gly Glu Gln Lys
 60 100 105 110
 Gly Ile Lys Thr Thr Ser Ser Val Trp Arg Asp Lys Glu Met Asp Ser
 115 120 125
 Asp Gln Gln Arg Ser Tyr Glu Ile Asp Ser Glu Ile Cys Pro Pro Asp
 400

130 135 140
 Asp Leu Ala Ser Leu Pro Ser Cys Lys Glu Asn Pro Glu Asp Val Leu
 145 150 155 160
 Ser Pro Thr Ser Val Ala Thr Tyr Leu Ser Ser Lys Ser Gln Pro Ser
 5 165 170 175
 Ala Lys Val Ser Val Met Gly Thr Asp Gln Ser Glu Ser Ile Asn Thr
 180 185 190
 Ser Asn Glu Thr Glu Tyr Leu Lys Gln Lys Xaa His Asp Leu Gly Asn
 195 200 205
 10 Trp Asn Leu Xaa Arg Leu Pro Xaa Ile Ser
 210 215

 <210> 1051
 <211> 96
 15 <212> PRT
 <213> Homo sapiens

 <400> 1051
 Ser Xaa Xaa Trp Arg Val Ser Leu Pro Xaa Asp Gly Gln Cys Pro Xaa
 20 1 5 10 15
 Xaa Cys Glu Gln Ile Gly Glu Met Lys Ala Glu Val Xaa Lys Leu His
 20 25 30
 Lys Lys Leu Phe Glu Gln Glu Lys Leu Gln Asn Xaa Met Lys Leu
 35 40 45
 25 Leu Gln Leu Ser Lys Arg Gln Glu Lys Val Ile Phe Asp Gln Leu Val
 50 55 60
 Val Thr His Lys Ile Leu Arg Lys Ala Arg Gly Asn Leu Glu Leu Arg
 65 70 75 80
 Pro Gly Gly Ala His Pro Gly Thr Cys Ser Pro Ser Arg Pro Gly Ser
 30 85 90 95

 <210> 1052
 <211> 106
 <212> PRT
 35 <213> Homo sapiens

 <400> 1052
 Ser Lys Met Thr Phe Ser Trp Arg Leu Leu Ser Cys Lys Ser Phe Met
 1 5 10 15
 40 Xaa Phe Cys Asn Phe Phe Ser Cys Ser Asn Asn Phe Leu Cys Ser Leu
 20 25 30
 Xaa Thr Ser Ala Phe Ile Ser Pro Ile Cys Ser Gln Xaa Xaa Gly His
 35 40 45
 Trp Pro Ser Xaa Gly Ser Glu Thr Leu Xaa Xaa Lys Leu Xaa Pro Ala
 50 55 60
 45 Val Xaa Pro Xaa Xaa Arg Val Ser Trp Ala Gly Ser His Xaa Leu Gln
 65 70 75 80
 Thr Cys Leu Xaa Xaa Ala Xaa Xaa Xaa Ala Leu Trp Phe Gln Xaa Leu
 85 90 95
 50 Thr Leu Xaa Asn Trp Xaa Pro Phe Trp Gly
 100 105

 <210> 1053
 <211> 219
 55 <212> PRT
 <213> Homo sapiens

 <400> 1053
 Cys Leu Asp Phe Ser Lys Ala Asp Ser Gly Val His Leu Cys Val Ile
 1 5 10 15
 Asp Asp Ser Asn Glu His Met Leu Thr Val Trp Asp Trp Gln Arg Lys
 20 25 30
 Ala Lys Gly Ala Glu Ile Lys Thr Thr Asn Glu Val Val Leu Ala Val

35 40 45
 Glu Phe His Pro Thr Asp Ala Asn Thr Ile Ile Thr Cys Gly Lys Ser
 50 55 60
 5 His Ile Phe Phe Trp Thr Trp Ser Gly Asn Ser Leu Thr Arg Lys Gln
 65 70 75 80
 Gly Ile Phe Gly Lys Tyr Glu Lys Pro Lys Phe Val Gln Cys Leu Ala
 85 90 95
 Phe Leu Gly Asn Gly Asp Val Leu Thr Gly Asp Ser Gly Gly Val Met
 100 105 110
 10 Leu Ile Trp Ser Lys Thr Thr Val Glu Pro Thr Pro Gly Lys Gly Pro
 115 120 125
 Lys Gly Val Tyr Gln Ile Ser Lys Gln Ile Lys Ala His Asp Gly Ser
 130 135 140
 Val Phe Thr Leu Cys Gln Met Arg Asn Gly Met Leu Leu Thr Gly Gly
 145 150 155 160
 15 Gly Lys Asp Arg Lys Ile Ile Leu Trp Asp His Asp Leu Asn Pro Glu
 165 170 175
 Arg Glu Ile Glu Gly Pro Asp Gln Tyr Gly Thr Ile Arg Ala Val Ala
 180 185 190
 20 Glu Gly Lys Gly Arg Ser Ile Phe Ser Arg Pro His His Arg Asn Phe
 195 200 205
 Ile Leu Arg Xaa Asn His Phe Asn Asp Gly Leu
 210 215
 25 <210> 1054
 <211> 126
 <212> PRT
 <213> Homo sapiens
 30 <400> 1054
 Pro Arg Xaa Phe Ser Thr Xaa Xaa Phe Pro Pro Leu Tyr Glu Arg Phe
 1 5 10 15
 Gly Val Cys Leu Lys Gly Gln Gly Asn Pro Leu Trp Val Xaa Xaa Asn
 20 25 30
 35 Lys Lys Ile Cys Pro Pro Leu Lys Ile Xaa Arg Xaa Ile Ser Tyr Gly
 35 40 45
 Glu Lys Xaa Ser Glu Ile Leu Pro Phe Gly Xaa His Leu Leu Lys Thr
 50 55 60
 Xaa Lys Ile Val Xaa Phe Lys Xaa Xaa Xaa Asp Ser Lys His Pro Ile
 65 70 75 80
 40 Phe Leu Gln Tyr Val Cys Ser Val His Thr Tyr Arg Ser Ala Pro Val
 85 90 95
 Ser Ile Arg His Ile Tyr Leu Ser Val Ser Asn Asp Tyr Tyr Ile Ile
 100 105 110
 45 Arg Ser Ala Cys Ala Ile Leu Pro Ala Arg Asn Ile Leu Thr
 115 120 125
 <210> 1055
 <211> 72
 50 <212> PRT
 <213> Homo sapiens
 <400> 1055
 Lys Asn Met Pro Pro Val Lys Asn Xaa Gln Gly Xaa Leu Leu Trp Gly
 1 5 10 15
 Lys Xaa Ile Gly Asn Pro Ser Leu Trp Xaa Xaa Pro Val Lys Asn Xaa
 20 25 30
 Gln Asn Ser Xaa Phe Gln Xaa Xaa Xaa Arg Phe Gln Ala Pro His Leu
 35 40 45
 60 Ser Ser Val Cys Met Phe Cys Thr Tyr Leu Ser Glu Arg Ala Ser Lys
 50 55 60
 Tyr Gln Ala Tyr Ile Ser Val Cys
 65 70

<210> 1056
 <211> 206
 <212> PRT
 5 <213> Homo sapiens

<400> 1056
 Met Leu Leu Thr Gly Gly Gly Lys Asp Arg Lys Ile Ile Leu Trp Asp
 1 5 10 15
 10 His Asp Leu Asn Pro Glu Arg Glu Ile Glu Val Pro Asp Gln Tyr Gly
 20 25 30
 Thr Ile Arg Ala Val Ala Glu Gly Lys Ala Asp Gln Phe Leu Val Gly
 35 40 45
 15 Thr Ser Arg Asn Phe Ile Leu Arg Gly Thr Phe Asn Asp Gly Phe Gln
 50 55 60
 Ile Glu Val Gln Gly His Thr Asp Glu Leu Trp Gly Leu Ala Thr His
 65 70 75 80
 Pro Phe Lys Asp Leu Leu Leu Thr Cys Ala Gln Asp Arg Gln Val Cys
 85 90 95
 20 Leu Trp Asn Ser Met Glu His Xaa Leu Glu Trp Thr Arg Leu Val Asp
 100 105 110
 Glu Pro Gly His Cys Ala Asp Phe His Pro Ser Gly Thr Val Val Ala
 115 120 125
 25 Ile Gly Thr His Ser Gly Arg Trp Phe Val Leu Asp Ala Glu Thr Arg
 130 135 140
 Asp Leu Val Ser Ile His Thr Asp Gly Asn Glu Gln Leu Ser Val Met
 145 150 155 160
 Arg Tyr Ser Ile Asp Gly Thr Phe Leu Ala Val Gly Ser His Asp Asn
 165 170 175
 30 Phe Ile Tyr Leu Tyr Val Val Ser Glu Asn Gly Arg Lys Xaa Ser Arg
 180 185 190
 Tyr Gly Arg Xaa Thr Gly His Ser Ser Tyr Ile Thr His Xaa
 195 200 205

35 <210> 1057
 <211> 70
 <212> PRT
 <213> Homo sapiens

40 <400> 1057
 Glu Asp Met Xaa His Val Glu Xaa Leu Ser Glu Ile Ser Met Xaa Ile
 1 5 10 15
 Gly Xaa Xaa Xaa Leu Pro Phe Gly Xaa Gln Leu Leu Lys Thr Leu Lys
 20 25 30
 45 Ile Val Leu Phe Lys Arg Arg Glu Ile Pro Ser Asn Pro Ser Phe Phe
 35 40 45
 Ser Met Tyr Val Leu Thr Tyr Leu Ser Glu Arg Ala Ser Lys Tyr Gln
 50 55 60
 Ala Tyr Ile Ser Val Cys
 50 65 70

55 <210> 1058
 <211> 99
 <212> PRT
 <213> Homo sapiens

<400> 1058
 Tyr Leu Leu Ala Arg Ser Asp Lys Tyr Val Arg Thr Tyr Ile Leu Lys
 1 5 10 15
 60 Lys Asp Gly Leu Leu Gly Ile Ser Leu Leu Leu Lys Arg Thr Ile Leu
 20 25 30
 Arg Val Phe Asn Ser Cys Xaa Pro Lys Gly Arg Xaa Xaa Asp Pro Ile
 35 40 45

Xaa Ile Glu Ile Ser Leu Ser Xaa Ser Thr Trp Xaa Ile Ser Ser Tyr
 50 55 60
 Leu Lys Lys His Thr Val Phe Ser Leu Xaa Pro Leu Asn Thr Pro Thr
 65 70 75 80
 5 Pro Phe His Tyr Xaa Gly Xaa Lys Xaa Met Val Xaa Asn Xaa Pro Trp
 85 90 95
 Glu Val Thr

10 <210> 1059
 <211> 219
 <212> PRT
 <213> Homo sapiens

15 <400> 1059
 Phe Leu Gln Pro Leu Gln Pro His Val Arg Val Trp Asp Ser Val Thr
 1 5 10 15
 Leu Ser Thr Leu Gln Ile Ile Gly Leu Gly Thr Phe Glu Arg Gly Val
 20 20 25 30
 Gly Cys Leu Asp Phe Ser Lys Ala Asp Ser Gly Val His Leu Cys Val
 35 40 45
 Ile Asp Asp Ser Asn Glu His Met Leu Thr Val Trp Asp Trp Gln Arg
 50 55 60
 Lys Ala Lys Gly Ala Glu Ile Lys Thr Thr Asn Glu Val Val Leu Ala
 25 65 70 75 80
 Val Glu Phe His Pro Thr Asp Ala Asn Thr Ile Ile Thr Cys Gly Lys
 85 90 95
 Ser His Ile Phe Phe Trp Thr Trp Ser Gly Asn Ser Leu Thr Arg Lys
 100 105 110
 30 Gln Gly Ile Phe Gly Lys Tyr Glu Lys Pro Lys Phe Val Gln Cys Leu
 115 120 125
 Ala Phe Leu Gly Asn Gly Asp Val Leu Thr Gly Asp Ser Gly Gly Val
 130 135 140
 Met Leu Ile Trp Ser Lys Thr Thr Val Glu Pro Thr Pro Gly Lys Gly
 35 145 150 155 160
 Pro Lys Gly Val Tyr Gln Ile Ser Lys Gln Ile Lys Ala His Asp Gly
 165 170 175
 Ser Val Phe Thr Leu Cys Gln Met Arg Asn Gly Met Leu Leu Thr Gly
 180 185 190
 40 Gly Xaa Lys Asp Arg Lys Ile Ile Leu Trp Asp His Asp Leu Asn Pro
 195 200 205
 Glu Arg Arg Asn Arg Xaa Ser Trp Ile Ser Met
 210 215

45 <210> 1060
 <211> 69
 <212> PRT
 <213> Homo sapiens

50 <400> 1060
 Leu Leu His His Gln Ile Ser Met Cys Tyr Thr Pro Cys Lys Lys Tyr
 1 5 10 15
 Thr Asp Met Asn Arg Gln Phe Leu Glu Lys Lys Glu His Phe Phe Lys
 20 25 30
 55 Tyr Leu Gly Asn Thr Ala Leu Ser Asp Gln Gln Gly Val Tyr Leu Arg
 35 40 45
 Thr Ser Val Thr Phe Gly Val Ala Met Tyr Asn Glu Ile Tyr Asn His
 50 55 60
 Asp Thr Leu Arg Trp
 60 65

<210> 1061
 <211> 86

<212> PRT

<213> Homo sapiens

<400> 1061

5 Arg Gly Xaa Trp Lys Pro Leu Cys Val Ser Leu Asp Lys Lys Ile Cys
 1 5 10 15
 Thr Xaa Val Glu Asn Thr Gln Cys Arg Ser Xaa Cys Gly Xaa Xaa Ile
 20 25 30
 Xaa Ile Ser Phe Pro Phe Gly Leu Pro Leu Leu Lys Xaa Leu Lys Ile
 35 40 45
 10 Val Xaa Phe Gln Lys Lys Arg Asp Ser Lys Xaa Pro Ile Phe Leu Gln
 50 55 60
 Tyr Val Cys Ser Cys Thr Tyr Leu Ser Glu Arg Ala Ser Lys Tyr Gln
 65 70 75 80
 15 Ala Tyr Ile Ser Val Cys
 85

<210> 1062

<211> 200

<212> PRT

<213> Homo sapiens

<400> 1062

25 Leu Ala Arg Ser Ala Asp Arg Arg Ala Ser Thr Asp Leu Thr Arg Lys
 1 5 10 15
 Met Lys Pro Asp Glu Thr Pro Met Phe Asp Pro Ser Leu Leu Lys Glu
 20 25 30
 Val Asp Trp Ser Gln Asn Thr Ala Thr Phe Ser Pro Ala Ile Ser Pro
 35 40 45
 30 Thr His Pro Gly Glu Gly Leu Val Leu Arg Pro Leu Cys Thr Ala Asp
 50 55 60
 Leu Asn Arg Gly Phe Phe Lys Val Leu Gly Gln Leu Thr Glu Thr Gly
 65 70 75 80
 Val Val Ser Pro Glu Gln Phe Met Lys Ser Phe Glu His Met Lys Lys
 85 90 95
 35 Ser Gly Asp Tyr Tyr Val Thr Val Val Glu Asp Val Thr Leu Gly Gln
 100 105 110
 Ile Val Ala Thr Ala Thr Leu Ile Ile Glu His Lys Phe Ile His Ser
 115 120 125
 40 Cys Ala Lys Arg Gly Arg Val Glu Asp Val Val Val Ser Asp Glu Cys
 130 135 140
 Arg Gly Lys Gln Leu Gly Lys Leu Leu Leu Ser Thr Leu Thr Leu Leu
 145 150 155 160
 Ser Lys Lys Leu Asn Cys Tyr Lys Ile Thr Leu Glu Cys Leu Pro Gln
 165 170 175
 45 Asn Val Gly Phe Tyr Lys Lys Phe Gly Tyr Thr Val Ser Glu Glu Asn
 180 185 190
 Tyr Met Cys Arg Arg Phe Leu Lys
 195 200

50

<210> 1063

<211> 110

<212> PRT

<213> Homo sapiens

55

<400> 1063

Tyr Val Gly Asn Asn Thr Pro Leu Ser Val Leu Arg Cys Phe Phe Glu
 1 5 10 15
 Thr Lys Ile Phe Asn Phe Met His Val Ile Asn Ser Leu Ile Gln Xaa
 20 25 30
 Tyr Phe Phe Xaa Met Ser His Pro Asp Xaa Asp Xaa Tyr Phe Leu Leu
 35 40 45
 60 Pro Ile Leu Leu Thr Pro Lys Lys Gly Ser Gln Leu Leu Glu Lys Tyr

50 55 60
 His Ala Gly Lys Asp Gln Val Lys Xaa Phe Ser Leu Xaa Lys Asn Ile
 65 70 75 80
 Pro Xaa Xaa Ile His Trp Lys Leu Asn Pro Xaa Gly Pro Pro Xaa Gln
 85 90 95
 5 Glu Ser Leu Lys Ala Phe Ser Trp Gly Phe Gln Gly Phe Pro
 100 105 110

 <210> 1064
 10 <211> 266
 <212> PRT
 <213> Homo sapiens

 <400> 1064
 15 Val Ala Ala Ser Leu Leu Ala Pro Leu Leu Pro Glu Gly Ile Lys Glu
 1 5 10 15
 Glu Glu Glu Arg Trp Arg Arg Lys Val Ile Cys Lys Glu Glu Pro Val
 20 20 25 30
 Ser Glu Val Lys Glu Thr Ser Thr Thr Val Glu Glu Ala Thr Thr Ile
 35 40 45
 20 Val Lys Pro Gln Glu Ile Met Leu Asp Asn Ile Glu Asp Pro Ser Gln
 50 55 60
 Glu Asp Leu Cys Ser Val Gln Ser Gly Glu Ser Glu Glu Glu Glu
 65 70 75 80
 25 Glu Gln Asp Thr Leu Glu Leu Glu Leu Val Leu Glu Arg Lys Lys Ala
 85 90 95
 Glu Leu Arg Ala Leu Glu Glu Gly Asp Gly Ser Val Ser Gly Ser Ser
 100 105 110
 Pro Arg Ser Asp Ile Ser Gln Pro Ala Ser Gln Asp Gly Met Arg Arg
 115 120 125
 30 Leu Met Ser Lys Arg Gly Lys Trp Lys Met Phe Val Arg Ala Thr Ser
 130 135 140
 Pro Glu Ser Thr Ser Arg Ser Ser Ser Lys Thr Gly Arg Asp Thr Pro
 145 150 155 160
 35 Glu Asn Gly Glu Thr Ala Ile Gly Ala Glu Asn Ser Glu Lys Ile Asp
 165 170 175
 Glu Asn Ser Asp Lys Glu Met Glu Val Glu Glu Ser Ser Glu Lys Ile
 180 185 190
 Lys Val Gln Thr Thr Pro Lys Val Glu Glu Glu Gln Asp Leu Lys Phe
 195 200 205
 40 Gln Ile Gly Glu Leu Ala Asn Thr Leu Pro Ser Lys Phe Arg Val Ser
 210 215 220
 Ser Ile Asn Arg Gln Ser Ile Phe Asn Phe His Val Leu Leu Phe Gln
 225 230 235 240
 45 Thr Gly Thr Arg Ile Ala Thr Gly Gly Lys Gly Leu Leu Met Thr Leu
 245 250 255
 Asn Glu Asn Phe Arg Met Gln Gln Asn Asn
 260 265

 50 <210> 1065
 <211> 114
 <212> PRT
 <213> Homo sapiens

 55 <400> 1065
 Asp Leu Pro Met His Asn Arg Val Ser Ser Phe Ile Asn Glu Gly Thr
 1 5 10 15
 Gln Ser Pro Arg Thr Leu Ile Ser Leu Pro Lys Lys Arg Thr Thr Lys
 20 25 30
 60 Phe Val Lys Gly Asp Ser Ser Pro Leu Gly Pro Trp Asn Ser His Phe
 35 40 45
 Ile Phe Leu Ile Ser Asn Thr Val Lys Ala Lys Glu Arg Glu Arg Ile
 50 55 60

Trp Glu Leu Lys Asn Lys Arg Ala Lys Ile Ser Asn Asn Glu Lys Lys
 65 70 75 80
 Ile Lys Lys Ser Gln Ile Tyr Lys Glu Met Phe Ser Ser Asp Leu Leu
 85 90 95
 5 Ala Glu Asp Ser Asn Leu Val Leu His Ser His Leu Gln Pro Arg Ser
 100 105 110
 Phe Pro

10 <210> 1066
 <211> 276
 <212> PRT
 <213> Homo sapiens

15 <400> 1066
 Val Ala Ala Ser Leu Leu Ala Pro Leu Leu Pro Glu Gly Ile Lys Glu
 1 5 10 15
 Glu Glu Glu Arg Trp Arg Arg Lys Val Ile Cys Lys Glu Glu Pro Val
 20 25 30
 Ser Glu Val Lys Glu Thr Ser Thr Thr Val Glu Glu Ala Thr Thr Ile
 35 40 45
 Val Lys Pro Gln Glu Ile Met Leu Asp Asn Ile Glu Asp Pro Ser Gln
 50 55 60
 Glu Asp Leu Cys Ser Val Val Gln Ser Gly Glu Ser Glu Glu Glu Glu
 25 65 70 75 80
 Glu Gln Asp Thr Leu Glu Leu Glu Leu Val Leu Glu Arg Lys Lys Ala
 85 90 95
 Glu Leu Arg Ala Leu Glu Glu Gly Asp Gly Ser Val Ser Gly Ser Ser
 100 105 110
 30 Pro Arg Ser Asp Ile Ser Gln Pro Ala Ser Gln Asp Gly Met Arg Arg
 115 120 125
 Leu Met Ser Lys Arg Gly Lys Trp Lys Met Phe Val Arg Ala Thr Ser
 130 135 140
 Pro Glu Ser Thr Ser Arg Ser Ser Ser Lys Thr Gly Arg Asp Thr Pro
 35 145 150 155 160
 Glu Asn Gly Glu Thr Ala Ile Gly Ala Glu Asn Ser Glu Lys Ile Asp
 165 170 175
 Glu Asn Ser Asp Lys Glu Met Glu Val Glu Glu Ser Ser Glu Lys Ile
 180 185 190
 40 Lys Val Gln Thr Thr Pro Lys Xaa Xaa Glu Glu Gln Asp Leu Lys Phe
 195 200 205
 Gln Ile Gly Glu Leu Ala Asn Thr Leu Pro Ser Lys Phe Arg Val Ser
 210 215 220
 Ser Ile Asn Arg Gln Xaa Ile Phe Asn Phe His Val Leu Leu Phe Gln
 225 230 235 240
 45 Thr Gly Thr Arg Ile Ala Thr Gly Xaa Lys Gly Xaa Phe Met Xaa Thr
 245 250 255
 Thr Leu Thr Lys Thr Leu Gly Cys Pro Xaa Thr Thr Xaa Pro Phe Glu
 260 265 270
 50 Ile Xaa Pro Ser
 275

<210> 1067
 <211> 114
 55 <212> PRT
 <213> Homo sapiens

<400> 1067
 Asp Leu Pro Met His Asn Arg Val Ser Ser Phe Ile Asn Glu Gly Thr
 1 5 10 15
 Gln Ser Pro Arg Thr Leu Ile Ser Leu Pro Lys Lys Arg Thr Thr Lys
 20 25 30
 Phe Val Lys Gly Asp Ser Ser Pro Leu Gly Pro Trp Asn Ser His Phe

35 40 45
 Ile Phe Leu Ile Ser Asn Thr Val Lys Ala Lys Glu Arg Glu Arg Ile
 50 55 60
 Trp Glu Leu Lys Asn Lys Arg Ala Lys Ile Ser Asn Asn Glu Lys Lys
 5 65 70 75 80
 Ile Lys Lys Ser Gln Ile Tyr Lys Glu Met Phe Ser Ser Asp Leu Leu
 85 90 95
 Ala Glu Asp Ser Asn Leu Val Leu His Ser His Leu Gln Pro Arg Ser
 100 105 110
 10 Phe Pro

<210> 1068
 <211> 87
 15 <212> PRT
 <213> Homo sapiens

<400> 1068
 Arg Thr Arg Leu Leu Ser Ser Ala Ser Arg Ser Asp Glu Asn Ile Ser
 20 1 5 10 15
 Leu Tyr Ile Trp Leu Phe Leu Ile Phe Phe Ser Leu Phe Glu Ile Phe
 20 25 30
 Ala Leu Leu Phe Phe Ser Ser Gln Ile Leu Ser Leu Ser Leu Ala Phe
 35 40 45
 25 Thr Val Phe Asp Ile Lys Asn Met Lys Cys Glu Phe His Gly Pro Arg
 50 55 60
 Gly Glu Glu Ser Pro Phe Thr Asn Phe Val Val Leu Phe Phe Gly Arg
 65 70 75 80
 Glu Ile Ser Val Leu Gly Asp
 30 85

<210> 1069
 <211> 265
 <212> PRT
 35 <213> Homo sapiens

<400> 1069
 Val Thr Lys Leu Ser Val Lys Asp Arg Leu Gly Phe Val Ser Lys Pro
 1 5 10 15
 40 Ser Val Ser Ala Thr Glu Lys Val Leu Ser Thr Ser Thr Gly Leu Thr
 20 25 30
 Lys Thr Val Tyr Asn Pro Ala Ala Leu Lys Ala Ala Gln Lys Thr Leu
 35 40 45
 Leu Val Ser Thr Ser Ala Val Asp Asn Asn Glu Ala Gln Lys Lys Lys
 50 55 60
 45 Gln Glu Ala Leu Lys Leu Gln Gln Asp Val Arg Lys Arg Lys Gln Glu
 65 70 75 80
 Ile Leu Glu Lys His Ile Glu Thr Gln Lys Met Leu Ile Ser Lys Leu
 85 90 95
 50 Glu Lys Asn Lys Thr Met Lys Ser Glu Asp Lys Ala Glu Ile Met Lys
 100 105 110
 Thr Leu Glu Val Leu Thr Lys Asn Ile Thr Lys Leu Lys Asp Glu Val
 115 120 125
 Lys Ala Ala Ser Pro Gly Arg Cys Leu Pro Lys Ser Ile Lys Thr Lys
 130 135 140
 55 Thr Gln Met Gln Lys Glu Leu Leu Asp Thr Glu Leu Asp Leu Tyr Lys
 145 150 155 160
 Lys Met Gln Ala Gly Glu Glu Val Thr Glu Leu Arg Arg Lys Tyr Thr
 165 170 175
 60 Glu Leu Gln Leu Glu Ala Ala Lys Arg Gly Ile Leu Ser Ser Gly Arg
 180 185 190
 Gly Arg Gly Ile His Ser Arg Xaa Arg Gly Ala Val His Gly Arg Ser
 195 200 205

Arg Gly Arg Arg Pro Arg Pro Ser Val Pro Gly Met Leu Trp Trp Ile
 210 215 220
 Pro Ser Lys Ala Leu Glu Ile Ser Ala Leu Pro Gly Ala Il Xaa Xaa
 225 230 235 240
 5 Ile Phe Phe Leu Xaa Ala Gln Ile Xaa Glu Ile Glu Xaa Gly Lys Ile
 245 250 255
 Gly Asp Xaa His Phe Met Pro Asn Tyr
 260 265
 10 <210> 1070
 <211> 27
 <212> PRT
 <213> Homo sapiens
 15 <400> 1070
 Val Leu Met His Pro Asp Val Ile Ile Lys Trp Asn Gly Leu Phe Lys
 1 5 10 15
 Lys Lys Lys Gly Lys Lys Arg Glu Lys Gln Cys
 20 25
 20 <210> 1071
 <211> 63
 <212> PRT
 <213> Homo sapiens
 25 <400> 1071
 Gln Leu Phe Thr Glu Val Lys Cys Lys His Gln Ser Phe Lys Ile Lys
 1 5 10 15
 Xaa Arg Xaa Glu Val Ser Ser Phe Leu Ala Ile Xaa Glu Ile His Leu
 20 25 30
 30 His Pro Phe Tyr Gln Lys Leu Phe Leu Gln Ile Cys Lys Ser Xaa Leu
 35 40 45
 Asp Asn Leu Met Lys His Arg Xaa Arg Ser Ser Tyr Xaa Asp Gln
 50 55 60
 35 <210> 1072
 <211> 190
 <212> PRT
 <213> Homo sapiens
 40 <400> 1072
 Asn Thr Ser Leu Val Ile Asp Glu Thr Leu Leu Glu Gln Gly Gln Leu
 1 5 10 15
 45 Asp Thr Pro Gly Val His Asn Val Thr Ala Leu Ser Asn Leu Ile Thr
 20 25 30
 Trp Gln Lys Val Asp Tyr Asp Phe Ser Tyr His Gln Met Glu Phe Pro
 35 40 45
 Cys Asn Ile Asn Val Phe Ile Thr Ser Glu Gly Arg Ser Leu Leu Pro
 50 55 60
 50 Ala Asp Cys Gln Ile His Leu Gln Pro Gln Leu Ile Pro Pro Asn Met
 65 70 75 80
 Glu Glu Tyr Met Asn Ser Leu Leu Ser Ala Val Leu Pro Ser Val Leu
 85 90 95
 Asn Lys Phe Arg Ile Tyr Leu Thr Leu Arg Phe Leu Glu Tyr Ser
 100 105 110
 55 Ile Ser Asp Glu Ile Thr Lys Ala Val Glu Asp Asp Phe Val Glu Met
 115 120 125
 Arg Lys Asn Asp Pro Gln Ser Ile Thr Ala Asp Asp Leu His Gln Leu
 130 135 140
 60 Leu Val Val Ala Arg Cys Leu Ser Leu Ser Ala Gly Gln Thr Thr Leu
 145 150 155 160
 Ser Arg Glu Arg Trp Leu Arg Ala Lys Gln Leu Glu Ser Leu Arg Arg
 165 170 175

Thr Arg Leu Gln Gln Gln Lys Cys Val Asn Gly Asn Glu Leu
 180 185 190

5 <210> 1073
 <211> 71
 <212> PRT
 <213> Homo sapiens

10 <400> 1073
 Leu Leu Ile Trp Asp Val Leu Phe Ile Gly Lys Val Leu Ser Arg Glu
 1 5 10 15
 Leu Phe Cys Lys Thr Lys Gln Cys Met Tyr Phe Ser Leu Val Asn Tyr
 20 25 30
 Asn Leu His Trp His Lys Lys His Met Val Thr Asn Val Leu Cys Ser
 15 35 40 45
 Arg Thr Ile Lys Glu Asn Val Phe Tyr Pro His Lys Ser Ser Glu Ala
 50 55 60
 Phe Ile Leu Phe Leu Lys Val
 65 70

20 <210> 1074
 <211> 71
 <212> PRT
 <213> Homo sapiens

25 <400> 1074
 Leu Ala Asp Leu Thr Tyr Phe Gly Thr Thr Asp Asp Pro Xaa Lys Asn
 1 5 10 15
 Ala Gln Asn Xaa Ile Xaa Ser Lys His Leu Met Thr Phe Xaa Lys Ile
 30 20 25 30
 Lys Leu Xaa Lys Xaa Xaa Met Xaa Phe Xaa Val Pro Ile Leu Phe His
 35 40 45
 Ile Xaa Ala Gln Leu Cys Xaa Pro Xaa Phe Pro Leu His Gly Ser Gln
 50 55 60
 35 Met Pro Trp Asp Trp Glu Lys
 65 70

40 <210> 1075
 <211> 214
 <212> PRT
 <213> Homo sapiens

45 <400> 1075
 Cys Ser Glu Lys Ala Ala Pro His Lys Ala Glu Gly Leu Glu Glu Ala
 1 5 10 15
 Asp Thr Gly Ala Ser Gly Cys His Ser His Pro Glu Glu Gln Pro Thr
 20 25 30
 Ser Ile Ser Pro Ser Arg His Gly Ala Leu Ala Glu Leu Cys Pro Pro
 35 40 45
 50 Gly Gly Ser His Arg Met Ala Leu Gly Thr Ala Ala Ala Leu Gly Ser
 50 55 60
 Asn Val Ile Arg Asn Glu Gln Leu Pro Leu Gln Tyr Leu Ala Asp Val
 65 70 75 80
 Asp Thr Ser Asp Glu Ser Ile Arg Ala His Val Met Ala Ser His
 55 85 90 95
 His Ser Lys Arg Arg Gly Arg Ala Ser Ser Glu Ser Gln Gly Leu Gly
 100 105 110
 Ala Gly Val Arg Thr Glu Ala Asp Val Xaa Glu Glu Ala Leu Arg Arg
 115 120 125
 60 Lys Leu Glu Glu Leu Thr Ser Asn Val Ser Asp Gln Glu Thr Ser Ser
 130 135 140
 Glu Glu Glu Glu Ala Lys Asp Glu Lys Ala Glu Pro Asn Arg Asp Lys
 145 150 155 160

Ser Val Gly Pro Leu Pro Gln Ala Asp Pro Glu Val Gly Thr Xaa Ala
 165 170 175
 Ile Lys Pro Thr Asp Arg Lys Lys Ala Pro Arg Thr Leu Gly Thr Pro
 180 185 190
 5 Ser Val Asn Arg Thr Thr Asp Glu Glu Leu Ser Xaa Leu Xaa Asp Arg
 195 200 205
 Xaa Ala Ile Asp Arg Leu
 210
 10 <210> 1076
 <211> 111
 <212> PRT
 <213> Homo sapiens
 15 <400> 1076
 Pro Ala Thr Ser Val Thr Arg Arg Pro Arg Pro Arg Arg Arg Lys Pro
 1 5 10 15
 Arg Thr Lys Arg Gln Ser Pro Thr Gly Thr Asn Gln Leu Gly Leu Ser
 20 25 30
 Pro Arg Arg Thr Arg Arg Trp Ala Arg Xaa Pro Ser Asn Gln Gln Thr
 35 40 45
 Gly Lys Lys Pro Pro Gly Pro Trp Gly Pro Arg Gln Ser Thr Gly Pro
 50 55 60
 Gln Met Arg Ser Cys Gln Xaa Trp Xaa Thr Xaa Trp Gln Leu Thr Gly
 65 70 75 80
 25 Phe Lys Ser Xaa Thr Gly Lys Xaa Ser Xaa Val Phe Xaa Thr Phe Glu
 85 90 95
 Xaa Lys Asp Cys Asn Pro Leu Arg Ala Pro Arg Ala Ser Thr Gly
 100 105 110
 30 <210> 1077
 <211> 236
 <212> PRT
 <213> Homo sapiens
 35 <400> 1077
 Ala Phe Leu Ala Ser Leu Glu Arg Gly Arg Arg Ile Ile Asp Arg Thr
 1 5 10 15
 Leu Arg Thr Leu Gly Pro Ser Asp Met Phe Pro Ala Glu Val Ala Trp
 40 20 25 30
 Ser Leu Ser Leu Cys Gly Asp Leu Gly Leu Pro Leu Asp Met Val Glu
 35 40 45
 Leu Met Leu Glu Glu Lys Gly Val Gln Leu Asp Ser Ala Gly Leu Glu
 50 55 60
 45 Arg Leu Ala Gln Glu Glu Ala Gln His Arg Ala Arg Gln Ala Glu Pro
 65 70 75 80
 Val Gln Lys Gln Gly Leu Trp Leu Asp Val His Ala Leu Gly Glu Leu
 85 90 95
 Gln Arg Gln Gly Val Pro Pro Thr Asp Asp Ser Pro Lys Tyr Asn Tyr
 100 105 110
 50 Ser Leu Arg Pro Ser Gly Ser Tyr Glu Phe Gly Thr Cys Glu Ala Gln
 115 120 125
 Val Leu Gln Leu Tyr Thr Glu Asp Gly Thr Ala Val Ala Ser Val Gly
 130 135 140
 55 Lys Gly Gln Arg Cys Gly Leu Leu Leu Asp Arg Thr Asn Phe Tyr Ala
 145 150 155 160
 Glu Gln Gly Gly Gln Ala Ser Asp Arg Gly Tyr Leu Val Arg Ala Gly
 165 170 175
 Gln Glu Asp Val Leu Phe Pro Val Ala Arg Ala Gln Val Cys Gly Gly
 180 185 190
 60 Phe Ile Leu His Glu Ala Ile Xaa Pro Glu Cys Leu Arg Leu Gly Asp
 195 200 205
 Gln Val Gln Leu His Val Asp Xaa Ala Trp Arg Leu Ser Cys Met Ala
 4//

	210		215		220
	Lys His Thr Gly Thr His	Leu Ala Glu Leu Gly Thr			
	225	230	235		

5 <210> 1078
 <211> 125
 <212> PRT
 <213> Homo sapiens

10 <400> 1078
 Thr Pro Leu Asp Trp Ser Gly Trp Pro Lys Arg Arg Pro Ser Thr Gly
 1 5 10 15
 His Gly Arg Leu Ser Gln Phe Arg Ser Arg Asp Cys Gly Leu Met Ser
 20 25 30
 15 Met Arg Leu Gly Ser Cys Ser Ala Lys Glu Cys Pro Gln Leu Thr Thr
 35 40 45
 Ala Pro Ser Thr Thr Thr Pro Cys Asp Pro Ala Glu Val Met Ser Ser
 50 55 60
 Ala Pro Val Arg Pro Arg Cys Cys Asn Cys Ile Gln Arg Thr Gly Gln
 20 65 70 75 80
 Gln Trp Pro Pro Trp Gly Lys Ala Ser Ala Val Ala Ser Ser Trp Thr
 85 90 95
 Gly Pro Thr Ser Thr Gln Asn Arg Gly Ala Arg Leu Gln Thr Val Ala
 100 105 110
 25 Thr Trp Cys Gly Gln Gly Lys Arg Thr Cys Cys Ser Gln
 115 120 125

 <210> 1079
 <211> 180
 <212> PRT
 <213> Homo sapiens

30 <400> 1079
 Asn Leu His Arg Pro Gly Pro Gly Leu Leu Gly Thr Ala Arg Pro Leu
 1 5 10 15
 Ala Leu Pro Ala Pro Gly Ser His Gly Leu Lys Pro Gly Pro Pro Val
 20 25 30
 Leu Arg Arg Ser Trp Ser Cys Pro Arg Gly Gly His Ser Ala Gly Leu
 35 40 45
 40 Ser Pro Arg Arg Pro Leu Leu Ser Arg Pro Leu Tyr Thr Val Ala Thr
 50 55 60
 Pro Gly Pro His Arg Cys Arg Thr His Asn Phe Arg Trp Val Ala Gly
 65 70 75 80
 Ser Ser Cys Thr Trp Gly Cys Arg Gln Leu Gly Ala Leu Leu Gly Ala
 45 85 90 95
 Ala Ala Pro Gln Ala His Gly His Gln Ala Thr Ile Pro Ala Ser Glu
 100 105 110
 Leu Ala Gln Pro Ala Val Pro Gly Ala Gly Pro Pro Leu Gly Pro Thr
 115 120 125
 50 Ala Pro Val Gln Arg Ser Leu Ala Gly Pro Leu Ser Pro Pro Ala Ser
 130 135 140
 Ala Leu Pro Cys Pro Arg Gly Val Pro Gly Leu His Thr Val Thr Arg
 145 150 155 160
 Thr Arg Pro Leu Gln Gly Thr Tyr Leu Lys Ala Pro Gly Ser Ser
 55 165 170 175
 Glu Ser Asp Gln
 180

 <210> 1080
 <211> 137
 <212> PRT
 <213> Homo sapiens

60

<400> 1080
 Thr Arg Ala Pro Xaa Ala Thr Xaa Trp Gly Phe Xaa Ile Gln Ala Pro
 1 5 10 15
 5 Gln Gly Pro Met Xaa Lys Xaa Phe Leu Leu Cys Pro Phe Gln Gly Xaa
 20 25 30
 Pro Arg Val Pro Ile Ala Pro Pro Phe His Asn Xaa Arg Ala Trp Gly
 35 40 45
 Thr Gly Lys Cys Ser Lys Pro Pro Ile Gly Gly Pro Arg Ala Trp Gly
 50 55 60
 10 Xaa Xaa Lys Trp Trp Ala Gln Gly Pro Gly Lys His Leu Xaa Asp Xaa
 65 70 75 80
 Gly Lys Leu Ala Leu Gln Tyr Ser Pro Lys Pro Met Xaa Ser Ser Gln
 85 90 95
 15 Leu Leu Thr Gln Val Arg Pro Arg Asp Pro Thr Trp Thr Lys Gly Asn
 100 105 110
 Ala Arg Ser Pro Glu Gly Ala Ser Arg Thr Phe Pro His Ala Glu Ala
 115 120 125
 Arg Thr Arg Gly Trp Arg Pro Ser Ser
 130 135
 20
 <210> 1081
 <211> 235
 <212> PRT
 <213> Homo sapiens
 25
 <400> 1081
 Ala Leu Asp Cys Asn Ser Glu Glu Asn Asn Phe Leu Thr Arg Glu Asn
 1 5 10 15
 30 Gly Glu Pro Asp Ala Phe Asp Glu Leu Phe Asp Ala Asp Gly Asp Gly
 20 25 30
 Glu Ser Tyr Thr Glu Glu Ala Asp Asp Gly Glu Thr Gly Glu Thr Arg
 35 40 45
 Asp Glu Lys Glu Asn Leu Ala Thr Leu Phe Gly Asp Met Glu Asp Leu
 50 55 60
 35 Thr Asp Glu Glu Glu Val Pro Ala Ser Gln Ser Thr Glu Asn Arg Val
 65 70 75 80
 Leu Pro Ala Pro Ala Pro Arg Arg Glu Lys Thr Asn Glu Glu Leu Gln
 85 90 95
 40 Glu Glu Leu Arg Asn Leu Gln Glu Gln Met Lys Ala Leu Gln Glu Gln
 100 105 110
 Leu Lys Val Thr Thr Ile Lys Gln Thr Ala Ser Pro Ala Arg Leu Gln
 115 120 125
 Lys Ser Pro Val Glu Lys Ser Pro Arg Pro Pro Leu Lys Glu Arg Arg
 130 135 140
 45 Val Gln Arg Ile Gln Glu Ser Thr Cys Phe Ser Ala Glu Leu Asp Val
 145 150 155 160
 Pro Ala Leu Pro Arg Thr Lys Arg Val Ala Arg Thr Pro Lys Ala Ser
 165 170 175
 50 Pro Pro Asp Pro Lys Ser Ser Ser Ser Arg Met Thr Ser Ala Pro Ser
 180 185 190
 Gln Pro Leu Gln Thr Ile Ser Arg Asn Lys Pro Ser Gly Ile Leu Glu
 195 200 205
 Val Lys Leu Xaa Gly Thr Pro Arg Lys Xaa Leu Gly Lys Arg Leu Xaa
 210 215 220
 55 Pro Ile Cys Val Glu Thr Phe Xaa Trp Ser Trp
 225 230 235
 <210> 1082
 <211> 72
 <212> PRT
 <213> Homo sapiens
 60
 <400> 1082

Val Glu Asn Gln Val Ile Ile Val Phe Ser Lys Leu Ser Val Asp Asp
 1 5 10 15
 Cys Ile Thr Ser Phe Thr Glu Val Phe Ala Gln Lys Leu Glu Gly Lys
 20 25 30
 5 Gln Arg Ala Met Phe Leu Tyr Leu Val Ile Glu Cys Ser Leu Leu
 35 40 45
 Tyr His Asn Lys Ile Leu Val Phe Ile Arg Thr Pro Arg Gly Lys Arg
 50 55 60
 Ile Trp Leu Asn Ser His Ser Arg
 10 65 70

<210> 1083

<211> 52

<212> PRT

15 <213> Homo sapiens

<400> 1083

Gly Thr Lys Asn Ser Pro Glu Thr Lys Xaa Xaa Ala Arg Xaa Leu Xaa
 1 5 10 15
 20 Ala Leu Pro Thr Lys Met Xaa Asn Gly Asp Gly Asn Val Lys Gly Lys
 20 25 30
 Xaa Leu Gly Pro Lys Asp Arg Arg Xaa Lys Phe Trp Phe Xaa Lys Xaa
 35 40 45
 Arg Arg Pro Cys
 25 50

<210> 1084

<211> 242

<212> PRT

30 <213> Homo sapiens

<400> 1084

Gln Arg Glu Arg Ala Arg Pro Ser Gly Ala Arg Arg Met Tyr Asp Asn
 1 5 10 15
 35 Met Ser Thr Met Val Tyr Ile Lys Glu Asp Lys Leu Glu Lys Leu Thr
 20 25 30
 Gln Asp Glu Ile Ile Ser Lys Thr Lys Gln Val Ile Gln Gly Leu Glu
 35 40 45
 Ala Leu Lys Asn Glu His Asn Ser Ile Leu Gln Ser Leu Leu Glu Thr
 40 50 55 60
 Leu Lys Cys Leu Lys Lys Asp Asp Glu Ser Asn Leu Val Glu Glu Lys
 65 70 75 80
 Ser Asn Met Ile Arg Lys Ser Leu Glu Met Leu Glu Leu Gly Leu Ser
 85 90 95
 45 Glu Ala Gln Val Met Met Ala Leu Ser Asn His Leu Asn Ala Val Glu
 100 105 110
 Ser Glu Lys Gln Lys Leu Arg Ala Gln Val Arg Arg Leu Cys Gln Glu
 115 120 125
 Asn Gln Trp Leu Arg Asp Glu Leu Ala Asn Thr Gln Gln Lys Leu Gln
 50 130 135 140
 Lys Ser Glu Gln Ser Val Ala Gln Leu Glu Glu Glu Lys Lys His Leu
 145 150 155 160
 Glu Phe Met Asn Gln Leu Lys Lys Tyr Asp Asp Ile Ser Pro Ser
 165 170 175
 55 Glu Asp Lys Asp Thr Asp Ser Thr Lys Glu Pro Leu Asp Asp Leu Phe
 180 185 190
 Pro Asn Asp Glu Asp Asp Pro Gly Gln Gly Ile Gln Gln Gln His Ser
 195 200 205
 Ser Ala Ala Ala Ala Ala Thr Gly Arg Xaa Arg Xaa Pro Arg Ala Gly
 60 210 215 220
 Xaa Asp Ala Pro Gln Pro Gly Asp Pro Val Pro Leu Ala Arg Ala Pro
 225 230 235 240
 Thr Arg

5 <210> 1085
 <211> 107
 <212> PRT
 <213> Homo sapiens

<400> 1085
 10 Gln Arg Glu Arg Ala Arg Pro Ser Gly Ala Arg Arg Met Tyr Asp Asn
 1 5 10 15
 Met Ser Thr Met Val Tyr Ile Lys Glu Asp Lys Leu Glu Lys Leu Thr
 20 25 30
 Gln Asp Glu Ile Ile Ser Lys Thr Lys Gln Val Ile Gln Gly Leu Glu
 35 40 45
 15 Ala Leu Lys Asn Glu His Asn Tyr Ile Leu Gln Ser Leu Leu Xaa Thr
 50 55 60
 Xaa Xaa Cys Leu Lys Lys Asp Asp Glu Ser Asn Phe Gly Gly Gly Glu
 65 70 75 80
 20 Ile Lys His Asp Arg Lys Ser Leu Xaa Met Phe Gly Ala Xaa Leu Xaa
 85 90 95
 Xaa Ala Gln Val Met Met Xaa Phe Ser Asn Tyr
 100 105

25 <210> 1086
 <211> 159
 <212> PRT
 <213> Homo sapiens

<400> 1086
 30 Gln Arg Glu Arg Ala Arg Pro Ser Gly Ala Arg Arg Met Tyr Asp Asn
 1 5 10 15
 Met Ser Thr Met Val Tyr Ile Lys Glu Asp Lys Leu Glu Lys Leu Thr
 20 25 30
 35 Gln Asp Glu Ile Ile Ser Lys Thr Lys Gln Val Ile Gln Gly Leu Glu
 35 40 45
 Ala Leu Lys Asn Glu His Asn Ser Ile Leu Gln Ser Leu Leu Glu Thr
 50 55 60
 Leu Lys Cys Leu Lys Lys Asp Asp Glu Ser Asn Leu Val Glu Glu Lys
 65 70 75 80
 40 Ser Asn Met Ile Arg Lys Ser Leu Glu Met Leu Glu Leu Gly Leu Ser
 85 90 95
 Glu Ala Gln Val Met Met Ala Leu Ser Asn His Leu Asn Ala Val Glu
 100 105 110
 Ser Glu Lys Gln Lys Leu Arg Ala Gln Val Arg Arg Leu Cys Gln Glu
 115 120 125
 45 Asn Gln Trp Leu Pro Asp Glu Leu Ala His Thr His Xaa Asn Cys Arg
 130 135 140
 Lys Met Thr Ile Cys Gly Leu Thr Gly Gly Gly Glu Lys Thr Ser
 145 150 155

50 <210> 1087
 <211> 132
 <212> PRT
 <213> Homo sapiens

55 <400> 1087
 Gln Arg Glu Arg Ala Arg Pro Ser Gly Ala Arg Arg Met Tyr Asp Asn
 1 5 10 15
 60 Met Ser Thr Met Val Tyr Ile Lys Glu Asp Lys Leu Glu Lys Leu Thr
 20 25 30
 Gln Asp Glu Ile Ile Ser Lys Thr Lys Gln Val Ile Gln Gly Leu Glu
 35 40 45
 Ala Leu Lys Asn Glu His Asn Ser Ile Leu Gln Ser Leu Leu Glu Thr

[illegible]

15 <210> 1088
 <211> 198
 <212> PRT
 <213> Homo sapiens

[illegible]

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      <210> 1089
      <211> 96
      <212> PRT
      <213> Homo sapiens

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		<400> 1089															
		Gln	Arg	Glu	Arg	Ala	Arg	Pro	Ser	Gly	Ala	Arg	Arg	Met	Tyr	Asp	Asn
		1				5					10					15	
55		Met	Ser	Thr	Met	Val	Tyr	Ile	Lys	Glu	Asp	Lys	Leu	Glu	Lys	Leu	Thr
					20					25					30		
		Gln	Asp	Glu	Ile	Ile	Ser	Lys	Thr	Lys	Gln	Val	Ile	Gln	Gly	Leu	Glu
				35					40						45		
		Ala	Leu	Lys	Asn	Glu	His	Asn	Ser	Ile	Leu	Gln	Ser	Leu	Leu	Glu	Thr
		50						55					60				
60		Leu	Lys	Cys	Leu	Lys	Lys	Asp	Asp	Glu	Ser	Asn	Leu	Val	Glu	Glu	Lys
		65					70					75				80	
		Ser	Asn	Met	Ile	Pro	Glu	Val	Thr	Gly	Asp	Val	Gly	Ala	Arg	Pro	Glu
						85					90					95	

24

<210> 1090
 <211> 646
 <212> PRT
 5 <213> Homo sapiens

 <400> 1090
 Ser Pro Arg Arg Glu Thr Gly Lys Glu Ser Arg Lys Ser Gln Ser Pro
 1 5 10 15
 10 Ser Pro Lys Asn Glu Ser Ala Arg Gly Arg Lys Lys Ser Arg Ser Gln
 20 25 30
 Ser Pro Lys Lys Asp Ile Ala Arg Glu Arg Arg Gln Ser Gln Ser Arg
 35 40 45
 15 Ser Pro Lys Arg Asp Thr Thr Arg Glu Ser Arg Arg Ser Glu Ser Leu
 50 55 60
 Ser Pro Arg Arg Glu Thr Ser Arg Glu Asn Lys Arg Ser Gln Pro Arg
 65 70 75 80
 Val Lys Asp Ser Ser Pro Gly Glu Lys Ser Arg Ser Gln Ser Arg Glu
 85 90 95
 20 Arg Glu Ser Asp Arg Asp Gly Gln Arg Arg Glu Arg Glu Arg Thr
 100 105 110
 Arg Lys Trp Ser Arg Ser Arg Ser His Ser Arg Ser Pro Ser Arg Cys
 115 120 125
 25 Arg Thr Lys Ser Lys Ser Ser Ser Phe Gly Arg Ile Asp Arg Asp Ser
 130 135 140
 Tyr Ser Pro Arg Trp Lys Gly Arg Trp Ala Asn Asp Gly Trp Arg Cys
 145 150 155 160
 Pro Pro Gly Asn Asp Arg Tyr Arg Lys Asn Asp Pro Xaa Lys Pro Asn
 165 170 175
 30 Glu Asn Thr Xaa Lys Glu Lys Asn Asp Ile His Leu Asp Ala Asp Asp
 180 185 190
 Pro Asn Ser Ala Asp Lys His Arg Asn Asp Cys Pro Asn Trp Ile Thr
 195 200 205
 35 Glu Lys Ile Asn Ser Gly Pro Asp Pro Arg Thr Arg Asn Pro Glu Lys
 210 215 220
 Leu Lys Glu Ser His Trp Glu Glu Asn Arg Asn Glu Asn Ser Gly Asn
 225 230 235 240
 Ser Trp Asn Lys Asn Phe Gly Ser Gly Trp Val Ser Asn Arg Gly Arg
 245 250 255
 40 Gly Arg Gly Asn Arg Gly Arg Gly Thr Tyr Arg Ser Ser Phe Ala Tyr
 260 265 270
 Lys Asp Gln Asn Glu Asn Arg Trp Gln Asn Arg Lys Pro Leu Ser Gly
 275 280 285
 45 Asn Ser Asn Ser Ser Gly Ser Glu Ser Phe Lys Phe Val Glu Gln Gln
 290 295 300
 Ser Tyr Lys Arg Lys Ser Glu Gln Glu Phe Ser Phe Asp Thr Pro Ala
 305 310 315 320
 Asp Arg Ser Gly Trp Thr Ser Ala Ser Ser Trp Ala Val Arg Lys Thr
 325 330 335
 50 Leu Pro Ala Asp Val Gln Asn Tyr Tyr Ser Arg Arg Gly Arg Asn Ser
 340 345 350
 Ser Gly Pro Gln Ser Gly Trp Met Lys Gln Glu Glu Glu Thr Ser Gly
 355 360 365
 55 Gln Asp Ser Ser Leu Lys Asp Gln Thr Asn Gln Gln Val Asp Gly Ser
 370 375 380
 Gln Leu Pro Ile Asn Met Met Gln Pro Gln Met Asn Val Met Gln Gln
 385 390 395 400
 Gln Met Asn Ala Gln His Gln Pro Met Asn Ile Phe Pro Tyr Pro Val
 405 410 415
 60 Gly Val His Ala Pro Leu Met Asn Ile Gln Arg Asn Pro Phe Asn Ile
 420 425 430
 His Pro Gln Leu Pro Leu His Leu His Thr Gly Val Pro Leu Met Gln
 435 440 445

Val Ala Thr Pro Thr Ser Val Ser Gln Gly Leu Pro Pro Pro Pro Pro
 450 455 460
 Pro Pro Pro Pro Ser Gln Gln Val Asn Tyr Ile Ala Ser Gln Pro Asp
 465 470 475 480
 5 Gly Lys Gln Leu Gln Gly Ile Pro Ser Ser Ser His Val Ser Asn Asn
 485 490 495
 Met Ser Thr Pro Val Leu Pro Ala Pro Thr Ala Ala Pro Gly Asn Thr
 500 505 510
 10 Gly Met Val Gln Gly Pro Ser Ser Gly Asn Thr Ser Ser Ser Ser His
 515 520 525
 Ser Lys Ala Ser Asn Ala Ala Val Lys Leu Ala Glu Ser Lys Val Ser
 530 535 540
 Val Ala Val Glu Ala Ser Ala Asp Ser Ser Lys Thr Asp Lys Lys Leu
 545 550 555 560
 15 Gln Ile Gln Glu Lys Ala Ala Gln Glu Val Lys Leu Ala Ile Lys Pro
 565 570 575
 Phe Tyr Gln Asn Lys Asp Ile Thr Lys Glu Glu Tyr Lys Glu Ile Val
 580 585 590
 20 Arg Lys Ala Val Asp Lys Val Cys His Ser Lys Ser Gly Glu Val Asn
 595 600 605
 Ser Thr Lys Val Ala Asn Leu Val Lys Ala Tyr Val Asp Lys Tyr Lys
 610 615 620
 Tyr Ser Arg Lys Gly Ser Gln Lys Lys Thr Leu Glu Glu Pro Val Ser
 625 630 635 640
 25 Thr Glu Lys Asn Ile Gly
 645

<210> 1091
 <211> 155
 30 <212> PRT
 <213> Homo sapiens

<400> 1091
 Arg Thr Arg Asn Pro Glu Lys Leu Lys Glu Ser His Trp Glu Glu Asn
 1 5 10 15
 Arg Asn Glu Asn Ser Gly Asn Ser Trp Asn Lys Asn Phe Gly Ser Gly
 20 25 30
 Trp Val Ser Asn Arg Gly Arg Gly Asn Arg Gly Arg Gly Thr
 35 40 45
 40 Tyr Arg Ser Ser Phe Ala Tyr Lys Asp Gln Asn Glu Asn Arg Trp Gln
 50 55 60
 Asn Arg Lys Pro Leu Ser Gly Asn Ser Asn Ser Ser Gly Ser Glu Ser
 65 70 75 80
 Phe Lys Phe Val Glu Gln Gln Ser Tyr Lys Arg Lys Ser Glu Gln Glu
 85 90 95
 45 Phe Ser Phe Asp Thr Pro Ala Asp Arg Ser Gly Trp Thr Ser Ala Ser
 100 105 110
 Ser Trp Ala Val Arg Lys Thr Leu Pro Ala Asp Val Gln Asn Tyr Tyr
 115 120 125
 50 Ser Arg Arg Gly Arg Asn Ser Ser Gly Pro Gln Ser Gly Trp Met Lys
 130 135 140
 Gln Glu Glu Glu Thr Ser Gly Arg Ile Leu Ala
 145 150 155

55 <210> 1092
 <211> 124
 <212> PRT
 <213> Homo sapiens

60 <400> 1092
 Val Lys Ser Val Cys His Ser Lys Ala Ser Asn Ala Ala Val Lys Leu
 1 5 10 15
 Ala Glu Ser Lys Val Ser Val Ala Val Glu Ala Ser Ala Asp Ser Ser

20 25 30
 Lys Thr Asp Lys Lys Leu Gln Ile Gln Glu Lys Ala Ala Gln Glu Val
 35 40 45
 5 Lys Leu Ala Ile Lys Pro Phe Tyr Gln Asn Lys Asp Ile Thr Lys Glu
 50 55 60
 Glu Tyr Lys Glu Ile Val Arg Lys Ala Val Asp Lys Val Cys His Ser
 65 70 75 80
 Lys Ser Gly Glu Val Asn Ser Thr Lys Val Ala Asn Leu Val Lys Ala
 85 90 95
 10 Tyr Val Asp Lys Tyr Lys Tyr Ser Arg Lys Gly Ser Gln Lys Lys Thr
 100 105 110
 Leu Glu Glu Pro Val Ser Thr Glu Lys Asn Ile Gly
 115 120
 15 <210> 1093
 <211> 199
 <212> PRT
 <213> Homo sapiens
 20 <400> 1093
 Ser Pro Arg Arg Glu Thr Gly Lys Glu Ser Arg Lys Ser Gln Ser Pro
 1 5 10 15
 Ser Pro Lys Asn Glu Ser Ala Arg Gly Arg Lys Lys Ser Arg Ser Gln
 20 25 30
 25 Ser Pro Lys Lys Asp Ile Ala Arg Glu Arg Arg Gln Ser Gln Ser Arg
 35 40 45
 Ser Pro Lys Arg Asp Thr Thr Arg Glu Ser Arg Arg Ser Glu Ser Leu
 50 55 60
 Ser Pro Arg Arg Glu Thr Ser Arg Glu Asn Lys Arg Ser Gln Pro Arg
 65 70 75 80
 30 Val Lys Asp Ser Ser Pro Gly Glu Lys Ser Arg Ser Gln Ser Arg Glu
 85 90 95
 Arg Glu Ser Asp Arg Asp Gly Gln Arg Arg Glu Arg Glu Arg Thr
 100 105 110
 35 Arg Lys Trp Ser Arg Ser Arg Ser His Ser Arg Ser Pro Ser Arg Cys
 115 120 125
 Arg Thr Lys Ser Lys Ser Ser Ser Phe Gly Arg Ile Asp Arg Asp Ser
 130 135 140
 Tyr Ser Pro Arg Trp Lys Gly Arg Trp Ala Asn Asp Gly Trp Arg Cys
 145 150 155 160
 40 Pro Pro Gly Asn Asp Arg Tyr Arg Lys Asn Asp Pro Xaa Lys Pro Asn
 165 170 175
 Glu Asn Thr Xaa Lys Glu Lys Asn Asp Ile His Leu Asp Ala Asp Asp
 180 185 190
 45 Pro Asn Ser Cys Gly Lys His
 195
 <210> 1094
 <211> 225
 50 <212> PRT
 <213> Homo sapiens
 <400> 1094
 Asn Asp Ile His Leu Asp Ala Asp Asp Pro Asn Ser Ala Asp Lys His
 1 5 10 15
 Arg Asn Asp Cys Pro Asn Trp Ile Thr Glu Lys Ile Asn Ser Gly Pro
 20 25 30
 Asp Pro Arg Thr Arg Asn Pro Glu Lys Leu Lys Glu Ser His Trp Glu
 35 40 45
 60 Glu Asn Arg Asn Glu Asn Ser Gly Asn Ser Trp Asn Lys Asn Phe Gly
 50 55 60
 Ser Gly Trp Val Ser Asn Arg Gly Arg Gly Arg Gly Asn Arg Gly Arg
 65 70 75 80

Gly Thr Tyr Arg Ser Ser Phe Ala Tyr Lys Asp Gln Asn Glu Asn Arg
 85 90 95
 Trp Gln Asn Arg Lys Pro Leu Ser Gly Asn Ser Asn Ser Ser Gly Ser
 100 105 110
 5 Glu Ser Phe Lys Phe Val Glu Gln Gln Ser Tyr Lys Arg Lys Ser Glu
 115 120 125
 Gln Glu Phe Ser Phe Asp Thr Pro Ala Asp Arg Ser Gly Trp Thr Ser
 130 135 140
 Ala Ser Ser Trp Ala Val Arg Lys Thr Leu Pro Ala Asp Val Gln Asn
 10 145 150 155 160
 Tyr Tyr Ser Arg Arg Gly Arg Asn Ser Ser Gly Pro Gln Ser Gly Trp
 165 170 175
 Met Lys Gln Glu Glu Glu Thr Ser Gly Gln Asp Ser Ser Leu Lys Asp
 180 185 190
 15 Gln Thr Asn Gln Gln Val Asp Gly Ser Gln Leu Pro Ile Asn Met Met
 195 200 205
 Gln Pro Ala Asn Glu Cys Asn Ala Ala Gln Met Asn Ala His Thr Ser
 210 215 220
 Leu
 20 225

<210> 1095

<211> 246

<212> PRT

25 <213> Homo sapiens

<400> 1095

Thr Leu Gly Leu Lys Thr Ser Gly Gln Asp Ser Ser Leu Lys Asp Gln
 1 5 10 15
 30 Thr Asn Gln Gln Val Asp Gly Ser Gln Leu Pro Ile Asn Met Met Gln
 20 25 30
 Pro Gln Met Asn Val Met Gln Gln Met Asn Ala Gln His Gln Pro
 35 40 45
 35 Met Asn Ile Phe Pro Tyr Pro Val Gly Val His Ala Pro Leu Met Asn
 50 55 60
 Ile Gln Arg Asn Pro Phe Asn Ile His Pro Gln Leu Pro Leu His Leu
 65 70 75 80
 His Thr Gly Val Pro Leu Met Gln Val Ala Thr Pro Thr Ser Val Ser
 85 90 95
 40 Gln Gly Leu Pro Pro Pro Pro Pro Pro Pro Pro Ser Gln Gln Val
 100 105 110
 Asn Tyr Ile Ala Ser Gln Pro Asp Gly Lys Gln Leu Gln Gly Ile Pro
 115 120 125
 45 Ser Ser Ser His Val Ser Asn Asn Met Ser Thr Pro Val Leu Pro Ala
 130 135 140
 Pro Thr Ala Ala Pro Gly Asn Thr Gly Met Val Gln Gly Pro Ser Ser
 145 150 155 160
 Gly Asn Thr Ser Ser Ser Ser His Ser Lys Ala Ser Asn Ala Ala Val
 165 170 175
 50 Lys Leu Ala Glu Ser Lys Val Ser Val Ala Val Glu Ala Ser Ala Asp
 180 185 190
 Ser Ser Lys Thr Asp Lys Lys Leu Gln Ile Gln Glu Lys Ala Ala Gln
 195 200 205
 55 Glu Val Lys Leu Ala Ile Lys Pro Phe Tyr Gln Asn Lys Asp Ile Thr
 210 215 220
 Lys Glu Glu Tyr Lys Glu Ile Val Arg Lys Ala Val Xaa Lys Val Gly
 225 230 235 240
 Ile Xaa Arg Val Glu Lys
 245

60

<210> 1096

<211> 214

<212> PRT

<213> Homo sapiens

<400> 1096

5 Lys Lys Val Phe L u Pro Thr Ser Leu Cys Ile Ser Tyr Gly Gln Trp
 1 5 10 15
 Met Glu Glu Lys Lys Glu Gln Met Glu Arg Asp Gly Cys Ser Glu Gln
 20 25 30
 Glu Ser Gln Pro Cys Ala Phe Ile Gly Ile Gly Asn Ser Asp Gln Glu
 35 40 45
 10 Met Gln Gln Leu Asn Leu Glu Gly Lys Asn Tyr Cys Thr Ala Lys Thr
 50 55 60
 Leu Tyr Ile Ser Asp Ser Asp Lys Arg Lys His Phe Met Leu Ser Val
 65 70 75 80
 15 Lys Met Phe Tyr Gly Asn Ser Asp Asp Ile Gly Val Phe Leu Ser Lys
 85 90 95
 Arg Ile Lys Val Ile Ser Lys Pro Ser Lys Lys Lys Gln Ser Leu Lys
 100 105 110
 Asn Ala Asp Leu Cys Ile Ala Ser Gly Thr Lys Val Ala Leu Phe Asn
 115 120 125
 20 Arg Leu Arg Ser Gln Thr Val Ser Thr Arg Tyr Leu His Val Glu Gly
 130 135 140
 Gly Asn Phe His Ala Ser Ser Gln Gln Trp Gly Ala Phe Phe Ile His
 145 150 155 160
 Leu Leu Asp Asp Asp Glu Ser Glu Gly Glu Glu Phe Thr Val Arg Asp
 165 170 175
 25 Gly Tyr Ile His Tyr Gly Gln Thr Val Lys Leu Val Cys Ser Val Thr
 180 185 190
 Gly Met Ala Leu Pro Arg Leu Ile Ile Arg Lys Val Asp Lys Xaa Thr
 195 200 205
 30 Ala Leu Phe Gly Cys Arg
 210

<210> 1097

<211> 214

35 <212> PRT

<213> Homo sapiens .

<400> 1097

40 Lys Lys Val Phe Leu Pro Thr Ser Leu Cys Ile Ser Tyr Gly Gln Trp
 1 5 10 15
 Met Glu Glu Lys Lys Glu Gln Met Glu Arg Asp Gly Cys Ser Glu Gln
 20 25 30
 Glu Ser Gln Pro Cys Ala Phe Ile Gly Ile Gly Asn Ser Asp Gln Glu
 35 40 45
 45 Met Gln Gln Leu Asn Leu Glu Gly Lys Asn Tyr Cys Thr Ala Lys Thr
 50 55 60
 Leu Tyr Ile Ser Asp Ser Asp Lys Arg Lys His Phe Met Leu Ser Val
 65 70 75 80
 50 Lys Met Phe Tyr Gly Asn Ser Asp Asp Ile Gly Val Phe Leu Ser Lys
 85 90 95
 Arg Ile Lys Val Ile Ser Lys Pro Ser Lys Lys Lys Gln Ser Leu Lys
 100 105 110
 Asn Ala Asp Leu Cys Ile Ala Ser Gly Thr Lys Val Ala Leu Phe Asn
 115 120 125
 55 Arg Leu Arg Ser Gln Thr Val Ser Thr Arg Tyr Leu His Val Glu Gly
 130 135 140
 Gly Asn Phe His Ala Ser Ser Gln Gln Trp Gly Ala Phe Phe Ile His
 145 150 155 160
 Leu Leu Asp Asp Asp Glu Ser Glu Gly Glu Glu Phe Thr Val Arg Asp
 165 170 175
 60 Gly Tyr Ile His Tyr Gly Gln Thr Val Lys Leu Val Cys Ser Val Thr
 180 185 190
 Gly Met Ala Leu Pro Arg Leu Ile Ile Arg Lys Val Asp Lys Xaa Thr

422

His Leu Leu Asp Asp Asp Glu Ser Glu Gly Glu Glu Phe Thr Val Pro
 180 185 190
 Arg Trp Leu His Pro Leu Trp Thr Asn Ser Gln Thr Cys Val Leu Ser
 195 200 205
 5 Tyr Trp His Gly Leu Pro Lys Ile Asp Asn
 210 215
 <210> 1100
 <211> 201
 10 <212> PRT
 <213> Homo sapiens
 <400> 1100
 Val Val Gln Ala Gly Val Phe Gly Arg Ala Trp Glu His Lys Ser Leu
 15 1 5 10 15
 Phe His His Val Ser Arg Thr Ser His Ser Gly Pro Gly Leu Val Ala
 20 20 25 30
 Lys Met Val Lys Pro Lys Tyr Lys Gly Arg Ser Thr Ile Asn Pro Ser
 35 40 45
 20 Lys Ala Ser Thr Asn Pro Asp Arg Val Gln Gly Ala Gly Gly Gln Asn
 50 55 60
 Met Arg Asp Arg Ala Thr Ile Arg Arg Leu Asn Met Tyr Arg Gln Lys
 65 70 75 80
 25 Glu Arg Arg Asn Ser Arg Gly Lys Ile Ile Lys Pro Leu Gln Tyr Gln
 85 90 95
 Ser Thr Val Ala Ser Gly Thr Val Ala Arg Val Glu Pro Asn Ile Lys
 100 105 110
 Trp Phe Gly Asn Thr Arg Val Ile Lys Gln Ser Ser Leu Gln Lys Phe
 115 120 125
 30 Gln Glu Glu Met Asp Thr Val Met Lys Asp Pro Tyr Lys Val Val Met
 130 135 140
 Lys Gln Ser Lys Leu Pro Met Ser Leu Leu His Asp Arg Ile Arg Pro
 145 150 155 160
 35 His Asn Leu Lys Gly His Ile Leu Asp Thr Glu Ser Phe Glu Thr Thr
 165 170 175
 Phe Gly Pro Xaa Ser Gln Lys Glu Thr Asp Gln Thr Tyr Phe Ala Ser
 180 185 190
 Asp Met Gln Ser Leu Ile Glu Asn Ala
 195 200
 40 <210> 1101
 <211> 210
 <212> PRT
 <213> Homo sapiens
 45 <400> 1101
 Ala Gly Xaa Phe Gly Arg Ala Trp Glu His Lys Ser Leu Phe His His
 1 5 10 15
 Val Ser Arg Thr Ser His Ser Gly Pro Gly Leu Val Ala Lys Met Val
 20 25 30
 Lys Pro Lys Tyr Lys Gly Arg Ser Thr Ile Asn Pro Ser Lys Ala Ser
 35 40 45
 Thr Asn Pro Asp Arg Val Gln Gly Ala Gly Gly Gln Asn Met Arg Asp
 50 55 60
 55 Arg Ala Thr Ile Arg Arg Leu Asn Met Tyr Arg Gln Lys Glu Arg Arg
 65 70 75 80
 Asn Ser Arg Gly Lys Ile Ile Lys Pro Leu Gln Tyr Gln Ser Thr Val
 85 90 95
 Ala Ser Gly Thr Val Ala Arg Val Glu Pro Asn Ile Lys Trp Phe Gly
 100 105 110
 60 Asn Thr Arg Val Ile Lys Gln Ser Ser Leu Gln Lys Phe Gln Glu Glu
 115 120 125
 Met Asp Thr Val Met Lys Asp Pro Tyr Lys Val Val Met Lys Gln Ser

130 135 140
 Lys Leu Pro Met Ser Leu Leu His Asp Arg Ile Arg Pro His Asn Leu
 145 150 155 160
 Lys Val His Ile Leu Asp Thr Glu Ser Phe Glu Thr Thr Phe Gly Pro
 5 165 170 175
 Lys Ser Gln Arg Lys Arg Pro Asn Leu Phe Ala Ser Asp Met Gln Ser
 180 185 190
 Leu Ile Glu Asn Ala Glu Met Ser Thr Glu Ser Tyr Asp Pro Gly Gln
 195 200 205
 10 Gly Ser
 210

 <210> 1102
 <211> 232
 15 <212> PRT
 <213> Homo sapiens

 <400> 1102
 Arg Val Gln Ile Pro Ser Phe Lys Glu Asp Xaa Arg Gly Pro Xaa Xaa
 20 1 5 10 15
 Val Arg Leu Pro Gln Xaa Cys Gly Arg Phe Phe His Glu Ser Xaa Asp
 20 25 30
 Phe Gly Lys Ile Gln Xaa Xaa Pro Gln Phe Phe Gly Asn Asp Leu Val
 35 40 45
 25 Xaa Val Xaa Val Ser Asp Leu Glu Lys Glu Leu Glu Ser Phe Phe Leu
 50 55 60
 Met Lys Arg Arg Arg Asn Arg Ser Thr Lys Glu Met Met Arg Glu Glu
 65 70 75 80
 Ser Ser Ser Glu Pro Glu Glu Glu Asn Val Gly Asn Asp Thr Lys Ala
 85 90 95
 30 Val Ile Lys Ala Leu Asp Glu Lys Ile Val Lys Tyr Gln Lys Phe Leu
 100 105 110
 Asp Lys Ala Lys Ala Lys Lys Phe Ser Ala Val Arg Ile Ser Lys Gly
 115 120 125
 35 Leu Ser Glu Lys Ile Phe Ala Lys Pro Glu Glu Gln Arg Lys Thr Leu
 130 135 140
 Glu Glu Asp Val Asp Asp Arg Xaa Pro Ser Lys Lys Lys Arg
 145 150 155 160
 Lys Ala Gln Arg Glu Glu Glu Gln Glu His Ser Asn Lys Ala Pro Arg
 165 170 175
 40 Ala Leu Thr Ser Lys Glu Arg Arg Arg Ala Val Arg Gln Gln Arg Pro
 180 185 190
 Lys Lys Val Gly Val Arg Tyr Tyr Glu Thr His Asn Val Lys Asn Arg
 195 200 205
 45 Asn Arg Asn Lys Lys Lys Thr Asn Asp Ser Glu Gly Gln Lys His Lys
 210 215 220
 Arg Lys Lys Phe Arg Gln Lys Gln
 225 230

 50 <210> 1103
 <211> 210
 <212> PRT
 <213> Homo sapiens

 55 <400> 1103
 Trp Ala Thr Lys Arg Trp Val Ala Val Leu Ser Gln Asp Tyr Pro Thr
 1 5 10 15
 Leu Ala Phe His Ala Ser Leu Thr Asn Pro Phe Gly Lys Gly Ala Phe
 20 25 30
 60 Ile Gln Leu Leu Arg Gln Phe Gly Lys Leu His Thr Asp Lys Lys Gln
 35 40 45
 Ile Ser Val Gly Phe Ile Gly Tyr Pro Asn Val Gly Lys Ser Ser Val
 50 55 60

Ile Asn Thr Leu Arg Ser Lys Lys Val Cys Asn Val Ala Pro Ile Ala
 65 70 75 80
 Gly Glu Thr Lys Val Trp Gln Tyr Ile Thr Leu Met Arg Arg Ile Phe
 85 90 95
 5 Leu Il Asp Cys Pro Gly Val Val Tyr Pro Ser Glu Asp Ser Glu Thr
 100 105 110
 Asp Ile Val Leu Lys Gly Val Val Gln Val Glu Lys Ile Lys Ser Pro
 115 120 125
 10 Glu Asp His Ile Gly Ala Val Leu Glu Arg Ala Lys Pro Glu Tyr Ile
 130 135 140
 Ser Lys Thr Tyr Lys Ile Asp Ser Trp Glu Asn Ala Glu Asp Phe Leu
 145 150 155 160
 Glu Lys Leu Ala Phe Arg Thr Gly Lys Leu Leu Lys Gly Gly Glu Pro
 165 170 175
 15 Asp Leu Gln Thr Val Gly Lys Met Val Leu Asn Asp Trp Gln Lys Gly
 180 185 190
 Arg Ile Xaa Phe Phe Val Lys Pro Pro Asn Ala Glu Pro Leu Trp Ala
 195 200 205
 20 Pro Thr
 210

<210> 1104

<211> 210

<212> PRT

25 <213> Homo sapiens

<400> 1104

Val Gln Ala Gly Val Phe Gly Arg Ala Trp Glu His Lys Ser Leu Phe
 1 5 10 15
 30 His His Val Ser Arg Thr Ser His Ser Gly Pro Gly Leu Val Ala Lys
 20 25 30
 Met Val Lys Pro Lys Tyr Lys Gly Arg Ser Thr Ile Asn Pro Ser Lys
 35 40 45
 35 Ala Ser Thr Asn Pro Asp Arg Val Gln Gly Ala Gly Gly Gln Asn Met
 50 55 60
 Arg Asp Arg Ala Thr Ile Arg Arg Leu Asn Met Tyr Arg Gln Lys Glu
 65 70 75 80
 Arg Arg Asn Ser Arg Gly Lys Ile Ile Lys Pro Leu Gln Tyr Gln Ser
 85 90 95
 40 Thr Val Ala Ser Gly Thr Val Ala Arg Val Glu Pro Asn Ile Lys Trp
 100 105 110
 Phe Gly Asn Thr Arg Val Ile Lys Gln Ser Ser Leu Gln Lys Phe Gln
 115 120 125
 45 Glu Glu Met Asp Thr Val Met Lys Asp Pro Tyr Lys Val Val Met Lys
 130 135 140
 Gln Ser Lys Leu Pro Met Ser Leu Leu His Asp Arg Ile Arg Pro His
 145 150 155 160
 Asn Leu Lys Val His Ile Leu Asp Thr Glu Ser Phe Glu Thr Thr Phe
 165 170 175
 50 Gly Pro Lys Ser Arg Xaa Asn Asp Gln Thr Tyr Leu Gln Val Ile Cys
 180 185 190
 Ser Leu Leu Ser Lys Met Leu Lys Cys Pro Leu Arg Ala Met Thr Arg
 195 200 205
 55 Ala Arg
 210

<210> 1105

<211> 368

<212> PRT

60 <213> Homo sapiens

<400> 1105

Glu Ile Asp Gln Val Val Pro Ala Ala Gln Ser Ser Pro Ile Asn Cys

1 5 10 15
 Glu Lys Arg Glu Asn Leu Leu Pro Phe Val Gly Leu Asn Asn Leu Gly
 20 25 30
 5 Asn Thr Cys Tyr Leu Asn Ser Ile Leu Gln Val Leu Tyr Phe Cys Pro
 35 40 45
 Gly Phe Lys Ser Gly Val Lys His Leu Phe Asn Ile Ile Ser Arg Lys
 50 55 60
 Lys Glu Ala Leu Lys Asp Glu Ala Asn Gln Lys Asp Lys Gly Asn Cys
 65 70 75 80
 10 Lys Glu Asp Ser Leu Ala Ser Tyr Glu Leu Ile Cys Ser Leu Gln Ser
 85 90 95
 Leu Ile Ile Ser Val Glu Gln Leu Gln Ala Ser Phe Leu Leu Asn Pro
 100 105 110
 15 Glu Lys Tyr Thr Asp Glu Leu Ala Thr Gln Pro Arg Arg Leu Leu Asn
 115 120 125
 Thr Leu Arg Glu Leu Asn Pro Met Tyr Glu Gly Tyr Leu Gln His Asp
 130 135 140
 Ala Gln Glu Val Leu Gln Cys Ile Leu Gly Asn Ile Gln Glu Thr Cys
 145 150 155 160
 20 Gln Leu Leu Lys Lys Glu Glu Val Lys Asn Val Ala Glu Leu Pro Thr
 165 170 175
 Lys Val Glu Glu Ile Pro His Pro Lys Glu Glu Met Asn Gly Ile Asn
 180 185 190
 25 Ser Ile Glu Met Asp Ser Met Arg His Ser Glu Asp Phe Lys Glu Lys
 195 200 205
 Leu Pro Lys Gly Asn Gly Lys Arg Lys Ser Asp Thr Glu Phe Gly Asn
 210 215 220
 Met Lys Lys Lys Val Lys Leu Ser Lys Glu His Gln Ser Leu Glu Glu
 225 230 235 240
 30 Asn Gln Arg Gln Thr Arg Ser Lys Arg Lys Ala Thr Ser Asp Thr Leu
 245 250 255
 Glu Ser Pro Pro Lys Ile Ile Pro Lys Tyr Ile Ser Glu Asn Glu Ser
 260 265 270
 35 Pro Arg Pro Ser Gln Lys Lys Ser Arg Val Lys Ile Asn Trp Leu Lys
 275 280 285
 Ser Ala Thr Lys Gln Pro Ser Ile Leu Ser Lys Phe Cys Ser Leu Gly
 290 295 300
 Lys Ile Thr Thr Asn Gln Gly Val Lys Gly Gln Ser Lys Glu Asn Glu
 305 310 315 320
 40 Cys Asp Pro Glu Glu Asp Leu Gly Lys Cys Glu Ser Asp Asn Thr Thr
 325 330 335
 Asn Gly Cys Gly Leu Glu Ser Pro Gly Asn Thr Val Thr Pro Val Asn
 340 345 350
 45 Val Asn Glu Val Lys Pro Ile Asn Lys Gly Glu Glu Gln Ile Gly Phe
 355 360 365

<210> 1106

<211> 218

<212> PRT

50 <213> Homo sapiens

<400> 1106

55 Glu Ile Asp Gln Val Val Pro Ala Ala Gln Ser Ser Pro Ile Asn Cys
 1 5 10 15
 Glu Lys Arg Glu Asn Leu Leu Pro Phe Val Gly Leu Asn Asn Leu Gly
 20 25 30
 Asn Thr Cys Tyr Leu Asn Ser Ile Leu Gln Val Leu Tyr Phe Cys Pro
 35 40 45
 60 Gly Phe Lys Ser Gly Val Lys His Leu Phe Asn Ile Ile Ser Arg Lys
 50 55 60
 Lys Glu Ala Leu Lys Asp Glu Ala Asn Gln Lys Asp Lys Gly Asn Cys
 65 70 75 80
 Lys Glu Asp Ser Leu Ala Ser Tyr Glu Leu Ile Cys Ser Leu Gln Ser

85 90 95
 Leu Ile Ile Ser Val Glu Gln Leu Gln Ala Ser Phe Leu Leu Asn Pro
 100 105 110
 5 Glu Lys Tyr Thr Asp Glu Leu Ala Thr Gln Pro Arg Arg Leu Leu Asn
 115 120 125
 Thr Leu Arg Glu Leu Asn Pro Met Tyr Glu Gly Tyr Leu Gln His Asp
 130 135 140
 Ala Gln Glu Val Leu Gln Cys Ile Leu Gly Asn Ile Gln Glu Thr Cys
 145 150 155 160
 10 Gln Leu Leu Lys Lys Glu Glu Val Lys Asn Val Ala Glu Phe Leu Leu
 165 170 175
 Arg Xaa Lys Lys Ser Ser Ser Glu Glu Glu Met Asn Gly Leu Gln His
 180 185 190
 Xaa Asp Gly Xaa Met Xaa Leu Leu Xaa Thr Phe Lys Arg Thr Pro Lys
 15 195 200 205
 Gly Met Gly Lys Glu Lys Val Pro Trp Ile
 210 215

 <210> 1107
 20 <211> 121
 <212> PRT
 <213> Homo sapiens

 <400> 1107
 25 Leu Asn Tyr Pro Lys Arg Arg His Leu Asn Thr Trp Ile Tyr Thr Ser
 1 5 10 15
 Leu Leu Cys Leu Leu Phe Lys Ile Lys Cys Ser Tyr Leu Tyr Ser Pro
 20 25 30
 Tyr Phe Gly Val Ile Ile Tyr Met Phe Ile Val Pro Val Val Phe
 30 35 40 45
 His Pro Arg Ser Arg Ile Ser Phe Ser Thr Phe Ser Phe Ile Arg Val
 50 55 60
 Met Lys Leu Asn Pro Trp Ala Met Ser Glu Ala Gln Ser Leu Glu Cys
 65 70 75 80
 35 Val Tyr Ser Gln Trp Cys Met Tyr Ile Leu Cys Leu Asp Ser Leu Arg
 85 90 95
 Ser Val Ser Glu Asn Leu Asp Ser Ser Leu Leu His Lys Asn Phe Ile
 100 105 110
 Cys Ile Tyr Glu Asp Asp Ser Val Pro
 40 115 120

 <210> 1108
 <211> 211
 <212> PRT
 45 <213> Homo sapiens

 <400> 1108
 Glu Thr Cys Gln Leu Leu Lys Lys Glu Glu Val Lys Asn Val Ala Glu
 1 5 10 15
 50 Leu Pro Thr Lys Val Glu Glu Ile Pro His Pro Lys Glu Glu Met Asn
 20 25 30
 Gly Ile Asn Ser Ile Glu Met Asp Ser Met Arg His Ser Glu Asp Phe
 35 40 45
 Lys Glu Lys Leu Pro Lys Gly Asn Gly Lys Arg Lys Ser Asp Thr Glu
 50 55 60
 Phe Gly Asn Met Lys Lys Lys Val Lys Leu Ser Lys Glu His Gln Ser
 65 70 75 80
 Leu Glu Glu Asn Gln Arg Gln Thr Arg Ser Lys Arg Lys Ala Thr Ser
 85 90 95
 60 Asp Thr Leu Glu Ser Pro Pro Lys Ile Ile Pro Lys Tyr Ile Ser Glu
 100 105 110
 Asn Glu Ser Pro Arg Pro Ser Gln Lys Lys Ser Arg Val Lys Ile Asn
 115 120 125

Trp Leu Lys Ser Ala Thr Lys Gln Pro Ser Ile Leu Ser Lys Phe Cys
 130 135 140
 Ser Leu Gly Lys Ile Thr Thr Asn Gln Gly Val Lys Gly Gln Ser Lys
 145 150 155 160
 5 Glu Asn Glu Cys Asp Pro Glu Glu Asp Leu Gly Lys Cys Glu Ser Asp
 165 170 175
 Asn Thr Thr Asn Gly Cys Gly Leu Glu Ser Pro Gly Asn Thr Val Thr
 180 185 190
 10 Pro Val Asn Val Asn Glu Val Lys Pro Ile Asn Lys Gly Glu Glu Gln
 195 200 205
 Ile Gly Phe
 210

15 <210> 1109
 <211> 187
 <212> PRT
 <213> Homo sapiens

<400> 1109
 20 Asn Val Ala Glu Leu Pro Thr Lys Val Glu Glu Ile Pro His Pro Lys
 1 5 10 15
 Glu Glu Met Asn Gly Ile Asn Ser Ile Glu Met Asp Ser Met Arg His
 20 25 30
 Ser Glu Asp Phe Lys Glu Lys Leu Pro Lys Gly Asn Gly Lys Arg Lys
 35 40 45
 25 Ser Asp Thr Glu Phe Gly Asn Met Lys Lys Lys Val Lys Leu Ser Lys
 50 55 60
 Glu His Gln Ser Leu Glu Glu Asn Gln Arg Gln Thr Arg Ser Lys Arg
 65 70 75 80
 30 Lys Ala Thr Ser Asp Thr Leu Glu Ser Pro Pro Lys Ile Ile Pro Lys
 85 90 95
 Tyr Ile Ser Glu Asn Glu Ser Pro Arg Pro Ser Gln Lys Lys Ser Arg
 100 105 110
 Val Lys Ile Asn Trp Leu Lys Ser Ala Thr Lys Gln Pro Ser Ile Leu
 115 120 125
 35 Ser Lys Phe Cys Ser Leu Gly Lys Ile Thr Thr Asn Gln Gly Val Lys
 130 135 140
 Gly Gln Ser Lys Glu Asn Glu Cys Asp Pro Glu Glu Asp Leu Gly Lys
 145 150 155 160
 40 Cys Glu Ser Asp Asn Thr Thr Asn Gly Cys Gly Leu Glu Ser Pro Gly
 165 170 175
 Asn Thr Val Thr Pro Val Asn Val Asn Glu Ser
 180 185

45 <210> 1110
 <211> 314
 <212> PRT
 <213> Homo sapiens

<400> 1110
 50 Ile Pro Thr Glu Val Ala Ile Glu Ser Thr Pro Met Ile Leu Glu Ser
 1 5 10 15
 Ser Ile Met Ser Ser His Val Met Lys Gly Ile Asn Leu Ser Ser Gly
 20 25 30
 55 Asp Gln Asn Leu Ala Pro Glu Ile Gly Ile Gln Glu Ile Ala Leu His
 35 40 45
 Ser Gly Glu Glu Pro His Ala Glu Glu His Leu Lys Gly Asp Phe Tyr
 50 55 60
 Glu Ser Glu His Gly Ile Asn Ile Asp Leu Asn Ile Asn Asn His Leu
 65 70 75 80
 60 Ile Ala Lys Glu Met Glu His Asn Thr Val Cys Ala Ala Gly Thr Ser
 85 90 95
 Pro Val Gly Glu Ile Gly Glu Glu Lys Ile Leu Pro Thr Ser Glu Thr

100 105 110
 Lys Gln Cys Thr Val Leu Asp Thr Tyr Pro Gly Val Ser Glu Ala Asp
 115 120 125
 5 Ala Gly Glu Thr Leu Ser Ser Thr Gly Pro Phe Ala Leu Glu Pro Asp
 130 135 140
 Ala Thr Gly Thr Ser Lys Gly Ile Glu Phe Thr Thr Ala Ser Thr Leu
 145 150 155 160
 Ser Leu Val Asn Lys Tyr Asp Val Asp Leu Ser Leu Thr Thr Gln Asp
 165 170 175
 10 Thr Glu His Asp Met Val Ile Ser Thr Ser Pro Ser Gly Gly Ser Glu
 180 185 190
 Ala Asp Ile Glu Gly Pro Leu Pro Ala Lys Asp Ile His Leu Asp Leu
 195 200 205
 15 Pro Ser Asn Asn Asn Leu Val Ser Lys Asp Thr Glu Glu Pro Leu Pro
 210 215 220
 Val Lys Glu Ser Asp Gln Thr Leu Ala Ala Leu Leu Ser Pro Lys Glu
 225 230 235 240
 Ser Ser Gly Gly Glu Lys Glu Val Pro Pro Pro Pro Lys Glu Thr Leu
 245 250 255
 20 Pro Asp Ser Gly Phe Ser Ala Asn Ile Glu Asp Ile Asn Glu Ala Asp
 260 265 270
 Leu Val Arg Pro Leu Leu Pro Lys Asp Met Glu Arg Leu Thr Ser Leu
 275 280 285
 25 Lys Ser Trp His Leu Lys Asp Leu Tyr Leu Gln Val Met Phe Gly Pro
 290 295 300
 Trp Thr Arg Ser Ala Gly Gln Pro Xaa Leu
 305 310

 <210> 1111
 30 <211> 218
 <212> PRT
 <213> Homo sapiens

 <400> 1111
 35 Pro Val Gly Glu Ile Gly Glu Glu Lys Ile Leu Pro Thr Ser Glu Thr
 1 5 10 15
 Lys Gln Cys Thr Val Leu Asp Thr Tyr Pro Gly Val Ser Glu Ala Asp
 20 25 30
 40 Ala Gly Glu Thr Leu Ser Ser Thr Gly Pro Phe Ala Leu Glu Pro Asp
 35 40 45
 Ala Thr Gly Thr Ser Lys Gly Ile Glu Phe Thr Thr Ala Ser Thr Leu
 50 55 60
 Ser Leu Val Asn Lys Tyr Asp Val Asp Leu Ser Leu Thr Thr Gln Asp
 65 70 75 80
 45 Thr Glu His Asp Met Val Ile Ser Thr Ser Pro Ser Gly Gly Ser Glu
 85 90 95
 Ala Asp Ile Glu Gly Pro Leu Pro Ala Lys Asp Ile His Leu Asp Leu
 100 105 110
 50 Pro Ser Asn Asn Asn Leu Val Ser Lys Asp Thr Glu Glu Pro Leu Pro
 115 120 125
 Val Lys Glu Ser Asp Gln Thr Leu Ala Ala Leu Leu Ser Pro Lys Glu
 130 135 140
 Ser Ser Gly Gly Glu Lys Glu Val Pro Pro Pro Pro Lys Glu Thr Leu
 145 150 155 160
 55 Pro Asp Ser Gly Phe Ser Ala Asn Ile Glu Asp Ile Asn Glu Ala Asp
 165 170 175
 Leu Val Arg Pro Leu Leu Pro Lys Asp Met Glu Arg Leu Thr Ser Leu
 180 185 190
 60 Lys Ser Trp His Leu Lys Asp Leu Tyr Leu Gln Val Met Phe Gly Pro
 195 200 205
 Trp Thr Arg Ser Ala Gly Gln Pro Xaa Leu
 210 215

<210> 1112
 <211> 163
 <212> PRT
 <213> Homo sapiens

5

<400> 1112

Ile Pro Thr Glu Val Ala Ile Glu Ser Thr Pro Met Ile Leu Glu Ser
 1 5 10 15
 Ser Ile Met Ser Ser His Val Met Lys Gly Ile Asn Leu Ser Ser Gly
 20 25 30
 Asp Gln Asn Leu Ala Pro Glu Ile Gly Ile Gln Glu Ile Ala Leu His
 35 40 45
 Ser Gly Glu Glu Pro His Ala Glu Glu His Leu Lys Gly Asp Phe Tyr
 50 55 60
 Glu Ser Glu His Gly Ile Asn Ile Asp Leu Asn Ile Asn Asn His Leu
 65 70 75 80
 Ile Ala Lys Glu Met Glu His Asn Thr Val Cys Ala Ala Gly Thr Ser
 85 90 95
 Pro Val Gly Glu Ile Gly Glu Glu Lys Ile Leu Pro Thr Ser Glu Thr
 100 105 110
 Lys Gln Arg Thr Val Leu Asp Thr Tyr Pro Gly Val Ser Glu Ala Asp
 115 120 125
 Ala Gly Glu Thr Leu Ser Ser Thr Gly Pro Phe Ala Leu Glu Pro Asp
 130 135 140
 Ala Thr Gly Thr Ser Lys Gly Ile Glu Phe Thr Thr Ala Ser Thr Leu
 145 150 155 160
 Ser Leu Ser

30

<210> 1113
 <211> 332
 <212> PRT
 <213> Homo sapiens

35

<400> 1113

Ser Gly Cys Gly Ala Pro Ala Ala Gly Ala Gly Pro Arg Gly Ala Glu
 1 5 10 15
 Leu Gly Ser Gly Ala Gln Ala Val Pro Arg Gly Ala Met Lys Gly Lys
 20 25 30
 Glu Glu Lys Glu Gly Gly Ala Arg Leu Gly Ala Gly Gly Gly Ser Pro
 35 40 45
 Glu Lys Ser Pro Ser Ala Gln Glu Leu Lys Glu Gln Gly Asn Arg Leu
 50 55 60
 Phe Val Gly Arg Lys Tyr Pro Glu Ala Ala Cys Tyr Gly Arg Ala
 65 70 75 80
 Ile Thr Arg Asn Pro Leu Val Ala Val Tyr Tyr Thr Asn Arg Ala Leu
 85 90 95
 Cys Tyr Leu Lys Met Gln Gln His Glu Gln Ala Leu Ala Asp Cys Arg
 100 105 110
 Arg Ala Leu Glu Leu Asp Gly Gln Ser Val Lys Ala His Phe Phe Leu
 115 120 125
 Gly Gln Cys Gln Leu Glu Met Glu Ser Tyr Asp Glu Ala Ile Ala Asn
 130 135 140
 Leu Gln Arg Ala Tyr Ser Leu Ala Lys Glu Gln Arg Leu Asn Phe Gly
 145 150 155 160
 Asp Asp Ile Pro Ser Ala Leu Arg Ile Ala Lys Xaa Lys Arg Trp Asn
 165 170 175
 Ser Ile Glu Glu Arg Arg Ile His Gln Glu Ser Glu Leu Xaa Phe Tyr
 180 185 190
 Xaa Phe Xaa Leu Ile Ala Xaa Asp Arg Glu Arg Lys Xaa Lys Xaa Cys
 195 200 205
 Gln Gly Asn His Glu Gly Tyr Glu Asp Asp Lys Pro Arg Pro Gly Pro
 210 215 220

Ser Arg Leu Ala Leu Arg Pro Ser Thr Thr Ser Thr Trp Arg Thr Trp
 225 230 235 240
 Thr Ser Phe Phe Phe Gln Val Asp Glu Arg Gly Arg Ser Glu Thr Ser
 245 250 255
 5 Pro Thr Tyr Leu Cys Gly Lys Ile Ser Phe Glu Pro Met Arg Glu Pro
 260 265 270
 Cys Ile Thr Pro Ser Gly Ile Thr Tyr Asp Arg Lys Asp Ile Glu Glu
 275 280 285
 10 His Leu Gln Arg Val Gly His Phe Asp Pro Val Thr Arg Ser Pro Leu
 290 295 300
 Thr Gln Glu Gln Leu Ile Pro Asn Leu Ala Met Lys Glu Val Ile Asp
 305 310 315 320
 Ala Phe Ile Ser Glu Asn Gly Trp Val Glu Asp Tyr
 325 330
 15
 <210> 1114
 <211> 259
 <212> PRT
 <213> Homo sapiens
 20
 <400> 1114
 Val Thr Gln Glu Phe Thr Gln Tyr Trp Ala Gln Arg Glu Ala Asp Phe
 1 5 10 15
 Lys Glu Thr Leu Leu Gln Glu Arg Glu Ile Leu Glu Glu Asn Ala Glu
 20 25 30
 25 Arg Arg Leu Ala Ile Phe Lys Asp Leu Val Gly Lys Cys Asp Thr Arg
 35 40 45
 Glu Glu Ala Ala Lys Asp Ile Cys Ala Thr Lys Val Glu Thr Glu Glu
 50 55 60
 30 Ala Thr Ala Cys Leu Glu Leu Lys Phe Asn Gln Ile Lys Ala Glu Leu
 65 70 75 80
 Ala Lys Thr Lys Gly Glu Leu Ile Lys Thr Lys Glu Glu Leu Lys Lys
 85 90 95
 35 Arg Glu Asn Glu Ser Asp Ser Leu Ile Gln Glu Leu Glu Thr Ser Asn
 100 105 110
 Lys Lys Ile Ile Thr Gln Asn Gln Arg Ile Lys Glu Leu Ile Asn Ile
 115 120 125
 Ile Asp Gln Lys Glu Asp Thr Ile Asn Glu Phe Gln Asn Leu Lys Ser
 130 135 140
 40 His Met Glu Asn Thr Phe Lys Cys Asn Asp Lys Ala Asp Thr Ser Ser
 145 150 155 160
 Leu Ile Ile Asn Asn Lys Leu Ile Cys Asn Glu Thr Val Glu Val Pro
 165 170 175
 Lys Asp Ser Lys Ser Lys Ile Cys Ser Glu Arg Lys Arg Val Asn Glu
 180 185 190
 45 Asn Glu Leu Gln Gln Asp Glu Pro Pro Ala Lys Lys Gly Ser Ile His
 195 200 205
 Cys Ser Ser Ala Ser Leu Lys Thr Lys Arg Lys Val Glu Glu Val Arg
 210 215 220
 50 Pro Glu His Cys Arg Lys Leu Lys Thr Xaa Arg Val Leu Gln Gly Lys
 225 230 235 240
 Ile Met Lys Gly Leu Glu Ser Ile Phe Ser Ser Leu Phe Glu Asn Asp
 245 250 255
 Leu Lys Lys
 55
 <210> 1115
 <211> 204
 <212> PRT
 <213> Homo sapiens
 60
 <400> 1115
 Arg Ile Ser Asn Ser Arg Xaa Pro Ile Gly Lys Ile Leu Ser Xaa Leu

1 5 10 15
 Val Leu Lys Pro Ile Trp Glu Glu Cys Lys Glu Ile Val Lys Ala Ser
 20 25 30
 5 Ser Lys Lys Ser His Gln Ile Glu Glu Leu Glu Gln Gln Ile Glu Lys
 35 40 45
 Leu Gln Ala Glu Val Lys Gly Tyr Lys Asp Glu Asn Asn Arg Leu Lys
 50 55 60
 Glu Lys Glu His Lys Asn Gln Asp Asp Leu Leu Lys Glu Lys Glu Thr
 65 70 75 80
 10 Leu Ile Gln Gln Leu Lys Glu Glu Leu Gln Glu Lys Asn Val Thr Leu
 85 90 95
 Asp Val Gln Ile Gln His Val Val Glu Gly Lys Arg Ala Leu Ser Glu
 100 105 110
 15 Leu Thr Gln Gly Val Thr Cys Tyr Lys Ala Lys Ile Lys Glu Leu Glu
 115 120 125
 Thr Ile Leu Glu Thr Gln Lys Val Glu Cys Ser His Ser Ala Lys Leu
 130 135 140
 Glu Gln Asp Ile Leu Glu Lys Glu Ser Ile Ile Leu Lys Leu Glu Arg
 145 150 155 160
 20 Asn Leu Lys Glu Phe Gln Glu His Leu Gln Asp Ser Val Lys Asn Thr
 165 170 175
 Lys Asp Leu Asn Val Lys Glu Leu Lys Leu Lys Glu Glu Ile Thr Gln
 180 185 190
 25 Leu Thr Asn Asn Leu Gln Asp Met Lys His Leu Leu
 195 200

<210> 1116

<211> 92

<212> PRT

30 <213> Homo sapiens

<400> 1116

Val Gln Leu Ser Gln Glu Lys Arg Tyr Thr Tyr Asp Lys Leu Gly Lys
 1 5 10 15
 35 Xaa Gln Arg Arg Asn Glu Glu Leu Glu Glu Gln Cys Val Gln His Gly
 20 25 30
 Arg Val His Glu Thr Met Lys Gln Arg Leu Arg Gln Leu Asp Lys His
 35 40 45
 Ser Gln Ala Thr Ala Gln Gln Leu Val Gln Leu Leu Ser Lys Gln Asn
 40 50 55 60
 Gln Leu Leu Leu Glu Arg Gln Ser Leu Ser Glu Glu Val Asp Arg Leu
 65 70 75 80
 Arg Thr Gln Leu Pro Ser Met Pro Gln Ser Asp Cys
 85 90

<210> 1117

<211> 224

<212> PRT

50 <213> Homo sapiens

<400> 1117

Gly Asn Ser Ser Leu Asn Ser Thr Ser Asn Thr Lys Val Ser Ala Val
 1 5 10 15
 55 Pro Thr Asn Met Ala Ala Lys Lys Thr Ser Thr Pro Lys Ile Asn Phe
 20 25 30
 Val Gly Gly Asn Lys Leu Gln Ser Thr Gly Asn Lys Ala Glu Asp Thr
 35 40 45
 Lys Gly Thr Glu Cys Val Lys Ser Thr Pro Val Thr Ser Ala Val Gln
 50 55 60
 60 Ile Pro Glu Val Lys Gln Asp Thr Val Ser Glu Pro Val Thr Pro Ala
 65 70 75 80
 Ser Leu Ala Ala Leu Gln Ser Asp Val Gln Pro Val Gly His Asp Tyr
 85 90 95

Val Glu Glu Val Arg Asn Asp Glu Gly Lys Val Ile Arg Phe His Cys
 100 105 110
 Lys Leu Cys Glu Cys Ser Phe Asn Asp Pro Asn Ala Lys Glu Met His
 115 120 125
 5 Leu Lys Gly Arg Arg His Arg Leu Gln Tyr Lys Lys Lys Val Asn Pro
 130 135 140
 Asp Leu Gln Val Glu Val Lys Pro Ser Ile Arg Xaa Arg Lys Ile Gln
 145 150 155 160
 10 Glu Glu Lys Met Arg Lys Gln Met Xaa Lys Glu Glu Tyr Trp Arg Xaa
 165 170 175
 Xaa Lys Glu Lys Gly Ala Leu Glu Asn Gly Asn Glu Thr Xaa Xaa Lys
 180 185 190
 Arg His Val Leu Glu Glu Asn Gly Xaa Arg Thr Thr Leu Phe Gly Met
 195 200 205
 15 Ile Ala Xaa Asn Ala Xaa Xaa Arg Xaa Ser His Xaa Pro Xaa Gly His
 210 215 220

<210> 1118

<211> 161

20 <212> PRT

<213> Homo sapiens

<400> 1118

25 Glu Arg Cys Gly Ala Ala Arg Phe Ala Cys Lys Cys Ile Thr Lys Arg
 1 5 10 15
 Gln Pro Arg Met Lys Lys Ala Ser Arg Ser Val Gly Ser Val Pro Lys
 20 25 30
 Val Ser Ala Ile Ser Lys Thr Gln Thr Ala Glu Lys Ile Lys Pro Glu
 35 40 45
 30 Asn Ser Ser Ser Ala Ser Thr Gly Gly Lys Leu Val Lys Pro Gly Thr
 50 55 60
 Ala Ala Ser Leu Ser Lys Thr Lys Ser Ser Asp Asp Leu Leu Ala Gly
 65 70 75 80
 35 Met Ala Gly Gly Val Thr Val Thr Asn Gly Val Lys Gly Lys Lys Ser
 85 90 95
 Thr Cys Pro Ser Ala Ala Pro Ser Ala Ser Ala Pro Ala Met Thr Thr
 100 105 110
 Val Glu Asn Lys Ser Lys Ile Ser Thr Gly Thr Ala Ser Ser Thr Lys
 115 120 125
 40 Arg Ser Thr Ser Thr Gly Gln Gly Ala Asn Asp Met Ala Leu Ala Lys
 130 135 140
 Arg Ser Arg Ser Arg Thr Ala Thr Glu Cys Asp Val Arg Met Ser Lys
 145 150 155 160
 Ser

45

<210> 1119

<211> 185

50 <212> PRT

<213> Homo sapiens

<400> 1119

Leu Ile Glu Ala Glu Gly Ile Glu Asp Ile Glu Lys Glu Asp Ile Glu
 1 5 10 15
 55 Ser Gln Glu Ile Glu Ala Gln Glu Gly Glu Asp Asp Thr Phe Leu Thr
 20 25 30
 Ala Gln Asp Gly Glu Glu Glu Glu Asn Glu Lys Asp Ile Ala Gly Ser
 35 40 45
 Gly Asp Gly Thr Gln Glu Val Ser Lys Pro Leu Pro Ser Glu Gly Ser
 50 55 60
 60 Leu Ala Glu Ala Asp His Thr Ala His Glu Glu Met Glu Ala His Thr
 65 70 75 80
 Thr Val Lys Glu Ala Glu Asp Asp Asn Ile Ser Val Thr Ile Gln Ala

85 90 95
 Glu Asp Ala Ile Thr Leu Asp Phe Asp Gly Asp Asp Leu Leu Glu Thr
 100 105 110
 Gly Lys Asn Val Lys Ile Thr Asp Ser Glu Ala Ser Lys Pro Lys Asp
 115 120 125
 5 Gly Gln Asp Ala Ile Ala Gln Ser Pro Glu Lys Glu Ser Lys Asp Tyr
 130 135 140
 Glu Met Asn Ala Asn His Lys Asp Gly Lys Lys Glu Asp Cys Val Lys
 145 150 155 160
 10 Gly Asp Pro Val Glu Lys Glu Ala Arg Glu Ser Ser Xaa Lys Ala Glu
 165 170 175
 Ser Gly Asp Gln Arg Lys Xaa Tyr Phe
 180 185
 15 <210> 1120
 <211> 236
 <212> PRT
 <213> Homo sapiens
 20 <400> 1120
 Lys Gln Val Ser Gln Lys Met Gly Arg Xaa Ala Ile Xaa Xaa Ser Pro
 1 5 10 15
 Xaa Lys Glu Ser Lys Asp Tyr Glu Met Asn Ala Xaa His Lys Asp Gly
 20 25 30
 25 Lys Lys Glu Asp Cys Val Lys Gly Asp Pro Val Glu Lys Glu Ala Arg
 35 40 45
 Glu Ser Ser Lys Lys Ala Glu Ser Gly Asp Lys Glu Lys Asp Thr Leu
 50 55 60
 Lys Lys Gly Pro Ser Ser Thr Gly Ala Xaa Gly Gln Ala Lys Ser Ser
 65 70 75 80
 30 Ser Lys Glu Ser Lys Asp Ser Lys Thr Ser Ser Lys Asp Xaa Lys Gly
 85 90 95
 Ser Xaa Ser Ser Thr Ser Gly Ser Ser Xaa Ser Ser Thr Lys Asn Xaa
 100 105 110
 35 Trp Val Ser Gly Leu Ser Ser Asn Thr Lys Ala Ala Asp Leu Lys Asn
 115 120 125
 Leu Phe Gly Lys Tyr Gly Lys Val Leu Ser Ala Lys Val Val Thr Asn
 130 135 140
 Ala Arg Ser Pro Gly Ala Lys Cys Tyr Gly Ile Val Thr Met Ser Ser
 145 150 155 160
 40 Ser Thr Glu Val Ser Arg Cys Ile Ala His Xaa His Arg Thr Glu Leu
 165 170 175
 His Gly Gln Leu Ile Ser Val Glu Lys Val Lys Gly Asp Pro Ser Lys
 180 185 190
 45 Lys Glu Met Lys Lys Glu Asn Asp Glu Lys Ser Ser Ser Arg Ser Ser
 Gly Asp Lys Lys Asn Thr Ser Asp Arg Ser Ser Lys Thr Gln Ala Ser
 210 215 220
 Val Lys Lys Glu Glu Lys Arg Ser Ser Glu Lys Xaa
 225 230 235
 50 <210> 1121
 <211> 205
 <212> PRT
 55 <213> Homo sapiens
 <400> 1121
 Ser Gly Cys Gly Ala Pro Ala Ala Gly Ala Gly Pro Arg Gly Ala Glu
 1 5 10 15
 60 Leu Gly Ser Gly Ala Gln Ala Val Pro Arg Gly Ala Met Lys Gly Lys
 20 25 30
 Glu Glu Lys Glu Gly Gly Ala Arg Leu Gly Ala Gly Gly Ser Pro
 35 40 45

85 90 95
 Ala Glu Lys Asn Glu Gly Arg Met Asp Ala Glu Lys Val Glu Lys Met
 100 105 110
 5 Ala Ala Met Lys Glu Lys Pro Ala Glu Asn Thr Leu Phe Lys Ala Tyr
 115 120 125
 Pro Asn Lys Gly Val Gly Gln Ala Asn Lys Pro Asp Glu Thr Ser Lys
 130 135 140
 Thr Ser Ile Leu Ala Val Ser Asp Val Ser Ser Lys Pro Ser Ile
 145 150 155 160
 10 Lys Ala Val Ile Val Ser Ser Pro Lys Ala Lys Ala Thr Val Ser Lys
 165 170 175
 Thr Glu Asn Gln Lys Ser Phe Pro Lys Ser Val Pro Arg Asp Gln Ile
 180 185 190
 15 Asn Ala Glu Lys Lys Leu Ser Ala Gln Xaa Ile Trp Ser Ala
 195 200 205

 <210> 1124
 <211> 94
 <212> PRT
 20 <213> Homo sapiens

 <400> 1124
 Gln Leu Asn Ser Thr Gln Arg Glu Leu Glu Leu Glu Asn Ser Ala Ile
 1 5 10 15
 25 Arg Lys Ser Cys Cys Ala Glu Pro Ala Lys Gly Glu Glu Ala Phe Gln
 20 25 30
 Met Ser Glu Val Asp Glu Glu Ser Gly Leu Lys Asp Ser Glu Pro Glu
 35 40 45
 Arg Lys Arg Lys Lys Thr Glu Asp Ser Ser Ser Gly Lys Ser Val Ala
 50 55 60
 30 Ser Asp Val Pro Glu Glu Leu Asp Phe Leu Asp Leu Arg Leu Asp Ser
 65 70 75 80
 Ser Val Gln Phe Val Pro Ser Ser Thr Gln Val Lys Lys Gln
 85 90
 35
 <210> 1125
 <211> 237
 <212> PRT
 <213> Homo sapiens
 40
 <400> 1125
 Arg Pro Gly Lys Arg Arg Cys Gly Val Gly Cys Phe Pro Glu Ala Gly
 1 5 10 15
 45 Leu Asn Gly Ser Arg Leu Ser His Arg Val Ser Ser Pro Pro Ser Pro
 20 25 30
 Asn Gln Glu Ile Ala Arg Glu Arg Cys Gly Ala Ala Arg Phe Ala Cys
 35 40 45
 Lys Cys Ile Thr Lys Arg Gln Pro Arg Met Lys Lys Ala Ser Arg Ser
 50 55 60
 Val Gly Ser Val Pro Lys Val Ser Ala Ile Ser Lys Thr Gln Thr Ala
 65 70 75 80
 Glu Lys Ile Lys Pro Glu Asn Ser Ser Ser Ala Ser Thr Gly Gly Lys
 85 90 95
 55 Leu Val Lys Pro Gly Thr Ala Ala Ser Leu Ser Lys Thr Lys Ser Ser
 100 105 110
 Asp Asp Leu Leu Ala Gly Met Ala Gly Gly Val Thr Val Thr Asn Gly
 115 120 125
 Val Lys Gly Lys Lys Ser Thr Cys Pro Ser Ala Ala Pro Ser Ala Ser
 130 135 140
 60 Ala Pro Ala Met Thr Thr Val Glu Asn Lys Ser Lys Ile Ser Thr Gly
 145 150 155 160
 Thr Xaa Ser Ser Thr Lys Arg Ser Thr Xaa Thr Gly Asn Lys Glu Ser
 165 170 175

Ser Ser Thr Arg Glu Arg Leu Arg Glu Arg Thr Arg Leu Asn Gln Ser
 180 185 190
 Lys Lys Leu Pro Xaa Ala Gly Xaa Gly Ala Asn Asp Met Ala Phe Gly
 195 200 205
 5 Gln Thr Xaa Xaa Gln Leu Asn Xaa Phe Gln Asn Val Thr Phe Arg Xaa
 210 215 220
 Xaa Gln Xaa Leu Ser Gln Thr Ile Xaa Asn Pro Val Xaa
 225 230 235

 10 <210> 1126
 <211> 195
 <212> PRT
 <213> Homo sapiens

 15 <400> 1126
 Leu Asn Glu Ile Tyr Thr Lys Thr Asp Ser Lys Ser Ile Met Arg Met
 1 5 10 15
 Lys Ser Gly Gln Met Phe Ala Lys Glu Asp Leu Lys Arg Lys Lys Leu
 20 25 30
 Val Arg Asp Gly Ser Val Phe Leu Lys Asn Ala Ala Gly Arg Leu Lys
 35 40 45
 Glu Val Gln Ala Val Leu Leu Thr Asp Ile Leu Val Phe Leu Gln Glu
 50 55 60
 Lys Asp Gln Lys Tyr Ile Phe Ala Ser Leu Asp Gln Lys Ser Thr Val
 25 65 70 75 80
 Ile Ser Leu Lys Lys Leu Ile Val Arg Glu Val Ala His Glu Glu Lys
 85 90 95
 Gly Leu Phe Leu Ile Ser Met Gly Met Thr Asp Pro Glu Met Val Glu
 100 105 110
 30 Val His Ala Ser Ser Lys Glu Glu Arg Asn Ser Trp Ile Gln Ile Ile
 115 120 125
 Gln Asp Thr Ile Asn Thr Leu Asn Arg Asp Glu Asp Glu Gly Ile Pro
 130 135 140
 Ser Glu Asn Glu Glu Glu Lys Lys Met Leu Asp Thr Arg Pro Arg Glu
 35 145 150 155 160
 Leu Lys Glu His Phe Pro Glu Gly Gln Lys Ile Ser Leu Val Glu Arg
 165 170 175
 Arg Asn Asp Phe Pro Xaa Trp Leu Met His Pro Leu Ser Arg Asp Trp
 180 185 190
 40 Ser His Pro
 195

 <210> 1127
 <211> 160
 45 <212> PRT
 <213> Homo sapiens

 <400> 1127
 Glu Glu Gly Arg Ala Leu His Asp Gly Ile Ala Ile Ala Tyr Ala Thr
 50 1 5 10 15
 Leu Glu Tyr Phe Ile Arg Asp Val Lys Ser Leu Thr Leu Phe Val Thr
 20 25 30
 His Tyr Pro Pro Val Cys Glu Leu Lys Asn Tyr Ser His Gln Val
 35 40 45
 55 Gly Asn Tyr His Met Gly Phe Leu Val Ser Glu Asp Glu Ser Lys Leu
 50 55 60
 Asp Pro Gly Thr Ala Glu Gln Val Pro Asp Phe Val Thr Phe Leu Tyr
 65 70 75 80
 Gln Ile Thr Arg Gly Ile Ala Ala Arg Ser Tyr Gly Leu Asn Val Ala
 85 90 95
 60 Lys Leu Ala Asp Val Pro Gly Glu Ile Leu Lys Lys Ala Ala His Lys
 100 105 110
 Ser Lys Glu Leu Glu Gly Leu Ile Asn Thr Lys Arg Lys Arg Leu Lys

Asp Pro Ala Asn Arg Ala His Leu Gly Leu Glu Glu Gln Leu Arg Glu
 260 265 270
 Leu Leu Asp Met Leu Asp Leu Thr Cys Ala Met Lys Ser Ser Gly Ser
 275 280 285
 5 Arg Ser Lys Arg Ala Lys Leu Leu Lys Lys Glu Ile Ala Leu Leu Arg
 290 295 300
 Asn Lys Leu Ser Gln Gln His Ser Gln Pro Leu Pro Thr Gly Pro Gly
 305 310 315 320
 Leu Glu Gly Phe Glu Glu Asp Gly Ala Ala Leu Gly Pro Gly Gly Gly
 325 330 335
 10 Arg Arg Ser Pro Ser Glu Val Gly Asp Ser Ser Ala Ala Lys Glu Lys
 340 345 350
 Val Ala Glu His Met Arg Arg Leu Xaa Xaa Trp Arg Arg Ser Xaa Xaa
 355 360 365
 15 Glu Lys Arg Leu Asp Ala Gly Leu His Gln Xaa Leu Leu Gly Cys Xaa
 370 375 380
 Glu Pro Thr Xaa Asn Pro Ala Gly Gly Leu Gly Gly Gly Arg Pro His
 385 390 395 400
 20 Pro Asp Asp Leu Gly Pro Ser Ser Ser Arg Phe Ser Phe Lys
 405 410

<210> 1130

<211> 178

<212> PRT

25 <213> Homo sapiens

<400> 1130

Ile Val Glu Arg Glu Ser Gly His Tyr Val Glu Met His Ala Arg Tyr
 1 5 10 15
 30 Ile Gly Thr Thr Val Phe Val Arg Gln Val Gly Arg Tyr Leu Thr Leu
 20 25 30
 Ala Ile Arg Met Pro Glu Asp Leu Ala Met Ser Tyr Glu Glu Ser Gln
 35 40 45
 Asp Leu Gln Leu Cys Val Asn Gly Cys Pro Leu Ser Glu Arg Ile Asp
 50 55 60
 35 Asp Gly Gln Gly Gln Val Ser Ala Ile Leu Gly His Ser Leu Pro Arg
 65 70 75 80
 Thr Ser Leu Val Gln Ala Trp Pro Gly Tyr Thr Leu Glu Thr Ala Asn
 85 90 95
 40 Thr Gln Cys His Glu Lys Met Pro Val Lys Asp Ile Tyr Phe Gln Ser
 100 105 110
 Cys Val Phe Asp Leu Leu Thr Thr Gly Asp Ala Asn Phe Thr Ala Ala
 115 120 125
 Ala His Ser Ala Leu Glu Asp Val Glu Ala Leu His Pro Arg Lys Glu
 130 135 140
 45 Arg Trp His Ile Phe Pro Ser Ser Gly Asn Gly Thr Pro Arg Gly Gly
 145 150 155 160
 Ser Asp Leu Ser Val Ser Leu Gly Leu Thr Cys Leu Ile Leu Ile Val
 165 170 175
 50 Phe Leu

<210> 1131

<211> 118

<212> PRT

55 <213> Homo sapiens

<400> 1131

Ala Gly Arg Arg His Arg Thr Gly Asn Arg Cys Pro Ser Leu Ala Ser
 1 5 10 15
 60 Ser His Gly Ile Glu Cys Trp Gln Ser Pro Val Cys Ser Gln Ala Arg
 20 25 30
 Pro Ala Pro Arg Arg Cys Glu Ala Gly Cys Val Pro Gly Trp Gln Thr

35 40 45
 Pro Gly Pro Ala Arg His Arg Cys Val His Ser Gly Gly Ser Arg Ser
 50 55 60
 5 Arg Thr Ala Ala Gly Pro Gly Ser Pro Arg Arg Thr Trp Pro Gly Leu
 65 70 75 80
 Gln Ala Tyr Gly Trp Gln Gly Ser Gly Ser Asp Pro Pro Ala Ala Gln
 85 90 95
 Thr Leu Trp Ser Leu Tyr Ser Gly Arg Ala Ser Pro His Ser Gly His
 100 105 110
 10 Ser Pro Phe Pro Arg Tyr
 115

<210> 1132

<211> 166

15 <212> PRT

<213> Homo sapiens

<400> 1132

20 Thr Asp Arg Gln Ile Thr Ala Ser Thr Gly Ser Pro Ile Ala Thr Ala
 1 5 10 15
 Gly Glu Asn Val Pro Ala Phe Leu Pro Trp Val Gln Gly Leu His Ile
 20 25 30
 Leu Gln Gly Thr Val Gly Cys Gly Ser Lys Val Gly Ile Thr Ser Gly
 35 40 45
 25 Glu Gln Val Glu Asp Thr Gly Leu Glu Ile Asp Val Leu His Trp His
 50 55 60
 Leu Leu Met Ala Leu Ser Val Gly Ser Leu Gln Cys Val Ala Arg Pro
 65 70 75 80
 Gly Leu His Gln Gly Gly Ala Arg Gln Ala Val Ser Gln Asp Gly Arg
 85 90 95
 30 His Leu Ala Leu Pro Val Ile Asp Ala Phe Thr Gln Gly Ala Ala Val
 100 105 110
 His Ala Gln Leu Gln Val Leu Ala Leu Val Gly His Gly Gln Val
 115 120 125
 35 Phe Arg His Thr Asp Gly Lys Gly Gln Val Ala Thr His Leu Pro His
 130 135 140
 Lys His Cys Gly Pro Tyr Ile Ala Gly Val His Leu His Ile Val Ala
 145 150 155 160
 40 Thr Leu Pro Phe His Asp
 165

<210> 1133

<211> 365

45 <212> PRT

<213> Homo sapiens

<400> 1133

Ser Ala His Ser Arg Leu Ala Ala Arg His Tyr Ser Gly Pro Gly Pro
 1 5 10 15
 50 Ala Pro Ala Arg Pro Arg Arg Arg Gln Phe Arg Leu Lys Lys Leu Ile
 20 25 30
 Asp Gln Glu Ile Lys Ser Gln Glu Glu Lys Glu Gln Glu Lys Glu Lys
 35 40 45
 Arg Val Thr Thr Leu Lys Glu Glu Leu Thr Lys Leu Lys Ser Phe Ala
 50 55 60
 55 Leu Met Val Val Asp Glu Gln Gln Arg Leu Thr Ala Gln Leu Thr Leu
 65 70 75 80
 Gln Arg Gln Lys Ile Gln Glu Leu Thr Thr Asn Ala Lys Glu Thr His
 85 90 95
 60 Thr Lys Leu Ala Leu Ala Glu Ala Arg Val Gln Glu Glu Glu Gln Lys
 100 105 110
 Ala Thr Arg Leu Glu Lys Glu Leu Gln Thr Gln Thr Thr Lys Phe His
 115 120 125

Gln Asp Gln Asp Thr Ile Met Ala Lys Leu Thr Asn Glu Asp Ser Gln
 130 135 140
 Asn Arg Gln Leu Gln Gln Lys Leu Ala Ala Leu Ser Arg Gln Ile Asp
 145 150 155 160
 5 Glu Leu Glu Glu Thr Asn Arg Ser Leu Arg Lys Ala Glu Glu Glu Leu
 165 170 175
 Gln Asp Ile Lys Glu Lys Ile Ser Lys Gly Glu Tyr Gly Asn Ala Gly
 180 185 190
 10 Ile Met Ala Glu Val Glu Glu Leu Arg Lys Arg Val Leu Asp Met Glu
 195 200 205
 Gly Lys Asp Glu Glu Leu Ile Lys Met Glu Glu Gln Cys Arg Asp Leu
 210 215 220
 Asn Lys Arg Leu Glu Arg Glu Thr Leu Gln Ser Lys Asp Phe Lys Leu
 225 230 235 240
 15 Glu Val Glu Lys Leu Ser Lys Arg Ile Met Ala Leu Glu Lys Leu Glu
 245 250 255
 Asp Ala Phe Asn Lys Ser Lys Gln Glu Cys Tyr Ser Leu Lys Cys Asn
 260 265 270
 20 Leu Glu Lys Glu Arg Met Thr Thr Lys Gln Leu Ser Gln Glu Leu Glu
 275 280 285
 Ser Leu Lys Val Arg Ile Lys Glu Leu Glu Ala Ile Glu Ser Arg Leu
 290 295 300
 Glu Lys Thr Glu Phe Thr Leu Lys Glu Asp Leu Thr Lys Leu Lys Thr
 305 310 315 320
 25 Leu Thr Val Met Phe Val Asp Glu Arg Lys Thr Met Ser Glu Lys Leu
 325 330 335
 Lys Lys Thr Glu Asp Lys Leu Gln Ala Ala Ser Ser Gln Leu Gln Val
 340 345 350
 30 Glu Gln Asn Lys Val Thr Thr Val Thr Glu Lys Val Asn
 355 360 365

<210> 1134

<211> 221

<212> PRT

35 <213> Homo sapiens

<400> 1134

Ser Gly Lys Met Ala Lys Val Ser Glu Leu Tyr Asp Val Thr Trp Glu
 1 5 10 15
 40 Glu Met Arg Asp Lys Met Arg Lys Trp Arg Glu Glu Asn Ser Arg Asn
 20 25 30
 Ser Glu Gln Ile Val Glu Val Gly Glu Glu Leu Ile Asn Glu Tyr Ala
 35 40 45
 45 Ser Lys Leu Gly Asp Asp Ile Trp Ile Ile Tyr Glu Gln Val Met Ile
 50 55 60
 Ala Ala Leu Asp Tyr Gly Arg Asp Asp Leu Ala Leu Phe Cys Leu Gln
 65 70 75 80
 Glu Leu Arg Arg Gln Phe Pro Gly Ser His Arg Val Lys Arg Leu Thr
 85 90 95
 50 Gly Met Arg Phe Glu Ala Met Glu Arg Tyr Asp Asp Ala Ile Gln Leu
 100 105 110
 Tyr Asp Arg Ile Leu Gln Glu Asp Pro Thr Asn Thr Ala Ala Arg Lys
 115 120 125
 Arg Lys Ile Ala Ile Arg Lys Ala Gln Gly Lys Asn Val Glu Ala Ile
 130 135 140
 55 Arg Glu Leu Asn Glu Tyr Leu Glu Gln Phe Val Gly Asp Gln Glu Ala
 145 150 155 160
 Trp His Glu Leu Ala Glu Leu Tyr Ile Asn Glu His Asp Tyr Ala Lys
 165 170 175
 60 Ala Ala Phe Cys Leu Glu Glu Leu Met Thr Asn Pro His Asn His
 180 185 190
 Leu Tyr Cys Gln Gln Tyr Ala Glu Val Lys Tyr Thr Gln Gly Gly Leu
 195 200 205

Glu Thr Leu Glu Leu Ser Arg Lys Phe Leu His Arg His
 210 215 220

5 <210> 1135
 <211> 118
 <212> PRT
 <213> Homo sapiens

<400> 1135
 10 Arg Glu Leu Glu Pro Ala Glu Phe Glu Thr Met Leu Leu Phe Cys Pro
 1 5 10 15
 Gly Cys Gly Asn Gly Leu Ile Val Glu Glu Gly Gln Arg Cys His Arg
 20 25 30
 Phe Ala Cys Asn Thr Cys Pro Tyr Val His Asn Ile Thr Arg Lys Val
 15 35 40 45
 Thr Asn Arg Lys Tyr Pro Lys Leu Lys Glu Val Asp Asp Val Leu Gly
 50 55 60
 Gly Ala Ala Ala Trp Glu Asn Val Asp Ser Thr Ala Glu Ser Cys Pro
 65 70 75 80
 20 Lys Cys Glu His Pro Arg Ala Tyr Phe Met Gln Leu Gln Thr Arg Ser
 85 90 95
 Ala Asp Glu Pro Met Thr Thr Phe Tyr Lys Cys Cys Asn Ala Gln Cys
 100 105 110
 Gly His Arg Trp Arg Asp
 25 115

<210> 1136
 <211> 126
 <212> PRT
 30 <213> Homo sapiens

<400> 1136
 Gly Ser Trp Ala Ile Leu Ala Leu Ile Pro Pro Ala Val Ser Thr Leu
 1 5 10 15
 35 Ser Ile Ala Ala Leu Val Glu Gly Gly His Arg Leu Ile Cys Arg Ala
 20 25 30
 Gly Leu Lys Leu His Glu Val Ser Thr Arg Met Phe Ala Phe Gly Thr
 35 40 45
 Arg Leu Cys Ser Arg Val Asn Ile Leu Pro Gly Ser Cys Ser Thr Lys
 40 50 55 60
 His Ile Ile His Phe Phe Gln Phe Trp Val Leu Pro Ile Cys Tyr Leu
 65 70 75 80
 Ala Gly Asp Val Val His Val Gly Ala Arg Val Ala Gly Glu Ala Val
 85 90 95
 45 Ala Ala Leu Ser Leu Leu His Asp Gln Pro Val Pro Ala Ala Gly Ala
 100 105 110
 Glu Gln Gln His Gly Leu Glu Leu Arg Arg Leu Gln Leu Pro
 115 120 125

50 <210> 1137
 <211> 208
 <212> PRT
 <213> Homo sapiens

55 <400> 1137
 Ser Leu Arg Phe Tyr Leu Ser Leu Gly Gln Leu Tyr Leu Ser Met Asn
 1 5 10 15
 Ile Asp Asp Lys Leu Glu Gly Leu Phe Leu Lys Cys Gly Gly Ile Asp
 20 25 30
 60 Glu Met Gln Ser Ser Arg Thr Met Val Val Met Gly Gly Val Ser Gly
 35 40 45
 Gln Ser Thr Val Ser Gly Glu Leu Gln Asp Ser Val Leu Gln Asp Arg
 50 55 60

Ser Met Pro His Gln Glu Ile Leu Ala Ala Asp Glu Val Leu Gln Glu
 65 70 75 80
 Ser Glu Met Arg Gln Gln Asp Met Ile Ser His Asp Glu Leu Met Val
 85 90 95
 5 His Glu Glu Thr Val Lys Asn Asp Glu Glu Gln Met Glu Thr His Glu
 100 105 110
 Arg Leu Pro Gln Gly Leu Gln Tyr Ala Leu Asn Val Pro Ile Ser Val
 115 120 125
 10 Lys Gln Glu Ile Thr Phe Thr Asp Val Ser Glu Gln Leu Met Arg Asp
 130 135 140
 Lys Lys Gln Ile Arg Glu Pro Val Asp Leu Gln Lys Lys Lys Lys Arg
 145 150 155 160
 Lys Gln Arg Ser Pro Ala Lys Ile Leu Thr Ile Asn Glu Asp Gly Ser
 165 170 175
 15 Leu Gly Leu Lys Thr Pro Lys Ser His Val Cys Glu His Cys Asn Ala
 180 185 190
 Ala Phe Arg Thr Asn Tyr Pro Tyr Arg Asp Met Ser Ser Tyr Arg
 195 200 205
 20 <210> 1138
 <211> 121
 <212> PRT
 <213> Homo sapiens
 25 <400> 1138
 Lys Arg Arg Leu Gln Gly Lys Glu Cys Cys Arg Val Glu Lys Glu Ile
 1 5 10 15
 Met Val Glu Phe Leu Pro Phe Ile Gly Phe Arg Asn Pro Gln Tyr His
 20 25 30
 30 Leu Asn His Leu Cys His Pro Ile Pro Pro Leu Asn Thr Leu Gly Lys
 35 40 45
 Arg Pro Ser Arg Gln Xaa Thr Cys Leu Asn Phe Gln Ala Xaa Asp Ser
 50 55 60
 Ser Leu Tyr Pro Arg Ala Gly Ala Glu Ser Arg Gly His Arg Xaa Gln
 65 70 75 80
 35 Ala Ala Ala Ala Pro Thr Phe Xaa Gly Ala Leu Arg Gly Gly Glu Gly
 85 90 95
 Gly Arg Gly Glu Asn Phe Cys Cys Gly Ser Phe Gly Asn Ser Ser His
 100 105 110
 40 Pro Xaa Ala Phe Leu Leu Phe Leu Pro
 115 120
 <210> 1139
 <211> 178
 <212> PRT
 <213> Homo sapiens
 45 <400> 1139
 Arg Ser Lys Gly Cys Asp Cys Cys Gly Glu Lys Ser Gln Pro Gln Glu
 1 5 10 15
 Lys Ser Leu Ile Gly Leu Lys Asn Thr Glu Asn Asn Asp Val Glu Ile
 20 25 30
 Ser Glu Thr Lys Lys Ala Asp Val Gln Ala Pro Val Ser Pro Ser Glu
 35 40 45
 55 Thr Ser Gln Ala Asn Pro Tyr Ser Glu Gly Gln Phe Leu Asp Glu His
 50 55 60
 His Ser Val Asn Phe His Leu Gly Leu Lys Glu Asp Asn Asp Thr Ile
 65 70 75 80
 Asn Asp Ser Leu Ile Val Ser Glu Thr Lys Ser Lys Glu Asn Thr Met
 85 90 95
 60 Gln Glu Ser Leu Pro Ser Gly Ile Val Asn Phe Arg Glu Glu Ile Cys
 100 105 110
 Asp Met Asp Ser Ser Glu Ala Met Ser Leu Glu Ser Gln Glu Ser Pro

115 120 125
 Asn Glu Asn Phe Lys Thr Val Gly Pro Cys Leu Gly Asp Ser Lys Asn
 130 135 140
 Val Ser Gln Glu Ser Leu Glu Thr Lys Glu Glu Lys Pro Glu Glu Thr
 5 145 150 155 160
 Pro Lys Met Glu Leu Ser Leu Glu Asn Val Leu Leu Lys Glu Met His
 165 170 175
 Val Lys

 10
 <210> 1140
 <211> 187
 <212> PRT
 <213> Homo sapiens

 15
 <400> 1140
 Phe Leu Asn Leu Arg Gly Asp Ile Gly Ser His Trp Leu Gln Phe Lys
 1 5 10 15
 Leu Leu Thr Glu Ile Ser Ser Ala Val Phe Ile Leu Thr Asp Asn Ile
 20 20 25 30
 Ser Lys Lys Glu Tyr Lys Leu Leu Tyr Ser Met Lys Glu Ser Thr Thr
 35 40 45
 Lys Tyr Tyr Phe Ile Leu Ser Pro Tyr Arg Gly Lys Arg Asn Thr Asn
 50 55 60
 25 Leu Arg Phe Leu Asn Lys Leu Ile Pro Val Leu Lys Ile Asp His Ser
 65 70 75 80
 His Val Leu Val Lys Val Ser Ser Thr Asp Ser Asp Ser Phe Val Lys
 85 90 95
 Arg Ile Arg Ala Ile Val Gly Asn Val Leu Arg Ala Pro Cys Arg Arg
 100 105 110
 30 Val Ser Val Glu Asp Met Ala His Ala Ala Arg Lys Leu Gly Leu Lys
 115 120 125
 Val Asp Glu Asp Cys Glu Glu Cys Gln Lys Ala Lys Asp Arg Met Glu
 130 135 140
 35 Arg Ile Thr Arg Lys Ile Lys Asp Ser Asp Ala Tyr Xaa Lys Asp Gln
 145 150 155 160
 Leu Arg Leu Xaa Gly Asp Pro Trp Arg Lys Ala Ala Gln Val Glu Lys
 165 170 175
 Glu Phe Cys Asn Phe Ser Gly Pro Trp Pro Pro
 180 185
 40
 <210> 1141
 <211> 145
 <212> PRT
 <213> Homo sapiens

 45
 <400> 1141
 Lys Trp Xaa Val Pro Ile Arg His Glu Lys Pro Ser Lys Xaa Gln Arg
 1 5 10 15
 50 Phe Xaa Ser Xaa Xaa Gln Gln Val Leu Lys Xaa Glu Ser Asp Xaa Thr
 20 25 30
 Asp Gln Phe Lys Arg Cys Tyr Gln Glu Tyr Xaa Ser Pro Gln Gly Arg
 35 40 45
 Xaa Thr Ser Ser Ser Leu Xaa Cys Xaa Ser Ser Cys Gln Gly Ser Cys
 50 55 60
 55 Gly Val Gly Pro Leu Xaa Ser Cys Xaa Leu Ser Leu Ala Pro Gly Val
 65 70 75 80
 Gly Ala Ala Ser Leu Val Thr Ala Gly Pro Gly Gly Gln Val Val Pro
 85 90 95
 60 Gly Xaa Arg Trp Gly Ser Cys Pro Glu Glu Ala Glu Val Gly Leu Ala
 100 105 110
 Pro Ala Gln Pro Lys Gly Leu Gln Trp Thr Ser Ile Gln Asp Val Ser
 115 120 125

Ala Arg Gly Val Gln Gly Thr Pro Met Ala Pro Tyr Leu Leu Thr Asp
 130 135 140
 Leu
 145

5
 <210> 1142
 <211> 67
 <212> PRT
 <213> Homo sapiens

10
 <400> 1142
 Xaa His Phe Xaa Phe Leu Thr Leu Val Xaa Xaa Asn Xaa Xaa Thr Phe
 1 5 10 15
 Xaa Phe Cys Ser Ala Ser His Val Glu Trp Ala Pro Xaa Ile Phe Lys
 15 20 25 30
 Xaa Pro Lys His Lys Pro His Met Gly Ala Pro Phe Lys Lys Xaa Val
 35 40 45
 Gly His Xaa Xaa Thr Phe Leu Asn Leu Xaa Thr Gly Val Phe Leu Asp
 50 55 60
 20 Xaa Leu Lys
 65

25
 <210> 1143
 <211> 149
 <212> PRT
 <213> Homo sapiens

30
 <400> 1143
 Glu Asn Glu Val Lys Leu Leu Val Glu Arg Met Met Ala Leu Gln Thr
 1 5 10 15
 Asp Ile Val Asp Leu Gln Arg Ser Pro Met Gly Arg Lys Gln Gly Gly
 20 25 30
 Thr Leu Asp Asp Leu Glu Glu Gln Ala Arg Glu Leu Tyr Arg Arg Leu
 35 35 40 45
 Arg Glu Lys Pro Arg Asp Gln Arg Thr Glu Gly Asp Ser Gln Glu Met
 50 55 60
 Val Arg Leu Leu Leu Gln Ala Ile Gln Ser Phe Glu Lys Lys Val Arg
 65 70 75 80
 Val Ile Tyr Thr Gln Leu Ser Lys Thr Val Val Cys Lys Gln Lys Ala
 40 85 90 95
 Leu Glu Leu Leu Pro Lys Val Glu Glu Val Val Ser Leu Met Asn Glu
 100 105 110
 Asp Glu Lys Thr Val Val Arg Leu Gln Glu Lys Arg Gln Lys Glu Leu
 115 120 125
 45 Trp Asn Leu Leu Lys Ile Ala Cys Thr Arg Ser Val Val Leu Ser Val
 130 135 140
 Glu Thr Pro Ile Ala
 145

50
 <210> 1144
 <211> 126
 <212> PRT
 <213> Homo sapiens

55
 <400> 1144
 His Pro Arg Pro Ala Arg Cys Pro Leu Val Thr Pro Thr Pro Thr Glu
 1 5 10 15
 Leu Glu Arg Leu Arg Leu Arg Ser Arg Pro Val Tyr Gly Val Cys Pro
 20 25 30
 60 Val Tyr Glu Asp Val Pro Ala Arg Asn Glu Arg Ile Tyr Val Tyr Glu
 35 40 45
 Asn Lys Lys Glu Ala Phe Ala Ser Cys Gln Asp Asp Gln Arg Val Arg
 50 55 60

1445

Phe Lys Ala Phe Ser Pro Xaa Lys Thr Leu Lys Asn Leu Xaa Lys Glu
 65 70 75 80
 Phe Val Asn Ile Ser Xaa Ser Asn Lys Thr Ser Leu His Xaa Phe Cys
 85 90 95
 5 Glu Asn Asn Phe Thr Leu Phe Asn Asp Lys Leu Lys Xaa Val Gly Leu
 100 105 110
 Xaa Asn Lys Thr Ala Pro Xaa Ala Ser Asp Ser Ser Lys Ile
 115 120 125
 10 <210> 1145
 <211> 152
 <212> PRT
 <213> Homo sapiens
 15 <400> 1145
 Arg Pro Ala Ala Pro Ala Ser Gly Glu Met Thr Met Asp Ala Leu Leu
 1 5 10 15
 Ala Arg Leu Lys Leu Leu Asn Pro Asp Asp Leu Arg Glu Glu Ile Val
 20 20 25 30
 Lys Ala Gly Leu Lys Cys Gly Pro Ile Thr Ser Thr Thr Arg Phe Ile
 35 40 45
 Phe Glu Lys Lys Leu Ala Gln Ala Leu Leu Glu Gln Gly Gly Arg Leu
 50 55 60
 Ser Ser Phe Tyr His His Glu Ala Gly Val Thr Ala Leu Ser Gln Asp
 25 65 70 75 80
 Pro Gln Arg Ile Leu Lys Pro Ala Glu Gly Asn Pro Thr Asp Gln Ala
 85 90 95
 Gly Phe Ser Glu Asp Arg Asp Phe Gly Tyr Ser Val Gly Leu Asn Pro
 100 105 110
 30 Pro Glu Glu Glu Ala Val Thr Ser Lys Thr Cys Ser Val Pro Pro Ser
 115 120 125
 Asp Thr Asp Thr Tyr Arg Ala Gly Ala Thr Ala Ser Lys Glu Pro Pro
 130 135 140
 Cys Leu Trp Gly Val Ser Ser Val
 35 145 150
 <210> 1146
 <211> 176
 <212> PRT
 40 <213> Homo sapiens
 <400> 1146
 Pro Arg Gly Ala Phe Met Gln Leu Ile Thr Val Ala Glu Gly Phe Ser
 1 5 10 15
 45 Gln Asp Leu Gly Cys Asp His Ile Leu Val Ile Asp Ser Gly Gly Leu
 20 25 30
 Ile Gly Gly Ala Leu Thr Ser Ala Gly Asp Arg Phe Glu Leu Glu Ala
 35 40 45
 Ser Leu Ala Thr Leu Leu Met Gly Leu Ser Asn Val Thr Val Ile Ser
 50 50 55 60
 Leu Ala Glu Thr Lys Asp Ile Pro Ala Ala Ile Leu His Ala Phe Leu
 65 70 75 80
 Arg Leu Glu Lys Thr Gly His Met Pro Asn Tyr Gln Phe Val Tyr Gln
 85 90 95
 55 Asn Leu His Asp Val Ser Val Pro Gly Pro Arg Pro Arg Asp Lys Arg
 100 105 110
 Gln Leu Leu Asp Pro Pro Gly Asp Leu Ser Arg Ala Ala Ala Gln Met
 115 120 125
 Glu Lys Gln Gly Asp Gly Phe Arg Ala Leu Ala Gly Leu Ala Phe Cys
 130 135 140
 60 Asp Pro Glu Asn Asn Thr Ser Gly Thr Ser Ser Leu Trp His Gly His
 145 150 155 160
 Leu His Gly Arg Ser Glu Leu Trp Pro Thr Val Lys Pro Tyr Leu Asn

165 170 175

<210> 1147
 <211> 113
 <212> PRT
 <213> Homo sapiens

<400> 1147

Met Phe Leu Phe Trp Phe Asp Xaa Xaa Phe Leu Met Phe Ser Ser Arg
 1 5 10 15
 Ile Ser Ser Ile Gln Ile Trp Phe His Cys Arg Pro Lys Leu Thr Ala
 20 25 30
 Ala Met Glu Val Ser Val Pro Gln Ala Gly Cys Ala Arg Cys Val Val
 35 40 45
 Leu Arg Val Ala Glu Gly Gln Ala Cys Gln Cys Pro Glu Ala Val Ala
 50 55 60
 Leu Phe Leu His Leu Gly Cys Ser Pro Ala Gln Val Thr Arg Trp Ile
 65 70 75 80
 Gln Glu Leu Ser Leu Val Ser Gly Pro Arg Ala Gly Asn Arg Tyr Ile
 85 90 95
 Met Lys Val Leu Val Tyr Lys Leu Val Val Gly His Val Pro Arg Phe
 100 105 110
 Phe

<210> 1148
 <211> 136
 <212> PRT
 <213> Homo sapiens

<400> 1148

Glu Asp Glu Gln Lys Thr Glu Gly Leu Glu Ser Pro Gln Thr Val Phe
 1 5 10 15
 Lys Xaa Xaa Ser Asp Leu Thr Asp Gln Leu Gln Arg Cys Tyr Gln Glu
 20 25 30
 Tyr Xaa Ser Pro Gln Gly Arg Glu Thr Ser Ser Ser Leu Xaa Cys Xaa
 35 40 45
 Ser Ser Cys Gln Gly Ser Cys Gly Val Gly Pro Leu Tyr Ser Cys Ser
 50 55 60
 Xaa Ser Leu Ala Pro Gly Val Gly Ala Ala Ser Leu Val Thr Ala Gly
 65 70 75 80
 Pro Gly Gly Gln Val Val Pro Gly Xaa Arg Trp Gly Ser Cys Pro Xaa
 85 90 95
 Glu Ala Xaa Val Gly Leu Ala Pro Ala Gln Pro Lys Gly Leu Gln Trp
 100 105 110
 Thr Ser Ile Gln Asp Val Ser Ala Arg Gly Val Gln Gly Thr Pro Met
 115 120 125
 Xaa Pro Tyr Leu Leu Thr Asp Leu
 130 135

<210> 1149
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 1149

Glu Gly Phe Leu Trp Xaa Thr Pro Phe Leu Met Gly Xaa Pro Asn Gly
 1 5 10 15
 Gly Val Val Xaa Leu Xaa Pro Xaa Lys Arg Ala Gly Ala Pro Ile Arg
 20 25 30
 His Glu Lys Thr Ser Lys Arg Gln Arg Val Trp Ser Leu Leu Lys Gln
 35 40 45
 Cys Leu Lys Xaa Xaa Val Thr Ser Gln Thr Ser Phe Arg Asp Val Thr

447

	65				70				75					80		
	Leu	Lys	Gln	Pro	Arg	Cys	Phe	Val	Leu	Met	Asp	His	Ile	Leu	Asn	Leu
					85					90					95	
5	Lys	Ile	Val	His	Ile	Leu	Asn	Met	Thr	Ser	Ala	Lys	Ile	Ile	Ser	Phe
				100					105					110		
	Leu	Leu	Pro	Pro	Asp	Glu	Ser	Leu	His	Ser	Leu	Gln	Ser	Arg	Ile	Glu
				115					120				125			
	Arg	Glu	Thr	Gly	Ile	Asn	Thr	Gly	Ser	Gln	Glu	Leu	Leu	Ser	Glu	Thr
				130				135				140				
10	Gly	Ile	Ser	Leu	Asp	Pro	Arg	Lys	Pro	Ala	Ser	Gln	Cys	Val	Leu	Asp
						150					155					160
	Gly	Val	Arg	Gly	Cys	Asp	Ser	Tyr	Met	Xaa	Tyr	Leu	Phe	Asp	Lys	Lys
					165					170					175	
15	<210>	1153														
	<211>	217														
	<212>	PRT														
	<213>	Homo sapiens														
20	<400>	1153														
	Glu	Ile	Val	Glu	Pro	Glu	Leu	Ser	Ile	Glu	Val	Cys	Glu	Glu	Lys	Ala
	1				5					10					15	
	Ser	Ala	Val	Leu	Pro	Pro	Thr	Cys	Ile	Gln	Leu	Leu	Asp	Ser	Ser	Asn
				20					25					30		
25	Trp	Lys	Glu	Arg	Leu	Ala	Cys	Met	Glu	Glu	Phe	Gln	Lys	Ala	Val	Glu
			35					40					45			
	Leu	Met	Asp	Arg	Thr	Glu	Met	Pro	Cys	Gln	Ala	Leu	Val	Arg	Met	Leu
			50				55					60				
	Ala	Lys	Lys	Pro	Gly	Trp	Lys	Glu	Thr	Asn	Phe	Gln	Val	Met	Gln	Met
30						70					75					80
	Lys	Leu	His	Ile	Val	Ala	Leu	Ile	Ala	Gln	Lys	Gly	Asn	Phe	Ser	Lys
				85						90					95	
	Thr	Ser	Ala	Gln	Val	Val	Leu	Asp	Gly	Leu	Val	Asp	Lys	Ile	Gly	Asp
				100					105					110		
35	Val	Lys	Cys	Gly	Asn	Asn	Ala	Lys	Glu	Ala	Met	Thr	Ala	Ile	Ala	Glu
			115					120					125			
	Ala	Cys	Met	Leu	Pro	Trp	Thr	Ala	Glu	Gln	Val	Val	Ser	Met	Ala	Phe
			130				135					140				
	Ser	Gln	Lys	Asn	Pro	Lys	Asn	Gln	Ser	Glu	Thr	Leu	Asn	Trp	Leu	Ser
40						150					155					160
	Asn	Ala	Ile	Lys	Glu	Phe	Gly	Phe	Ser	Gly	Leu	Asn	Val	Lys	Ala	Phe
					165					170					175	
	Ile	Asn	Asn	Val	Lys	Thr	Ala	Leu	Ala	Ala	Thr	Asn	Pro	Ala	Val	Arg
				180					185					190		
45	Thr	Ala	Ala	Ile	Thr	Leu	Leu	Gly	Val	Met	Tyr	Leu</				

Cys Leu Asp Leu Ile Leu Lys Trp Leu Thr Leu Arg Phe Phe Asp Thr
 65 70 75 80
 Asn Thr Ser Val Leu Met Lys Ala Leu Glu Tyr Leu Lys Leu Leu Phe
 85 90 95
 5 Thr Leu Leu Ser Glu Glu Glu Tyr His Leu Thr Glu Asn Glu Ala Ser
 100 105 110
 Ser Phe Ile Pro Tyr Leu Val Val Lys Val Gly Glu Pro Lys Asp Val
 115 120 125
 10 Ile Arg Lys Asp Val Arg Ala Ile Leu Asn Arg Met Cys Leu Val Tyr
 130 135 140
 Pro Ala Ser Lys Met Phe Pro Phe Ile Met Glu Gly Thr Lys Ser Lys
 145 150 155 160
 Asn Ser Lys Gln Arg Ala Glu Cys Leu Glu Glu Leu Gly Cys Leu Val
 165 170 175
 15 Glu Ser Tyr Gly Met Asn Val Cys Gln Pro Thr Pro Gly Lys Ala Leu
 180 185 190
 Lys Glu Ile Ala Val His Ile Gly Asp Arg Asp Asn Ala Val Arg Asn
 195 200 205
 20 Ala Ala Leu Asn Thr Ile Val Thr Val Tyr Asn Val His Gly Asp Gln
 210 215 220
 Val Phe Lys Leu Ile Gly Asn Leu Ser Glu Lys Asp Met Ser Met Leu
 225 230 235 240
 Glu Ser Thr Ser Arg Ala Ala Ala Gly Pro Ser Ile Phe His Pro Gly
 245 250 255
 25 Gly Tyr Gln Val Ser
 260

<210> 1155
 <211> 174
 30 <212> PRT
 <213> Homo sapiens

<400> 1155
 Thr Glu Pro Cys Arg Thr Ala Glu Asn Cys Thr Ala Thr Met Ser Glu
 1 5 10 15
 Asn Asn Lys Asn Ser Leu Glu Ser Ser Leu Arg Gln Leu Lys Cys His
 20 25 30
 Phe Thr Trp Asn Leu Met Glu Gly Glu Asn Ser Leu Asp Asp Phe Glu
 35 40 45
 40 Asp Lys Val Phe Tyr Arg Thr Glu Phe Gln Asn Arg Glu Phe Lys Ala
 50 55 60
 Thr Met Cys Asn Leu Leu Ala Tyr Leu Lys His Leu Lys Gly Gln Asn
 65 70 75 80
 45 Glu Ala Ala Leu Glu Cys Leu Arg Lys Ala Glu Glu Leu Ile Gln Gln
 85 90 95
 Glu His Ala Asp Gln Ala Glu Ile Arg Ser Leu Val Thr Trp Gly Asn
 100 105 110
 Tyr Ala Trp Val Tyr Tyr His Met Gly Arg Leu Ser Asp Val Gln Ile
 115 120 125
 50 Tyr Val Asp Lys Val Lys His Val Cys Glu Lys Phe Ser Ser Pro Tyr
 130 135 140
 Arg Ile Glu Ser Pro Glu Leu Asp Cys Glu Glu Gly Trp Thr Arg Leu
 145 150 155 160
 55 Lys Cys Gly Gly Asn Gln Asn Glu Arg Ala Lys Val Cys Phe
 165 170

<210> 1156
 <211> 211
 <212> PRT
 60 <213> Homo sapiens

<400> 1156
 Ala Ala Ala Ala Thr Thr Ala Phe Gly Cys Arg Ile Trp Asn Pro Cys

1 5 10 15
 Ala Ala Leu Thr Met Lys Gln Ser Ser Asn Val Pro Ala Phe Leu Ser
 20 25 30
 Lys Leu Trp Thr Leu Val Glu Glu Thr His Thr Asn Glu Phe Ile Thr
 35 40 45
 Trp Ser Gln Asn Gly Gln Ser Phe Leu Val Leu Asp Glu Gln Arg Phe
 50 55 60
 Ala Lys Glu Ile Leu Pro Lys Tyr Phe Lys His Asn Asn Met Ala Ser
 65 70 75 80
 10 Phe Val Arg Gln Leu Asn Met Tyr Gly Phe Arg Lys Val Val His Ile
 85 90 95
 Asp Ser Gly Ile Val Lys Gln Glu Arg Asp Gly Pro Val Glu Phe Gln
 100 105 110
 His Pro Tyr Phe Lys Gln Gly Gln Asp Asp Leu Leu Glu Asn Ile Lys
 115 120 125
 15 Arg Lys Val Ser Ser Ser Lys Pro Glu Glu Asn Lys Ile Arg Gln Glu
 130 135 140
 Asp Leu Thr Lys Ile Ile Ser Ser Ala Gln Lys Val Gln Ile Lys Gln
 145 150 155 160
 20 Glu Thr Ile Glu Ser Arg Leu Ser Glu Leu Lys Ser Glu Asn Glu Ser
 165 170 175
 Leu Trp Xaa Glu Xaa Ser Glu Phe Gln Gln Lys His Xaa Gln Gln Gln
 180 185 190
 Gln Val Ile Xaa Lys Asn Val Ser Leu Leu Val His Trp Phe Lys Ile
 195 200 205
 25 Thr Gln Leu
 210

 <210> 1157
 30 <211> 231
 <212> PRT
 <213> Homo sapiens

 <400> 1157
 35 Arg Gln Asp Leu Tyr Ser Ala Arg Asp Leu Gln Gly Leu Thr Val Glu
 1 5 10 15
 His Ala Ile Asp Ser Phe Arg Glu Gly Glu Thr Met Ile Leu Thr Leu
 20 25 30
 Lys Asp Lys Gly Val Leu Gln Glu Glu Glu Asp Val Leu Val Asn Val
 35 40 45
 Asn Leu Val Asp Lys Glu Arg Ala Glu Lys Asn Val Glu Leu Arg Lys
 50 55 60
 Lys Lys Pro Asp Tyr Leu Pro Tyr Ala Glu Asp Glu Ser Val Asp Asp
 65 70 75 80
 45 Leu Ala Gln Gln Lys Pro Arg Ser Ile Leu Ser Lys Tyr Asp Glu Glu
 85 90 95
 Leu Glu Gly Glu Arg Pro His Ser Phe Arg Leu Glu Gln Gly Gly Thr
 100 105 110
 Ala Asp Gly Leu Arg Glu Arg Glu Leu Glu Glu Ile Arg Ala Lys Leu
 115 120 125
 50 Arg Leu Gln Ala Gln Ser Leu Ser Thr Val Gly Pro Arg Leu Ala Ser
 130 135 140
 Glu Tyr Leu Thr Pro Glu Met Val Thr Phe Lys Lys Thr Lys Arg
 145 150 155 160
 55 Arg Val Lys Lys Ile Arg Lys Lys Glu Lys Glu Val Val Val Arg Ala
 165 170 175
 Asp Asp Leu Leu Pro Leu Gly Asp Gln Thr Gln Asp Gly Asp Phe Gly
 180 185 190
 Phe Lys Leu Xaa Gly Thr Gly Ser Pro Pro Lys Cys Pro Lys Xaa Glu
 195 200 205
 60 Glu Glu Glu Arg Thr Phe Ala Leu Xaa Pro Xaa Arg Arg Thr Thr Pro
 210 215 220
 Arg S r Gly Arg Thr Leu Asp

225

230

5

<210> 1158
 <211> 76
 <212> PRT
 <213> Homo sapiens

10

15

20

25

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60

<400> 1158
 Ser Leu Arg Phe Tyr Leu Ser Leu Gly Gln Leu Tyr Leu Ser Met Asn
 1 5 10 15
 Ile Asp Asp Lys Leu Glu Gly Leu Phe Leu Lys Cys Gly Gly Ile Xaa
 20 25 30
 Xaa Met Gln Ser Ser Arg Thr Met Val Xaa Met Gly Gly Val Ser Xaa
 35 40 45
 Xaa Leu Leu Cys Xaa Gly Lys Leu Pro Gly Phe Xaa Thr Xaa Lys Ile
 50 55 60
 Glu Xaa Xaa Pro Xaa Xaa Glu Asp Pro Cys Cys Xaa
 65 70 75

<210> 1159
 <211> 148
 <212> PRT
 <213> Homo sapiens

<400> 1159
 Thr Ser Arg Xaa Met Xaa Pro Cys Pro Ser Ile Ala Phe Asp Pro Gly
 1 5 10 15
 Met Asn Phe Xaa Leu Arg Thr Thr Pro Asp Lys Ser His Phe Gly Leu
 20 25 30
 Ile Val Gly Asp Ser Gln His Ser Phe Pro Phe Ser Gly Asp Glu Thr
 35 40 45
 Asn His Val Xaa Ala Thr Ser Thr Gln Asp Phe Xaa Asp Gln Val Thr
 50 55 60
 Ser Gln Lys Lys Ala Glu Ala Gln Pro Val His Gln Ala Tyr Gln Met
 65 70 75 80
 Ser Ser Phe Glu Gln Pro Phe Arg Ala Pro Tyr His Gly Ser Arg Ala
 85 90 95
 Gly Ile Ala Thr Gln Phe Ser Thr Ala Asn Gly Gln Val Asn Leu Arg
 100 105 110
 Gly Pro Gly Thr Ser Ala Glu Phe Ser Glu Phe Pro Leu Val Asn Val
 115 120 125
 Asn Asp Asn Arg Ala Gly Met Thr Ser Ser Pro Asp Ala Thr Thr Gly
 130 135 140
 Gln Thr Phe Gly
 145

<210> 1160
 <211> 217
 <212> PRT
 <213> Homo sapiens

<400> 1160
 Ser Leu Pro Ala Ser Phe Ser Pro Leu Val Pro Ser Thr Ser Cys Glu
 1 5 10 15
 Gly Ile His Leu Cys Ala Glu Leu Leu Gly Thr Met Ala Ser Leu Ser
 20 25 30
 Leu Ala Pro Val Asn Ile Phe Lys Ala Gly Ala Asp Glu Glu Arg Ala
 35 40 45
 Glu Thr Ala Arg Leu Thr Ser Phe Ile Gly Ala Ile Ala Ile Gly Asp
 50 55 60
 Leu Val Lys Ser Thr Leu Gly Pro Lys Gly Met Asp Lys Ile Leu Leu
 65 70 75 80
 Ser Ser Gly Arg Asp Ala Ser Leu Met Val Thr Asn Asp Gly Ala Thr

85 90 95
 Ile Leu Lys Asn Ile Gly Val Asp Asn Pro Ala Ala Lys Val Leu Val
 100 105 110
 5 Asp Met Ser Arg Val Gln Asp Asp Glu Val Gly Asp Gly Thr Thr Ser
 115 120 125
 Val Thr Val Leu Ala Ala Glu Leu Leu Arg Glu Ala Glu Ser Leu Ile
 130 135 140
 Ala Lys Lys Ile His Pro Gln Thr Ile Ile Ala Gly Trp Arg Glu Ala
 145 150 155 160
 10 Thr Lys Ala Ala Arg Xaa Ala Leu Leu Ser Ser Ala Val Asp His Gly
 165 170 175
 Ser His Glu Xaa Xaa Phe Arg Xaa Glu Leu Met Asn Ile Xaa Gly Pro
 180 185 190
 15 His Tyr Pro Gln Asn Phe Leu Leu Xaa Thr Lys Thr Thr Leu Gln Lys
 195 200 205
 Xaa Ala Val Xaa Xaa Val Leu Lys Leu
 210 215

 20 <210> 1161
 <211> 226
 <212> PRT
 <213> Homo sapiens

 <400> 1161
 25 Pro Asp Gln Leu Asp Pro Xaa Val Ala Arg Lys Leu Leu Xaa Lys Lys
 1 5 10 15
 Asn Pro Ser Cys Phe Pro Arg Arg Arg Arg Ser Arg Leu Met Thr Leu
 20 25 30
 30 Thr Glu Val Ser Xaa Ser Met Lys Ala Phe Ile Ser Lys Val Ser Thr
 35 40 45
 Xaa Lys Gly Ala Glu Leu Pro Arg Glu Pro Phe Glu Ala Pro Ile Thr
 50 55 60
 Phe Asp Ala Asp Ser Phe Leu Asn Tyr Phe Asp Lys Ile Leu Gly Pro
 65 70 75 80
 35 Arg Pro Asn Glu Ser Asp Ser Asp Asp Leu Asp Asp Glu Asp Phe Glu
 85 90 95
 Cys Leu Asp Ser Asp Asp Asp Leu Asp Phe Glu Thr His Glu Pro Gly
 100 105 110
 40 Glu Glu Ala Ser Leu Lys Gly Thr Leu Asp Asn Leu Lys Ser Tyr Met
 115 120 125
 Ala Gln Met Asp Gln Glu Leu Ala His Thr Cys Ile Ser Lys Ser Phe
 130 135 140
 Thr Thr Arg Asn Gln Val Glu Pro Val Ser Gln Thr Thr Asp Asn Asn
 145 150 155 160
 45 Ser Asp Glu Glu Asp Xaa Gly Thr Gly Glu Ser Val Met Ala Pro Val
 165 170 175
 Asp Val Asp Leu Asn Leu Val Ser Asn Ile Leu Glu Ser Tyr Ser Ser
 180 185 190
 50 Gln Ala Gly Leu Ala Gly Pro Ala Ser Asn Leu Leu Gln Ser Met Gly
 195 200 205
 Val Gln Leu Pro Asp Asn Thr Asp His Arg Pro Thr Ser Lys Pro Thr
 210 215 220
 Lys Asn
 225

 55 <210> 1162
 <211> 237
 <212> PRT
 <213> Homo sapiens

 60 <400> 1162
 Glu Val Thr Arg Ser Leu Leu Gln Arg Trp Gly Ala Ser Phe Arg Arg
 1 5 10 15

Gly Ala Asp Phe Asp Ser Trp Gly Gln Leu Val Glu Ala Ile Asp Glu
 20 25 30
 Tyr Gln Ile Leu Ala Arg His Leu Gln Lys Glu Ala Gln Ala Gln His
 35 40 45
 5 Asn Asn Ser Glu Phe Thr Glu Glu Gln Lys Lys Thr Ile Gly Lys Ile
 50 55 60
 Ala Thr Cys Leu Glu Leu Arg Ser Ala Ala Leu Gln Ser Thr Gln Ser
 65 70 75 80
 10 Gln Glu Glu Phe Lys Leu Glu Asp Leu Lys Lys Leu Glu Pro Ile Leu
 85 90 95
 Lys Asn Ile Leu Thr Tyr Asn Lys Glu Phe Pro Phe Asp Val Gln Pro
 100 105 110
 Val Pro Leu Arg Arg Ile Leu Ala Pro Gly Glu Glu Glu Asn Leu Glu
 115 120 125
 15 Phe Glu Glu Asp Glu Glu Glu Gly Gly Ala Gly Ala Gly Ser Pro Asp
 130 135 140
 Ser Phe Pro Ala Arg Val Pro Gly Thr Leu Leu Pro Arg Leu Pro Ser
 145 150 155 160
 20 Glu Pro Gly Met Thr Leu Leu Thr Ile Arg Ile Glu Lys Ile Gly Leu
 165 170 175
 Lys Asp Ala Gly Gln Cys Ile Asp Pro Tyr Ile Thr Val Ser Val Lys
 180 185 190
 Asp Leu Asn Gly Ile Asn Leu Thr Pro Val Pro Arg Xaa Xaa Xaa Gly
 195 200 205
 25 Phe Lys Lys Lys Lys Ile His Met Phe Ile Leu Met Xaa Gly His Trp
 210 215 220
 Ser Phe Gln Lys Xaa Cys Trp Xaa Lys Leu Thr Gln Lys
 225 230 235

 30 <210> 1163
 <211> 189
 <212> PRT
 <213> Homo sapiens

 35 <400> 1163
 Gly Ser Arg Phe Ser Ser Thr Leu Thr Gly Trp Leu Gly Gln Leu Arg
 1 5 10 15
 Arg Gly Ser Gln Leu Thr Met Gly Asp Pro Ser Lys Gln Asp Ile Leu
 20 25 30
 40 Thr Ile Phe Lys Arg Leu Arg Ser Val Pro Thr Asn Lys Val Cys Phe
 35 40 45
 Asp Cys Gly Ala Lys Asn Pro Ser Trp Ala Ser Ile Thr Tyr Gly Val
 50 55 60
 45 Phe Leu Cys Ile Asp Cys Ser Gly Ser His Arg Ser Leu Gly Val His
 65 70 75 80
 Leu Ser Phe Ile Arg Ser Thr Glu Leu Asp Ser Asn Trp Ser Trp Phe
 85 90 95
 Gln Leu Arg Cys Met Gln Val Gly Gly Asn Ala Ser Ala Ser Ser Phe
 100 105 110
 50 Phe His Gln His Gly Cys Ser Thr Asn Asp Thr Asn Ala Lys Tyr Asn
 115 120 125
 Ser Arg Ala Ala Gln Leu Tyr Arg Glu Lys Ile Lys Ser Leu Ala Ser
 130 135 140
 55 Gln Ala Thr Arg Lys His Gly Thr Asp Leu Trp Leu Asp Ser Cys Val
 145 150 155 160
 Val Pro Pro Leu Ser Pro Pro Pro Lys Glu Glu Asp Phe Phe Ala Ser
 165 170 175
 His Val Ser Ser Glu Val Ser Asp Thr Xaa Val Gly Ile
 180 185

 60 <210> 1164
 <211> 167
 <212> PRT

<213> Homo sapiens

<400> 1164

5 Gly Glu Asp Val Arg Gly Val Leu Lys Arg Arg Val Glu Thr Arg Gln
 1 5 10 15
 His Thr Xaa Glu Ala Ile Arg Gln Gln Glu Val Glu Gln Leu Asp Phe
 20 25 30
 Arg Asp Leu Leu Gly Lys Lys Val Ser Thr Lys Thr Leu Ser Glu Asp
 35 40 45
 10 Asp Leu Lys Glu Ile Pro Ala Glu Gln Met Asp Phe Arg Ala Asn Leu
 50 55 60
 Gln Arg Gln Val Lys Pro Lys Thr Val Ser Glu Glu Glu Arg Lys Val
 65 70 75 80
 His Ser Pro Gln Gln Val Asp Phe Arg Ser Val Leu Ala Lys Lys Gly
 15 85 90 95
 Thr Ser Lys Thr Pro Val Pro Glu Lys Val Pro Pro Pro Lys Pro Ala
 100 105 110
 Thr Pro Asp Phe Arg Ser Val Leu Gly Gly Lys Lys Lys Leu Pro Ala
 115 120 125
 20 Glu Asn Gly Ser Ser Ser Ala Glu Thr Leu Asn Ala Lys Ala Val Glu
 130 135 140
 Ser Ser Lys Pro Leu Ser Asn Ala Gln Pro Ser Gly Pro Leu Lys Pro
 145 150 155 160
 25 Val Gly Asn Ala Gln Ala Cys
 165

<210> 1165

<211> 242

<212> PRT

30 <213> Homo sapiens
 <400> 1165

Tyr Leu Gln Pro Thr Trp Asp Phe Asp Xaa Arg Gly His Ser Met Arg
 1 5 10 15
 35 Phe Xaa Asp Asp Ala Lys Asp Phe Ile Ser Ile Leu Leu Lys Lys Asp
 20 25 30
 Met Lys Thr Xaa Leu Asp Cys Thr Gln Cys Xaa Gln His Pro Trp Xaa
 35 40 45
 40 Met Lys Asp Xaa Xaa Glu His Gly Gly Gln Glu Thr Phe Gln Gly Xaa
 50 55 60
 Met Lys Lys Tyr Met Ala Arg Xaa Lys Trp Gln Lys Thr Gly Asn Ala
 65 70 75 80
 Val Arg Ala Ile Gly Arg Leu Ser Ser Met Ala Met Ile Ser Gly Leu
 85 90 95
 45 Ser Gly Arg Lys Ser Ser Thr Gly Ser Pro Thr Ser Pro Leu Asn Ala
 100 105 110
 Glu Lys Leu Glu Ser Glu Asp Val Ser Gln Ala Phe Leu Glu Ala Val
 115 120 125
 50 Ala Glu Glu Lys Pro His Val Lys Pro Tyr Phe Ser Lys Thr Ile Arg
 130 135 140
 Asp Leu Glu Val Val Glu Gly Ser Ala Ala Arg Phe Asp Cys Lys Ile
 145 150 155 160
 Glu Gly Tyr Pro Asp Pro Glu Val Xaa Trp Phe Lys Asp Asp Gln Ser
 165 170 175
 55 Ile Arg Glu Ser Arg His Phe Gln Ile Asp Tyr Asp Glu Asp Gly Asn
 180 185 190
 Cys Ser Leu Ile Ile Ser Asp Val Cys Gly Asp Asp Ala Lys Tyr
 195 200 205
 60 Thr Cys Lys Ala Val Asn Ser Leu Gly Glu Ala Thr Cys Thr Ala Glu
 210 215 220
 Leu Ile Val Glu Thr Met Glu Glu Gly Glu Gly Glu Glu Glu
 225 230 235 240
 Glu Glu

5 <210> 1166
 <211> 221
 <212> PRT
 <213> Homo sapiens

<400> 1166
 10 Ser Gly Lys Met Ala Lys Val Ser Glu Leu Tyr Asp Val Thr Trp Glu
 1 5 10 15
 Glu Met Arg Asp Lys Met Arg Lys Trp Arg Glu Glu Asn Ser Arg Asn
 20 25 30
 Ser Glu Gln Ile Val Glu Val Gly Glu Glu Leu Ile Asn Glu Tyr Ala
 35 40 45
 15 Ser Lys Leu Gly Asp Asp Ile Trp Ile Ile Tyr Glu Gln Val Met Ile
 50 55 60
 Ala Ala Leu Asp Tyr Gly Arg Asp Asp Leu Ala Leu Phe Cys Leu Gln
 65 70 75 80
 20 Glu Leu Arg Arg Gln Phe Pro Gly Ser His Arg Val Lys Arg Leu Thr
 85 90 95
 Gly Met Arg Phe Glu Ala Met Glu Arg Tyr Asp Asp Ala Ile Gln Leu
 100 105 110
 Tyr Asp Arg Ile Leu Gln Glu Asp Pro Thr Asn Thr Ala Ala Arg Lys
 115 120 125
 25 Arg Lys Ile Ala Ile Arg Lys Ala Gln Gly Lys Asn Val Glu Ala Ile
 130 135 140
 Arg Glu Leu Asn Glu Tyr Leu Glu Gln Phe Val Gly Asp Gln Glu Ala
 145 150 155 160
 30 Trp His Glu Leu Ala Glu Leu Tyr Ile Asn Glu His Asp Tyr Ala Lys
 165 170 175
 Ala Ala Phe Cys Leu Glu Glu Leu Met Met Thr Asn Pro His Asn His
 180 185 190
 Leu Tyr Cys Gln Gln Tyr Ala Glu Val Lys Tyr Thr Gln Xaa Gly Leu
 195 200 205
 35 Glu Asn Leu Asp Phe Gln Glu Ser Ile Leu His Arg His
 210 215 220

40 <210> 1167
 <211> 167
 <212> PRT
 <213> Homo sapiens

<400> 1167
 45 His Val Leu Ser Leu Ser Phe Pro Ile Arg Arg Asp Asp Gly Ser Trp
 1 5 10 15
 Glu Val Ile Glu Gly Tyr Arg Ala Gln His Ser Gln His Arg Thr Pro
 20 25 30
 Cys Lys Gly Gly Ile Arg Tyr Ser Thr Asp Val Ser Val Asp Glu Val
 35 40 45
 50 Lys Ala Leu Ala Ser Leu Met Thr Tyr Lys Cys Ala Val Val Asp Val
 50 55 60
 Pro Phe Gly Gly Ala Lys Ala Gly Val Lys Ile Asn Pro Lys Asn Tyr
 65 70 75 80
 55 Thr Asp Asn Glu Leu Glu Lys Ile Thr Arg Arg Phe Thr Met Glu Leu
 85 90 95
 Ala Lys Lys Gly Phe Ile Gly Pro Gly Ile Asp Val Pro Ala Pro Asp
 100 105 110
 Met Ser Thr Gly Glu Arg Glu Met Ser Trp Ile Ala Asp Thr Tyr Ala
 115 120 125
 60 Ser Thr Ile Gly His Tyr Asp Ile Asn Ala His Ala Cys Val Thr Gly
 130 135 140
 Lys Pro Ile Ser Gln Gly Gly Ile His Gly Arg Ile Ser Ala Thr Gly
 145 150 155 160

Pro Trp Cys Leu Pro Trp Asp
165

5 <210> 1168
<211> 112
<212> PRT
<213> Homo sapiens

<400> 1168
10 Ile Phe Ile Ser Xaa Xaa Xaa Pro Tyr Phe Xaa Asn Lys Asp Leu Ser
1 5 10 15
Xaa Gln Xaa Tyr Xaa Ile Xaa Xaa Gly Asp Xaa Ser Ser Thr Ser Xaa
20 25 30
Xaa Leu Xaa Trp Xaa Ser Ala Xaa Asp Leu Thr Xaa Arg Xaa Xaa Xaa
15 35 40 45
Pro Ala Glu Xaa Ser His Gln Gly Xaa Gly Ile His Glu Glu Pro Glu
50 55 60
Ser Phe Phe Thr Trp Phe Thr Asp His Ser Asp Ala Gly Ala Asp Xaa
65 70 75 80
20 Leu Xaa Glu Val Xaa Lys Asp Asp Ile Trp Pro Asn Pro Leu Gln Xaa
85 90 95
Tyr Leu Val Pro Asp Met Asp Asp Glu Xaa Xaa Xaa Gly Glu Arg Arg
100 105 110

25 <210> 1169
<211> 67
<212> PRT
<213> Homo sapiens

<400> 1169
30 Thr His Ile Arg Tyr Asn Lys Ile Gly Val Val Lys Thr Met Ser Cys
1 5 10 15
Gly Asn Glu Phe Val Glu Thr Leu Lys Lys Ile Gly Tyr Pro Lys Ala
20 25 30
35 Asp Asn Leu Asn Gly Glu Asp Phe Asp Trp Leu Phe Glu Gly Val Glu
35 40 45
Xaa Glu Ser Phe Leu Lys Trp Phe Cys Gly Asn Val Asn Glu Gln Asn
50 55 60
Val Leu Ser
40 65

<210> 1170
<211> 208
<212> PRT
45 <213> Homo sapiens

<400> 1170
Glu Ser Ser Gly Thr Tyr Ile Val Asn Leu Glu Asn Leu Val Gln Glu
1 5 10 15
50 Leu Ser Gln Ser Asn Met Met Leu Xaa Lys Gln Leu Glu Met Leu Thr
20 25 30
Asp Pro Ser Val Ser Gln Gln Ile Asn Pro Arg Asn Thr Ile Asp Thr
35 40 45
Lys Asp Tyr Ser Thr His Arg Leu Tyr Gln Val Leu Glu Gly Glu Asn
55 50 55 60
Lys Lys Lys Glu Leu Phe Leu Thr His Gly Asn Leu Glu Glu Val Ala
65 70 75 80
Glu Lys Leu Lys Gln Asn Ile Ser Leu Val Gln Asp Gln Leu Ala Val
85 90 95
60 Ser Ala Gln Glu His Ser Phe Phe Leu Ser Lys Arg Asn Lys Asp Val
100 105 110
Asp Met Leu Cys Asp Thr Leu Tyr Gln Gly Gly Asn Gln Leu Leu Leu
115 120 125

Ser Asp Gln Glu Leu Thr Glu Gln Phe His Lys Val Glu Ser Gln Leu
 130 135 140
 Asn Lys Leu Asn His Leu Leu Thr Asp Ile Leu Ala Asp Val Lys Thr
 145 150 155 160
 5 Lys Arg Lys Thr Leu Ala Asn Asn Lys Leu His Gln Met Glu Arg Glu
 165 170 175
 Phe Tyr Val Tyr Phe Leu Lys Asp Glu Asp Tyr Leu Lys Asp Ile Val
 180 185 190
 10 Glu Asn Leu Glu Thr Gln Ser Lys Ile Lys Ala Val Ser Leu Glu Asp
 195 200 205

<210> 1171

<211> 227

<212> PRT

15 <213> Homo sapiens

<400> 1171

Arg Leu Tyr Asn Ser Ala Val Val Thr Met Pro Val Val Arg Lys Ile
 1 5 10 15
 20 Phe Arg Arg Arg Arg Gly Asp Ser Glu Ser Glu Glu Asp Glu Gln Asp
 20 25 30
 Ser Glu Glu Val Arg Leu Lys Leu Glu Glu Thr Arg Glu Val Gln Asn
 35 40 45
 25 Leu Arg Lys Arg Pro Asn Gly Val Ser Ala Val Ala Leu Leu Val Gly
 50 55 60
 Glu Lys Val Gln Glu Glu Thr Thr Leu Val Asp Asp Pro Phe Gln Met
 65 70 75 80
 Lys Thr Gly Gly Met Val Asp Met Lys Lys Leu Lys Glu Arg Gly Lys
 85 90 95
 30 Asp Lys Ile Ser Glu Glu Glu Asp Leu His Leu Gly Thr Ser Phe Ser
 100 105 110
 Ala Glu Thr Asn Arg Arg Asp Glu Asp Ala Asp Met Met Lys Tyr Ile
 115 120 125
 35 Glu Thr Glu Leu Lys Lys Arg Lys Gly Ile Val Glu His Glu Glu Gln
 130 135 140
 Lys Val Lys Pro Lys Asn Ala Glu Asp Cys Leu Tyr Glu Leu Pro Glu
 145 150 155 160
 Asn Ile Arg Val Ser Ser Ala Lys Lys Thr Glu Glu Met Leu Ser Asn
 165 170 175
 40 Gln Met Leu Ser Gly Ile Pro Glu Val Asp Leu Gly Ile Asp Ala Lys
 180 185 190
 Ile Lys Asn Ile Ile Xaa Thr Glu Asp Ala Lys Ala Arg Leu Leu Ala
 195 200 205
 45 Glu Xaa Arg Thr Arg Lys Lys Asp Arg Glu Thr Ser Leu Cys Leu Pro
 210 215 220
 Thr Trp Leu
 225

<210> 1172

50 <211> 209

<212> PRT

<213> Homo sapiens

<400> 1172

Glu Arg Leu Arg Asp Ile Tyr Arg Pro Pro Xaa Lys Phe Gly Ser Lys
 1 5 10 15
 Asn Leu Ser Gln Ser Asn Met Met Leu Xaa Lys Gln Leu Glu Met Leu
 20 25 30
 60 Thr Asp Pro Ser Val Ser Xaa Gln Ile Asn Pro Arg Asn Thr Ile Asp
 35 40 45
 Thr Lys Asp Tyr Ser Thr His Arg Leu Tyr Gln Val Leu Glu Gly Glu
 50 55 60
 Asn Lys Lys Lys Glu Leu Phe Leu Thr His Gly Asn Leu Glu Glu Val

65 70 75 80
 Ala Glu Lys Leu Lys Gln Asn Ile Ser Leu Val Gln Asp Gln Leu Ala
 85 90 95
 Val Ser Ala Gln Glu His Ser Phe Phe Leu Ser Lys Arg Asn Lys Asp
 100 105 110
 Val Asp Met Leu Cys Asp Thr Leu Tyr Gln Gly Gly Asn Gln Leu Leu
 115 120 125
 Leu Ser Asp Gln Glu Leu Thr Glu Gln Phe His Lys Val Glu Ser Gln
 130 135 140
 10 Leu Asn Lys Leu Asn His Leu Leu Thr Asp Ile Leu Ala Asp Val Lys
 145 150 155 160
 Thr Lys Arg Lys Thr Leu Ala Asn Asn Lys Leu His Gln Met Glu Arg
 165 170 175
 15 Glu Phe Tyr Val Tyr Phe Leu Lys Asp Glu Asp Tyr Leu Lys Asp Ile
 180 185 190
 Val Glu Asn Leu Glu Thr Gln Ser Lys Ile Lys Ala Val Ser Leu Glu
 195 200 205
 Asp

20

<210> 1173
 <211> 178
 <212> PRT
 <213> Homo sapiens

25

<400> 1173
 Ile Val Glu Arg Glu Ser Gly His Tyr Val Glu Met His Ala Arg Tyr
 1 5 10 15
 Ile Gly Thr Thr Val Phe Val Arg Gln Val Gly Arg Tyr Leu Thr Leu
 20 25 30
 30 Ala Ile Arg Met Pro Glu Asp Leu Ala Met Ser Tyr Glu Glu Ser Gln
 35 40 45
 Asp Leu Gln Leu Cys Val Asn Gly Cys Pro Leu Ser Glu Arg Ile Asp
 50 55 60
 35 Asp Gly Gln Gly Gln Val Ser Ala Ile Leu Gly His Ser Leu Pro Arg
 65 70 75 80
 Thr Ser Leu Val Gln Ala Trp Pro Gly Tyr Thr Leu Glu Thr Ala Asn
 85 90 95
 Thr Gln Cys His Glu Lys Met Pro Val Lys Asp Ile Tyr Phe Gln Ser
 100 105 110
 40 Cys Val Phe Asp Leu Leu Thr Thr Gly Asp Ala Asn Phe Thr Ala Ala
 115 120 125
 Ala His Ser Ala Leu Glu Asp Val Glu Ala Leu His Pro Arg Lys Glu
 130 135 140
 45 Arg Trp His Ile Phe Pro Ser Ser Gly Asn Gly Thr Pro Arg Gly Gly
 145 150 155 160
 Ser Asp Leu Ser Val Ser Leu Gly Leu Thr Cys Leu Ile Leu Ile Val
 165 170 175
 Phe Leu

50

<210> 1174
 <211> 166
 <212> PRT
 <213> Homo sapiens

55

<400> 1174
 Thr Asp Arg Gln Ile Thr Ala Ser Thr Gly Ser Pro Ile Ala Thr Ala
 1 5 10 15
 60 Gly Glu Asn Val Pro Ala Phe Leu Pro Trp Val Gln Gly Leu His Ile
 20 25 30
 Leu Gln Gly Thr Val Gly Cys Gly Ser Lys Val Gly Ile Thr Ser Gly
 35 40 45

Glu Gln Val Glu Asp Thr Gly Leu Glu Ile Asp Val Leu His Trp His
 50 55 60
 Leu Leu Met Ala Leu Ser Val Gly Ser Leu Gln Cys Val Ala Arg Pro
 65 70 75 80
 5 Gly Leu His Gln Gly Gly Ala Arg Gln Ala Val Ser Gln Asp Gly Arg
 85 90 95
 His Leu Ala Leu Pro Val Ile Asp Ala Phe Thr Gln Gly Ala Ala Val
 100 105 110
 His Ala Gln Leu Gln Val Leu Ala Leu Val Gly His Gly Gln Val
 115 120 125
 10 Phe Arg His Thr Asp Gly Lys Gly Gln Val Ala Thr His Leu Pro His
 130 135 140
 Lys His Cys Gly Pro Tyr Ile Ala Gly Val His Leu His Ile Val Ala
 145 150 155 160
 15 Thr Leu Pro Phe His Asp
 165

<210> 1175
 <211> 118
 20 <212> PRT
 <213> Homo sapiens

<400> 1175
 Ala Gly Arg Arg His Arg Thr Gly Asn Arg Cys Pro Ser Leu Ala Ser
 25 1 5 10 15
 Ser His Gly Ile Glu Cys Trp Gln Ser Pro Val Cys Ser Gln Ala Arg
 20 25 30
 Pro Ala Pro Arg Arg Cys Glu Ala Gly Cys Val Pro Gly Trp Gln Thr
 35 40 45
 30 Pro Gly Pro Ala Arg His Arg Cys Val His Ser Gly Gly Ser Arg Ser
 50 55 60
 Arg Thr Ala Ala Gly Pro Gly Ser Pro Arg Arg Thr Trp Pro Gly Leu
 65 70 75 80
 Gln Ala Tyr Gly Trp Gln Gly Ser Gly Ser Asp Pro Pro Ala Ala Gln
 85 90 95
 35 Thr Leu Trp Ser Leu Tyr Ser Gly Arg Ala Ser Pro His Ser Gly His
 100 105 110
 Ser Pro Phe Pro Arg Tyr
 115

<210> 1176
 <211> 82
 <212> PRT
 <213> Homo sapiens

<400> 1176
 Lys Lys Cys Cys Leu His Met Leu Val Xaa Glu Thr Leu Ala Arg Arg
 1 5 10 15
 Ile Ser Gly His Thr Asn Met Trp Ile Gly Xaa Ser Cys Ser Glu Xaa
 20 25 30
 Ser Trp Gly Ser Leu Lys Arg Gly Lys Xaa Trp Phe Ser Xaa Met Leu
 35 40 45
 His Met Ala Xaa Phe Lys Arg Leu Lys Thr Phe Phe Cys Pro Leu Cys
 50 55 60
 55 Xaa Ala Trp Lys Leu Pro Pro Xaa Gln Cys Val Glu Xaa Leu Gln Arg
 65 70 75 80
 Asn Leu

<210> 1177
 <211> 44
 <212> PRT
 <213> Homo sapiens

<400> 1177
 Thr Gln Thr Tyr Xaa Asn Ser Ser Ile Xaa Phe Thr Ser Leu Ser Ser
 1 5 10 15
 5 Ile Cys Gln Lys Xaa Gly Val Ser Pro Asp Phe Phe Xaa Leu Gly Pro
 20 25 30
 Pro Xaa Xaa Lys Gln Ile Phe Thr Met Leu Leu Asn
 35 40

10 <210> 1178
 <211> 216
 <212> PRT
 <213> Homo sapiens

15 <400> 1178
 Leu Ser Glu Lys Phe Phe Lys Ala Ala Ser Asn Cys Gly Ile Val Glu
 1 5 10 15
 Ser Ile Leu Asn Trp Val Lys Phe Lys Ala Gln Thr Gln Leu Asn Lys
 20 25 30
 Lys Cys Ser Ser Val Lys Tyr Ser Lys Ile Lys Gly Ile Pro Lys Leu
 35 40 45
 Asp Asp Ala Asn Asp Ala Gly Gly Lys His Ser Leu Glu Cys Thr Leu
 50 55 60
 Ile Leu Thr Glu Gly Asp Ser Ala Lys Ser Leu Ala Val Ser Gly Leu
 25 65 70 75 80
 Gly Val Ile Gly Arg Asp Arg Tyr Gly Val Phe Pro Leu Arg Gly Lys
 85 90 95
 Ile Leu Asn Val Arg Glu Ala Ser His Lys Gln Ile Met Glu Asn Ala
 100 105 110
 30 Glu Ile Asn Asn Ile Ile Lys Ile Val Gly Leu Gln Tyr Lys Lys Ser
 115 120 125
 Tyr Asp Asp Ala Glu Ser Leu Lys Thr Leu Arg Tyr Gly Lys Ile Met
 130 135 140
 Ile Met Thr Asp Gln Asp Gln Asp Gly Ser His Ile Lys Gly Leu Leu
 35 145 150 155 160
 Ile Asn Phe Ile His His Asn Trp Pro Ser Leu Leu Lys His Gly Phe
 165 170 175
 Leu Glu Glu Phe Ile Thr Pro Ile Xaa Lys Ala Ser Lys Asn Lys Gln
 180 185 190
 40 Glu Leu Ser Phe Tyr Ser Ile Pro Glu Phe Ala Asn Gly Lys Asn Ile
 195 200 205
 Xaa Lys Thr Arg Lys Pro Gly Lys
 210 215

45 <210> 1179
 <211> 110
 <212> PRT
 <213> Homo sapiens

50 <400> 1179
 Lys Pro Phe Ser Xaa Pro Val Leu Lys Pro Xaa Xaa Thr Xaa Lys Thr
 1 5 10 15
 Lys Xaa Arg Xaa Lys Gly Cys Xaa Leu Xaa Leu Gly Ile Gln Asn Leu
 20 25 30
 55 Ala Phe Gln Xaa Lys Pro Xaa Pro Lys Gly Lys Gly Xaa Gly Ala
 35 40 45
 Xaa Lys Arg Lys Ala Xaa Gly Phe Glu Asn Glu Gly Asp Tyr Asn Pro
 50 55 60
 Gly Arg Xaa Xaa Ser Lys Xaa Xaa Ser Lys Lys Pro Lys Lys Thr Xaa
 60 65 70 75 80
 Phe Asp Gln Asp Ser Asp Val Asp Ile Phe Pro Ser Xaa Phe Pro Asn
 85 90 95
 Glu Xaa Pro Phe Leu Pro Arg Thr Gly Xaa Val Xaa Xaa Lys

	100	105	110
	<210> 1180		
	<211> 176		
5	<212> PRT		
	<213> Homo sapiens		
	<400> 1180		
10	Val Gly Arg Tyr Leu Thr Leu Ala Ile Arg Met Pro Glu Asp Leu Ala		
	1 5 10 15		
	Met Ser Tyr Glu Glu Ser Gln Asp Leu Gln Leu Cys Val Asn Gly Cys		
	20 25 30		
	Pro Leu Ser Glu Arg Ile Asp Asp Gly Gln Gly Gln Val Ser Ala Ile		
	35 40 45		
15	Leu Gly His Ser Leu Pro Arg Thr Ser Leu Val Gln Ala Trp Pro Gly		
	50 55 60		
	Tyr Thr Leu Glu Thr Ala Asn Thr Gln Cys His Glu Lys Met Pro Val		
	65 70 75 80		
	Lys Asp Ile Tyr Phe Gln Ser Cys Val Phe Asp Leu Leu Thr Thr Gly		
20	85 90 95		
	Asp Ala Asn Phe Thr Ala Ala Ala His Ser Ala Leu Glu Asp Val Glu		
	100 105 110		
	Ala Leu His Pro Arg Lys Glu Arg Trp His Ile Phe Pro Ser Ser Gly		
	115 120 125		
25	Asn Gly Thr Pro Arg Gly Gly Ser Asp Leu Ser Val Lys Ser Arg Thr		
	130 135 140		
	His Leu Leu Asp Pro Tyr Arg Val Phe Val Gly Val Xaa Phe Xaa Phe		
	145 150 155 160		
	Gly Phe Leu Phe Phe Xaa Tyr Asn Lys Ile Leu Lys Tyr Ile Leu Xaa		
30	165 170 175		
	<210> 1181		
	<211> 87		
	<212> PRT		
35	<213> Homo sapiens		
	<400> 1181		
	Lys Lys Cys Cys Leu His Met Leu Val Xaa Glu Thr Leu Ala Arg Arg		
	1 5 10 15		
40	Ile Ser Gly His Thr Asn Met Trp Ile Gly Tyr Ser Cys Ser Glu Xaa		
	20 25 30		
	Ser Trp Gly Ser Leu Lys Arg Gly Lys His Trp Phe Ser Gln Met Leu		
	35 40 45		
	His Met Ala Xaa Phe Lys Arg Leu Lys Thr Phe Phe Cys Pro Leu Cys		
45	50 55 60		
	Xaa Ala Trp Lys Leu Pro Pro Pro His Ser Val Ser Ser Leu Cys Lys		
	65 70 75 80		
	Glu Thr Phe Arg Cys Gly Ser		
	85		
50	<210> 1182		
	<211> 85		
	<212> PRT		
	<213> Homo sapiens		
55	<400> 1182		
	Phe Arg Ser Xaa Val Lys Ile Cys Phe Xaa Ile Trp Xaa Ala Gln Xaa		
	1 5 10 15		
60	Arg Lys Lys Ser Gly Xaa Tyr Pro Pro Phe Phe Val Gln Lys Tyr Glu		
	20 25 30		
	Ser Glu Val Lys Xaa Ile Glu Glu Phe Xaa Lys Asp Leu Gly Xaa Glu		
	35 40 45		
	Cys Val Ser Leu Ile Xaa Asn Leu Cys Ser Phe Gln Xaa Lys Tyr His		

50 55 60
 Xaa Xaa Leu Leu Asp Ser Gly Lys Arg Arg Leu Gly Tyr Phe Ala Ile
 65 70 75 80
 Ser Phe Ser Trp Lys
 85
 <210> 1183
 <211> 83
 <212> PRT
 10 <213> Homo sapiens
 <400> 1183
 Asn Gly Gly Asn Thr Gly Phe His Arg Cys Ser Thr Trp Leu Xaa Leu
 1 5 10 15
 15 Lys Asp Ser Lys Leu Phe Phe Val Leu Phe Val Xaa Leu Gly Ser Ser
 20 25 30
 Pro Pro Pro Thr Val Cys Arg Val Phe Ala Lys Lys Pro Leu Asp Val
 35 40 45
 Val His Arg Tyr Met Asn Thr Tyr Leu Cys Lys Thr Val Ser Val Gln
 50 55 60
 20 Cys Val Asn Thr Leu Asn Tyr Tyr Ala Arg Lys Ile Lys Leu His Thr
 65 70 75 80
 Leu Leu Trp
 25
 <210> 1184
 <211> 229
 <212> PRT
 30 <213> Homo sapiens
 <400> 1184
 Glu Ile Thr Glu Leu Lys Val Lys Glu Phe Glu Asn Ile Lys Leu Gln
 1 5 10 15
 35 Leu Gln Glu Asn His Glu Asp Glu Val Lys Lys Val Lys Ala Glu Val
 20 25 30
 Glu Asp Leu Lys Tyr Xaa Leu Asp Gln Ser Gln Lys Glu Ser Gln Cys
 35 40 45
 Leu Lys Ser Glu Leu Gln Ala Gln Lys Glu Ala Asn Ser Arg Ala Pro
 50 55 60
 40 Thr Thr Thr Met Arg Asn Leu Val Glu Arg Leu Lys Ser Gln Leu Ala
 65 70 75 80
 Leu Lys Glu Lys Gln Gln Lys Ala Leu Ser Arg Ala Leu Leu Glu Leu
 85 90 95
 Arg Ala Glu Met Thr Ala Ala Ala Glu Arg Ile Ile Ser Ala Thr
 100 105 110
 45 Ser Gln Lys Glu Ala His Leu Asn Val Gln Gln Ile Val Asp Arg His
 115 120 125
 Thr Arg Glu Leu Lys Thr Gln Val Glu Asp Leu Asn Glu Asn Leu Leu
 130 135 140
 50 Lys Leu Lys Glu Ala Leu Lys Thr Ser Lys Asn Arg Glu Asn Ser Leu
 145 150 155 160
 Thr Asp Asn Leu Asn Asp Leu Asn Asn Glu Leu Gln Lys Lys Gln Lys
 165 170 175
 Ala Tyr Asn Lys Ile Leu Arg Glu Lys Glu Glu Ile Asp Gln Glu Asn
 180 185 190
 55 Asp Glu Leu Lys Arg Gln Ile Lys Arg Leu Thr Xaa Gly Leu Gln Gly
 195 200 205
 Lys Pro Leu Thr Asp Asn Lys Pro Arg Ser Asn Trp Arg Asn Ser Xaa
 210 215 220
 60 Gly Arg Leu Lys Thr
 225

<210> 1185

<211> 182
 <212> PRT
 <213> Homo sapiens

5 <400> 1185
 Cys Lys Xaa Gly Pro Gln Xaa Gly Xaa Gln Lys Gly Phe Pro Asn Pro
 1 5 10 15
 Met Lys Pro Leu Xaa Thr Arg Leu Arg Xaa Leu Asn His Val Xaa Xaa
 20 25 30
 10 Gly Val Glu Thr Glu Gln Ala Phe Lys Gly Ser Phe Gln Val Phe Arg
 35 40 45
 Xaa Ala Asn His Pro Ala Asp Lys Glu Lys Ala Glu Leu Ile His Gln
 50 55 60
 15 Ile Glu Ala Thr Lys Asp Gln Ser Gly Ala Glu Ser Xaa Ile Pro Asp
 65 70 75 80
 Ala Asp Gln Leu Lys Glu Lys Ile Lys Asp Leu Glu Xaa Gln Leu Lys
 85 90 95
 Met Ser Asp Xaa Glu Lys Gln His Leu Lys Glu Glu Ile Lys Lys Leu
 100 105 110
 20 Lys Lys Glu Leu Glu Asn Phe Asp Pro Ser Phe Phe Glu Glu Ile Glu
 115 120 125
 Asp Xaa Lys Tyr Asn Tyr Lys Glu Glu Val Lys Lys Asn Ile Xaa Leu
 130 135 140
 Glu Glu Lys Val Lys Lys Leu Ser Glu Gln Leu Gly Val Glu Leu Thr
 25 145 150 155 160
 Ser Pro Val Ala Ala Xaa Glu Glu Phe Glu Asp Glu Glu Glu Ser Pro
 165 170 175
 Val Asn Phe Pro Ile Tyr
 180

30
 <210> 1186
 <211> 118
 <212> PRT
 <213> Homo sapiens

35 <400> 1186
 Arg Glu Leu Glu Pro Ala Glu Phe Glu Thr Met Leu Leu Phe Cys Pro
 1 5 10 15
 Gly Cys Gly Asn Gly Leu Ile Val Glu Glu Gly Gln Arg Cys His Arg
 20 25 30
 40 Phe Ala Cys Asn Thr Cys Pro Tyr Val His Asn Ile Thr Arg Lys Val
 35 40 45
 Thr Asn Arg Lys Tyr Pro Lys Leu Lys Glu Val Asp Asp Val Leu Gly
 50 55 60
 45 Gly Ala Ala Ala Trp Glu Asn Val Asp Ser Thr Ala Glu Ser Cys Pro
 65 70 75 80
 Lys Cys Glu His Pro Arg Ala Tyr Phe Met Gln Leu Gln Thr Arg Ser
 85 90 95
 50 Ala Asp Glu Pro Met Thr Thr Phe Tyr Lys Cys Cys Asn Ala Gln Cys
 100 105 110
 Gly His Arg Trp Arg Asp
 115

55 <210> 1187
 <211> 84
 <212> PRT
 <213> Homo sapiens

60 <400> 1187
 Cys Asn Thr Cys Pro Leu Arg Ala Gln His His Xaa Gln Gly Asn Lys
 1 5 10 15
 Ser Xaa Asp Pro Lys Leu Lys Glu Val Asp Xaa Val Leu Gly Gly Ala
 20 25 30

Ala Ala Trp Glu Asn Val Asp Ser Thr Ala Glu Ser Cys Pro Lys Cys
 35 40 45
 Glu His Pro Arg Ala Tyr Phe Met Gln Leu Gln Thr Arg Ser Ala Asp
 50 55 60
 5 Glu Pro Met Thr Xaa Phe Tyr Lys Cys Cys Asn Ala Gln Cys Gly His
 65 70 75 80
 Arg Trp Arg Asp

10 <210> 1188
 <211> 190
 <212> PRT
 <213> Homo sapiens

15 <400> 1188
 Leu Gln Asp Ile Lys Glu Lys Ile Ser Lys Gly Glu Tyr Gly Asn Ala
 1 5 10 15
 Gly Ile Met Ala Glu Val Glu Glu Leu Arg Lys Arg Val Leu Asp Met
 20 25 30
 20 Glu Gly Lys Asp Glu Glu Leu Ile Lys Met Glu Glu Gln Cys Arg Asp
 35 40 45
 Leu Asn Lys Arg Leu Glu Arg Glu Thr Leu Gln Ser Lys Asp Phe Lys
 50 55 60
 Leu Glu Val Glu Lys Leu Ser Lys Arg Ile Met Ala Leu Glu Lys Leu
 25 65 70 75 80
 Glu Asp Ala Phe Asn Lys Ser Lys Gln Glu Cys Tyr Ser Leu Lys Cys
 85 90 95
 Asn Leu Glu Lys Glu Arg Met Thr Thr Lys Gln Leu Ser Gln Glu Leu
 100 105 110
 30 Glu Ser Leu Lys Val Arg Ile Lys Glu Leu Glu Ala Ile Glu Ser Arg
 115 120 125
 Leu Glu Lys Thr Glu Phe Thr Leu Lys Glu Asp Leu Thr Lys Leu Lys
 130 135 140
 Thr Leu Thr Val Met Phe Val Asp Glu Arg Lys Thr Met Ser Glu Lys
 35 145 150 155 160
 Leu Lys Lys Thr Glu Asp Lys Leu Gln Ala Ala Ser Ser Gln Leu Gln
 165 170 175
 Val Glu Gln Asn Lys Val Thr Thr Val Thr Glu Lys Val Asn
 180 185 190

40 <210> 1189
 <211> 214
 <212> PRT
 <213> Homo sapiens

45 <400> 1189
 Val Arg Val Asp Ser Thr Ala Lys Val Ala Glu Ile Glu His Ala Glu
 1 5 10 15
 Lys Glu Lys Met Lys Glu Lys Val Glu Arg Ile Leu Lys His Gly Ile
 20 25 30
 50 Asn Cys Phe Ile Asn Arg Gln Leu Ile Tyr Asn Tyr Pro Glu Gln Leu
 35 40 45
 Phe Gly Ala Ala Gly Val Met Ala Ile Glu His Ala Asp Phe Ala Gly
 50 55 60
 55 Val Glu Arg Leu Ala Leu Val Thr Gly Gly Glu Ile Ala Ser Thr Phe
 65 70 75 80
 Asp His Pro Glu Leu Val Lys Leu Gly Ser Cys Lys Leu Ile Glu Glu
 85 90 95
 Val Met Ile Gly Glu Asp Lys Leu Ile His Phe Ser Gly Val Ala Leu
 100 105 110
 60 Gly Glu Ala Cys Thr Ile Val Leu Arg Gly Ala Thr Gln Gln Ile Leu
 115 120 125
 Asp Glu Ala Glu Arg Ser Leu His Asp Ala Leu Cys Val Leu Ala Gln

130 135 140
 Thr Val Lys Asp Ser Arg Thr Val Tyr Gly Gly Gly Cys Ser Glu Met
 145 150 155 160
 Leu Met Ala His Ala Val Thr Gln Leu Ala Asn Arg Thr Pro Gly Lys
 5 165 170 175
 Glu Ala Val Ala Met Glu Ser Tyr Ala Lys Ala Leu Arg Met Leu Pro
 180 185 190
 Thr Ile Ile Ala Asp Asn Ala Ala Met Thr Val Gln Thr Trp Trp His
 195 200 205
 10 Ser Ser Arg Leu Leu Gln
 210

<210> 1190
 <211> 245
 15 <212> PRT
 <213> Homo sapiens

<400> 1190
 Ser Arg Thr Arg Thr Ser Asp Arg Leu Asn Arg Ile Ala Asn Gln Val
 20 1 5 10 15
 Ala Ile Gln Arg Lys Lys Gln Phe Val Glu Arg Ala His Ser Tyr Trp
 20 25 30
 Leu Leu Lys Arg Leu Ser Arg Asn Gly Ala Pro Leu Leu Arg Arg Leu
 35 40 45
 25 Gln Ser Ser Leu Gln Ser Gln Arg Ser Ser Gln Gln Arg Glu Asn Asp
 50 55 60
 Glu Glu Met Lys Ala Ala Lys Glu Lys Leu Lys Tyr Trp Gln Arg Leu
 65 70 75 80
 Arg His Asp Leu Glu Arg Ala Arg Leu Leu Ile Glu Leu Leu Arg Lys
 30 85 90 95
 Arg Glu Lys Leu Lys Arg Glu Gln Val Lys Val Glu Gln Val Ala Met
 100 105 110
 Glu Leu Arg Leu Thr Pro Leu Thr Val Leu Leu Arg Ser Val Leu Asp
 115 120 125
 35 Gln Leu Gln Asp Lys Asp Pro Ala Arg Ile Phe Ala Gln Pro Val Ser
 130 135 140
 Leu Lys Glu Val Pro Asp Tyr Leu Asp His Ile Lys His Pro Met Asp
 145 150 155 160
 Phe Ala Thr Met Arg Lys Arg Leu Glu Ala Gln Gly Tyr Lys Asn Leu
 40 165 170 175
 His Glu Phe Glu Glu Asp Phe Asp Leu Ile Ile Asp Asn Cys Met Lys
 180 185 190
 Tyr Asn Ala Arg Asp Thr Val Phe Tyr Lys Xaa Arg Gly Glu Ala Cys
 195 200 205
 45 Ala Ile Lys Glu Val Leu Phe Leu Xaa Gln Ala Pro Xaa Arg Xaa Gly
 210 215 220
 Thr Ser Ile Arg Leu Gly Lys Arg Xaa Ser Gly Ile Ala Pro Cys Leu
 225 230 235 240
 Lys Pro Gly Leu Leu
 50 245

<210> 1191
 <211> 190
 <212> PRT
 55 <213> Homo sapiens

<400> 1191
 Pro Glu Ala Glu Thr Thr Gly Cys Gly Ala Ala Gly Arg Asp Thr Cys
 1 5 10 15
 60 Ser Pro Phe Asp Pro Ile Met Ser Arg Gly Ser Ile Glu Ile Pro Leu
 20 25 30
 Arg Asp Thr Asp Glu Val Ile Glu Leu Asp Phe Asp Gln Leu Pro Glu
 35 40 45

Gly Asp Glu Val Ile Ser Ile Leu Lys Gln Glu His Thr Gln Leu His
 50 55 60
 Ile Trp Ile Ala Leu Ala Leu Glu Tyr Tyr Lys Gln Gly Lys Thr Glu
 65 70 75 80
 5 Glu Phe Val Lys Leu Leu Glu Ala Ala Arg Ile Asp Gly Asn Leu Asp
 85 90 95
 Tyr Arg Asp His Glu Lys Asp Gln Met Thr Cys Leu Asp Thr Leu Ala
 100 105 110
 10 Ala Tyr Tyr Val Gln Gln Ala Arg Lys Glu Lys Asn Lys Asp Asn Lys
 115 120 125
 Lys Asp Leu Ile Thr Gln Ala Thr Leu Leu Tyr Thr Met Ala Asp Lys
 130 135 140
 Ile Ile Met Tyr Asp Gln Asn His Leu Leu Gly Arg Ala Cys Phe Cys
 145 150 155 160
 15 Leu Leu Glu Gly Asp Lys Met Asp Gln Ala Asp Ala Gln Phe His Phe
 165 170 175
 Val Leu Asn Gln Ser Xaa Asn Asn Ile Xaa Ser Pro Ser Trp
 180 185 190
 20 <210> 1192
 <211> 114
 <212> PRT
 <213> Homo sapiens
 25 <400> 1192
 Ala Glu Ala Gly Ser Ser Gln Gln Met Val Leu Ile Ile His Asn Asn
 1 5 10 15
 Phe Ile Gly His Cys Ile Gln Gln Gly Gly Leu Cys Asn Lys Ile Leu
 20 25 30
 30 Phe Ile Val Leu Ile Leu Phe Phe Pro Ser Leu Leu Tyr Ile Ile Arg
 35 40 45
 Cys Gln Cys Ile Gln Ala Ser His Leu Val Phe Phe Met Val Ser Ile
 50 55 60
 Val Gln Ile Ala Ile Tyr Thr Cys Cys Phe Gln Gln Phe Tyr Lys Leu
 65 70 75 80
 35 Phe Cys Phe Ser Leu Leu Val Val Phe Gln Arg Gln Ser Asn Pro Tyr
 85 90 95
 Val Gln Leu Cys Val Phe Leu Phe Gln Asn Thr Asp Asn Phe Ile Ser
 100 105 110
 40 Leu Arg
 <210> 1193
 <211> 40
 45 <212> PRT
 <213> Homo sapiens
 <400> 1193
 Lys Arg Phe Leu Thr Asn Glu Gly Ser Gly Xaa Lys Xaa Leu Glu Met
 1 5 10 15
 Asn Xaa Asn Gln Arg Asp Pro Pro Pro Lys Xaa Ser Asp Lys Gly Ser
 20 25 30
 Glu His Gly Ser Asp Asp Ser Asp
 35 40
 55 <210> 1194
 <211> 196
 <212> PRT
 <213> Homo sapiens
 60 <400> 1194
 Glu Arg Xaa Leu Glu Arg Ala Arg Glu Arg Asp Lys Glu Arg Glu Arg
 1 5 10 15

Gln Arg Asp Trp Glu Asp Lys Asp Lys Gly Arg Asp Asp Arg Arg Glu
 20 25 30
 Lys Arg Glu Glu Ile Arg Glu Asp Arg Asn Pro Arg Asp Gly His Asp
 35 40 45
 5 Glu Arg Lys Ser Lys Lys Arg Tyr Arg Asn Glu Gly Ser Pro Ser Pro
 50 55 60
 Arg Gln Ser Pro Lys Arg Arg Arg Glu His Ser Pro Asp Ser Asp Ala
 65 70 75 80
 10 Tyr Asn Ser Gly Asp Asp Lys Asn Glu Lys His Arg Leu Leu Ser Gln
 85 90 95
 Val Val Arg Pro Gln Glu Ser Arg Ser Leu Ser Pro Ser His Leu Thr
 100 105 110
 Glu Asp Arg Gln Gly Arg Trp Lys Glu Glu Asp Arg Lys Pro Glu Arg
 115 120 125
 15 Lys Glu Ser Ser Arg Arg Tyr Glu Glu Gln Glu Leu Lys Glu Lys Val
 130 135 140
 Ser Ser Val Asp Lys Gln Arg Glu Gln Thr Glu Ile Leu Glu Ser Ser
 145 150 155 160
 20 Arg Met Arg Ala Gln Asp Ile Ile Gly His His Gln Ser Glu Asp Arg
 165 170 175
 Glu Thr Ser Asp Arg Ala Leu Met Lys Thr Arg Arg Lys Pro Lys Phe
 180 185 190
 Lys Glu Xaa Ile
 195
 25
 <210> 1195
 <211> 194
 <212> PRT
 <213> Homo sapiens
 30
 <400> 1195
 Glu Lys Ser Glu Lys Lys Xaa Ile Lys Xaa Glu Xaa Pro Lys Gly Leu
 1 5 10 15
 35 Gly Xaa Xaa Xaa Xaa Lys Ala Glu Met Xaa Xaa Xaa Lys Ser Xaa Lys
 20 25 30
 Arg Ser Glu Lys Ile Gly Ile Gln Glu Met Xaa Met Met Lys Glu Asn
 35 40 45
 Gln Arg Ser Gly Tyr Arg Asn Glu Gly Xaa Pro Ser Pro Arg Gln Ser
 50 55 60
 40 Pro Lys Arg Arg Gly Glu His Xaa Pro Asp Ser Asp Ala Xaa Xaa Xaa
 65 70 75 80
 Gly Asp Asp Lys Asn Glu Lys Pro Arg Xaa Leu Ser Gln Val Val Xaa
 85 90 95
 45 Xaa Gln Xaa Phe Xaa Phe Phe Ser Pro Ser Pro Leu Xaa Xaa Asp Arg
 100 105 110
 Gln Gly Arg Trp Lys Xaa Glu Xaa Cys Xaa Pro Glu Arg Lys Xaa Ser
 115 120 125
 Ser Arg Xaa Tyr Glu Glu Gln Glu Leu Lys Xaa Lys Val Phe Phe Val
 130 135 140
 50 Asp Lys Gln Arg Glu Gln Thr Glu Ile Leu Glu Ser Ser Arg Met Xaa
 145 150 155 160
 Xaa Gln Xaa Ile Ile Xaa Pro Pro Gln Phe Glu Asp Arg Xaa Thr Xaa
 165 170 175
 55 Asp Xaa Ala His Asp Glu Asn Lys Lys Lys Ala Lys Ile Gln Lys Xaa
 180 185 190
 Xaa Xaa
 60
 <210> 1196
 <211> 232
 <212> PRT
 <213> Homo sapiens

<400> 1196
 Gln Asp Leu Tyr Ser Ala Arg Asp Leu Gln Gly Leu Thr Val Glu His
 1 5 10 15
 5 Ala Ile Asp Ser Phe Arg Glu Gly Glu Thr Met Ile Leu Thr Leu Lys
 20 25 30
 Asp Lys Gly Val Leu Gln Glu Glu Asp Val Leu Val Asn Val Asn
 35 40 45
 Leu Val Asp Lys Glu Arg Ala Glu Lys Asn Val Glu Leu Arg Lys Lys
 50 55 60
 10 Lys Pro Asp Tyr Leu Pro Tyr Ala Glu Asp Glu Ser Val Asp Asp Leu
 65 70 75 80
 Ala Gln Gln Lys Pro Arg Ser Ile Leu Ser Lys Tyr Asp Glu Glu Leu
 85 90 95
 15 Glu Gly Glu Arg Pro His Ser Phe Arg Leu Glu Gln Gly Gly Thr Ala
 100 105 110
 Asp Gly Leu Arg Glu Arg Glu Leu Glu Glu Ile Arg Ala Lys Leu Arg
 115 120 125
 Leu Gln Ala Gln Ser Leu Ser Thr Val Gly Pro Arg Leu Ala Ser Glu
 130 135 140
 20 Tyr Leu Thr Pro Glu Glu Met Val Thr Phe Lys Lys Thr Lys Arg Arg
 145 150 155 160
 Val Lys Lys Ile Arg Lys Lys Glu Lys Glu Val Val Val Arg Ala Asp
 165 170 175
 25 Asp Leu Leu Pro Leu Gly Asp Gln Thr Gln Asp Gly Asp Phe Gly Ser
 180 185 190
 Xaa Thr Ala Gly Asp Xaa Val Pro Pro Gln Cys Xaa Glu Trp Arg Lys
 195 200 205
 Lys Xaa Glu Pro Cys Ala Leu Thr Pro Gly Val Gly Arg His Pro Asn
 210 215 220
 30 Xaa Arg Thr Leu Asp Ile Ile Asp
 225 230

<210> 1197
 <211> 165
 35 <212> PRT
 <213> Homo sapiens.

<400> 1197
 Ile Gly Gly Trp Gln Leu Pro Cys Ser Cys Val Arg Thr Lys Gly Cys
 1 5 10 15
 40 Trp Arg Pro Gln Ser Glu Gly Gly Pro Gly Lys Ala Pro Asn Lys Ser
 20 25 30
 Leu Pro Ser Ala Val Xaa Cys Ile Glu Asp Lys Met Ala Ile Asp Asp
 35 40 45
 45 Lys Tyr Ser Arg Arg Glu Glu Tyr Arg Gly Phe Thr Gln Asp Phe Lys
 50 55 60
 Glu Lys Asp Gly Tyr Lys Pro Asp Val Lys Ile Glu Tyr Val Asp Glu
 65 70 75 80
 Thr Gly Arg Lys Leu Thr Pro Lys Glu Ala Phe Arg Gln Leu Ser His
 85 90 95
 50 Arg Phe His Gly Lys Gly Ser Gly Lys Met Lys Thr Glu Arg Arg Met
 100 105 110
 Lys Lys Leu Asp Glu Glu Ala Leu Leu Lys Lys Met Ser Ser Asp
 115 120 125
 55 Thr Pro Leu Gly Thr Val Ala Leu Leu Gln Glu Lys Gln Lys Ala Gln
 130 135 140
 Lys Thr Pro Tyr Ile Val Leu Ser Gly Ser Gly Lys Ser Met Asn Ala
 145 150 155 160
 60 Asn Thr Ile Thr Lys
 165

<210> 1198
 <211> 206

<212> PRT

<213> Homo sapiens

<400> 1198

5 Lys Met Ala Lys Val Ser Glu Leu Tyr Asp Val Thr Trp Glu Glu Met
 1 5 10 15
 Arg Asp Lys Met Arg Lys Trp Arg Glu Asn Ser Arg Asn Ser Glu
 20 25 30
 10 Gln Ile Val Glu Val Gly Glu Glu Leu Ile Asn Glu Tyr Ala Ser Lys
 35 40 45
 Leu Gly Asp Asp Ile Trp Ile Ile Tyr Glu Gln Val Met Ile Ala Ala
 50 55 60
 Leu Asp Tyr Gly Arg Asp Asp Leu Ala Leu Phe Cys Leu Gln Glu Leu
 65 70 75 80
 15 Arg Arg Gln Phe Pro Gly Ser His Arg Val Lys Arg Leu Thr Gly Met
 85 90 95
 Arg Phe Glu Ala Met Glu Arg Tyr Asp Asp Ala Ile Gln Leu Tyr Asp
 100 105 110
 20 Arg Ile Leu Gln Glu Asp Pro Thr Asn Thr Ala Ala Arg Lys Arg Lys
 115 120 125
 Ile Ala Ile Arg Lys Ala Gln Gly Lys Asn Val Glu Ala Ile Arg Glu
 130 135 140
 Leu Asn Glu Tyr Leu Glu Gln Phe Val Gly Asp Gln Glu Ala Trp His
 145 150 155 160
 25 Glu Leu Ala Glu Leu Tyr Ile Asn Glu His Asp Tyr Ala Lys Ala Ala
 165 170 175
 Phe Cys Leu Glu Glu Leu Met Met Thr Asn Pro His Asn His Leu Tyr
 180 185 190
 30 Cys Gln Gln Tyr Ala Glu Val Lys Tyr Thr Gln Xaa Trp Thr
 195 200 205

<210> 1199

<211> 62

<212> PRT

35 <213> Homo sapiens

<400> 1199

Cys Gln Gln Tyr Ala Glu Val Lys Tyr Thr Gln Gly Xaa Leu Glu Thr
 1 5 10 15
 40 Leu Glu Leu Ser Arg Lys Tyr Phe Ala Gln Ala Leu Lys Leu Asn Asn
 20 25 30
 Arg Asn Met Arg Ala Leu Phe Gly Leu Tyr Met Ser Ala Ser His Ile
 35 40 45
 45 Ala Xaa Asn Pro Lys Ala Ser Ala Lys Thr Lys Lys Ala Thr
 50 55 60

<210> 1200

<211> 147

<212> PRT

50 <213> Homo sapiens

<400> 1200

Ser Pro Cys Arg Ser Pro His Arg Trp Val Asn Ser Thr Cys Arg Ser
 1 5 10 15
 55 Thr Leu Lys Thr Arg Arg Leu Trp Tyr Asn Thr Pro His Thr His Ser
 20 25 30
 Gln Pro Pro Asp Lys Thr His Ser Leu Pro Leu Pro Cys Thr Ile Pro
 35 40 45
 Met Arg His Asn Tyr Asn Lys Leu His Leu Pro Thr Thr Asn Arg Pro
 50 55 60
 60 Lys Ile Ala His Cys Ile Leu Phe Asn Gln Pro His Ser Pro Arg Ser
 65 70 75 80
 Asn Ser His Ser His Pro Asn Pro Leu Lys Leu His Arg Arg Ser His

85 90 95
 Ser His Asn Arg Pro Arg Thr Tyr Ile Leu Ile Thr Ile Leu Pro Ser
 100 105 110
 5 Lys Leu Lys Leu Arg Thr His Ser Gln Ser His His Asn Pro Leu Ser
 115 120 125
 Arg Thr Ser Asn Ser Thr Pro Thr Asn Ser Phe Leu Met Thr Ser Ser
 130 135 140
 Lys Pro Arg
 145
 10 <210> 1201
 <211> 71
 <212> PRT
 <213> Homo sapiens
 15 <400> 1201
 Ser Asn Ile Thr Leu Leu Leu Thr Gly Leu Asn Ile Leu Val Thr Ala
 1 5 10 15
 20 Leu Tyr Ser Leu Tyr Ile Phe Thr Thr Thr Gln Trp Gly Ser Leu Thr
 20 25 30
 His His Ile Asn Asn Ile Lys Pro Ser Phe Thr Arg Glu Asn Thr Leu
 35 40 45
 Met Phe Ile His Leu Ser Pro Ile Leu Leu Leu Ser Leu Asn Pro Asp
 50 55 60
 25 Ile Ile Thr Gly Phe Ser Ser
 65 70
 <210> 1202
 <211> 93
 30 <212> PRT
 <213> Homo sapiens
 <400> 1202
 35 Ala His His Ser Leu Ile Glu Asn Asn Arg Asn Gln Ile Ile Gln Ala
 1 5 10 15
 Leu Leu Ile Thr Ile Leu Leu Gly Leu Tyr Phe Thr Leu Leu Gln Ala
 20 25 30
 Ser Glu Tyr Phe Glu Ser Pro Phe Thr Ile Ser Asp Gly Ile Tyr Gly
 35 40 45
 40 Ser Thr Phe Phe Val Ala Thr Gly Phe His Gly Leu His Val Ile Ile
 50 55 60
 Gly Ser Thr Phe Leu Thr Ile Cys Phe Ile Arg Gln Leu Ile Phe His
 65 70 75 80
 Phe Thr Ser Lys His His Phe Gly Phe Glu Ala Ala Ala
 45 85 90
 <210> 1203
 <211> 159
 <212> PRT
 50 <213> Homo sapiens
 <400> 1203
 Val Ser Ser Arg Tyr Xaa Pro Asn Glu Gly Ser His His Xaa Phe Leu
 1 5 10 15
 55 Lys Xaa Gln Arg Lys Ser Lys Ser Xaa Lys Ile Ile Phe Asn Tyr Xaa
 20 25 30
 Xaa Asp Ala Xaa Arg Glu Xaa Thr Leu Val Ser Glu Xaa Ala Gln Arg
 35 40 45
 Ala Gln Arg Glu Xaa Gln Cys Gln Met Lys Glu Ala Glu His Met Tyr
 50 55 60
 60 Gln Asn Glu Gln Asp Asn Val Asn Lys Xaa Xaa Gln Xaa Xaa Ser
 65 70 75 80
 Leu Asp Gln Lys Leu Phe Gln Leu Gln Ser Lys Asn Met Trp Leu Xaa

85 90 95
 Gln Gln Leu Val Xaa Xaa His Lys Lys Xaa Ala Xaa Lys Ser Lys Ile
 100 105 110
 5 Xaa Ile Asp Ile His Phe Leu Glu Arg Lys Xaa Xaa His His Xaa Leu
 115 120 125
 Lys Glu Lys Asn Glu Glu Ile Phe Asn Ser Asn Xaa His Leu Lys Xaa
 130 135 140
 Arg Ile Tyr Gln Tyr Glu Lys Glu Lys Ala Glu Xaa Glu Asn Ser
 145 150 155
 10
 <210> 1204
 <211> 53
 <212> PRT
 <213> Homo sapiens
 15
 <400> 1204
 Ser Gln Pro Tyr Thr Pro Ser Thr Tyr Leu Pro Gln His Asn Gly Ala
 1 5 10 15
 20 His Ser Pro His Ile Asn Asn Ile Lys Pro Ser Phe Thr Arg Glu Asn
 20 25 30
 Thr Leu Met Ser Tyr Thr Tyr Pro His Ser Leu Tyr Ser Ser Thr Arg
 35 40 45
 Ile Leu Pro Gly Phe
 50
 25
 <210> 1205
 <211> 71
 <212> PRT
 <213> Homo sapiens
 30
 <400> 1205
 Ser Asn Ile Thr Leu Leu Leu Thr Gly Leu Asn Ile Leu Val Thr Ala
 1 5 10 15
 35 Leu Tyr Ser Leu Tyr Ile Phe Thr Thr Thr Gln Trp Gly Ser Leu Thr
 20 25 30
 His His Ile Asn Asn Ile Lys Pro Ser Phe Thr Arg Glu Asn Thr Leu
 35 40 45
 Met Phe Ile His Leu Ser Pro Ile Leu Leu Leu Ser Leu Asn Pro Asp
 50 55 60
 40 Ile Ile Thr Gly Phe Ser Ser
 65 70
 <210> 1206
 <211> 279
 45 <212> PRT
 <213> Homo sapiens
 <400> 1206
 50 Glu Ile His Arg Lys Leu Ser Glu Ala Thr Arg Glu Leu Gln Asn Ala
 1 5 10 15
 Pro Asp Ala Ile Pro Glu Ser Gly Val Glu Pro Pro Ala Leu Asp Thr
 20 25 30
 Ala Trp Val Glu Ala Thr Arg Lys Lys Ala Leu Leu Lys Leu Glu Lys
 35 40 45
 55 Leu Asp Thr Asp Leu Lys Asn Tyr Lys Gly Asn Ser Ile Lys Glu Ser
 50 55 60
 Ile Arg Arg Gly His Asp Asp Leu Gly Asp His Tyr Leu Asp Cys Gly
 65 70 75 80
 Asp Leu Ser Asn Ala Leu Lys Cys Tyr Ser Arg Ala Arg Asp Tyr Cys
 85 90 95
 60 Thr Ser Ala Lys His Val Ile Asn Met Cys Leu Asn Val Ile Lys Val
 100 105 110
 Ser Val Tyr Leu Gln Asn Trp Ser His Val Leu Ser Tyr Val Ser Lys

115 120 125
 Ala Glu Ser Thr Pro Glu Ile Ala Glu Gln Arg Gly Glu Arg Asp Ser
 130 135 140
 Gln Thr Gln Ala Ile Leu Thr Lys Leu Lys Cys Ala Ala Gly Leu Ala
 145 150 155 160
 Glu Leu Ala Ala Arg Lys Tyr Lys Gln Ala Ala Lys Cys Leu Leu Leu
 165 170 175
 Ala Ser Phe Asp His Cys Asp Phe Pro Glu Leu Leu Ser Pro Ser Asn
 180 185 190
 10 Val Ala Ile Tyr Gly Gly Leu Cys Ala Leu Ala Thr Phe Asp Arg Gln
 195 200 205
 Glu Leu Gln Arg Asn Val Ile Phe Ser Ser Ser Phe Lys Leu Phe Leu
 210 215 220
 Glu Leu Glu Pro Xaa Val Arg Asp Ile Ile Phe Lys Phe Tyr Glu Xaa
 15 225 230 235 240
 Lys Tyr Ala Ser Cys Leu Lys Asn Ala Gly Pro Arg Met Lys Gly Gln
 245 250 255
 Pro Cys Ser Leu Asp Ile Val Xaa Trp Ala Pro Ile Val Lys Asp Pro
 260 265 270
 20 Cys Thr Pro Gln Ile Ser Lys
 275

 <210> 1207
 <211> 178
 25 <212> PRT
 <213> Homo sapiens

 <400> 1207
 Glu Ile His Arg Lys Leu Ser Glu Ala Thr Arg Glu Leu Gln Asn Ala
 1 5 10 15
 Pro Asp Ala Ile Pro Glu Ser Gly Val Glu Pro Pro Ala Leu Asp Thr
 20 25 30
 Ala Trp Val Glu Ala Thr Arg Lys Lys Ala Leu Leu Lys Leu Glu Lys
 35 35 40 45
 Leu Asp Thr Asp Leu Lys Asn Tyr Lys Gly Asn Ser Ile Lys Glu Ser
 50 55 60
 Ile Arg Arg Gly His Asp Asp Leu Gly Asp His Tyr Leu Asp Cys Gly
 65 70 75 80
 Asp Leu Ser Asn Ala Leu Lys Cys Tyr Ser Arg Ala Arg Asp Tyr Cys
 40 85 90 95
 Thr Ser Ala Lys His Val Ile Asn Met Cys Leu Asn Val Ile Lys Val
 100 105 110
 Ser Val Tyr Leu Gln Asn Trp Ser His Val Leu Ser Tyr Val Ser Lys
 115 120 125
 45 Ala Glu Ser Thr Pro Glu Ile Ala Glu Gln Arg Gly Glu Arg Asp Ser
 130 135 140
 Gln Thr Gln Ala Ile Leu Thr Lys Leu Lys Cys Ala Ala Ser Leu Ala
 145 150 155 160
 Lys Leu Xaa Ala Arg Xaa Tyr Lys Gln Ala Cys Gln Val Leu Cys Trp
 50 165 170 175
 Leu Leu

 <210> 1208
 55 <211> 120
 <212> PRT
 <213> Homo sapiens

 <400> 1208
 60 Ser Phe Gln Tyr Phe Lys Pro Leu Arg Phe Lys Pro Thr Met His Xaa
 1 5 10 15
 Met Gly Gln Pro Phe Lys Tyr His Gly Ala Xaa Leu Xaa Gly Arg Val
 20 25 30

Asp Ala Val Asn Leu Glu Gly Val Asp Gln Cys Xaa Cys Gly Leu Thr
 35 40 45
 Gln Ala Arg Ser Tyr Thr Ala Xaa Xaa Val Asp Gln Arg Ser Thr Thr
 50 55 60
 5 Phe Glu Lys Xaa Leu Leu Met Gly Lys Glu Phe Gln Arg Arg Ala Lys
 65 70 75 80
 Ala Met Met Leu Arg Ala Ala Val Leu Arg Asn Gln Ile His Val Lys
 85 90 95
 Ser Pro Pro Arg Glu Gly Ser Gln Gly Glu Leu Thr Pro Ala Asn Ser
 10 100 105 110
 Gln Ser Arg Met Ser Thr Asn Met
 115 120

 <210> 1209
 15 <211> 182
 <212> PRT
 <213> Homo sapiens

 <400> 1209
 20 Gly Val Glu Pro Pro Ala Leu Asp Thr Ala Trp Val Glu Ala Thr Arg
 1 5 10 15
 Lys Lys Ala Leu Leu Lys Leu Glu Lys Leu Asp Thr Asp Leu Lys Asn
 20 25 30
 Tyr Lys Gly Asn Ser Ile Lys Glu Ser Ile Arg Arg Gly His Asp Asp
 25 35 40 45
 Leu Gly Asp His Tyr Leu Asp Cys Gly Asp Leu Ser Asn Ala Leu Lys
 50 55 60
 Cys Tyr Ser Arg Ala Arg Asp Tyr Cys Thr Ser Ala Lys His Val Ile
 65 70 75 80
 30 Asn Met Cys Leu Asn Val Ile Lys Val Ser Val Tyr Leu Gln Asn Trp
 85 90 95
 Ser His Val Leu Ser Tyr Val Ser Lys Ala Glu Ser Thr Pro Glu Ile
 100 105 110
 Ala Glu Gln Arg Gly Glu Arg Asp Ser Gln Thr Gln Ala Ile Leu Thr
 35 115 120 125
 Lys Leu Lys Cys Ala Ala Gly Leu Ala Glu Leu Ala Ala Arg Lys Tyr
 130 135 140
 Lys Gln Ala Ala Lys Cys Leu Leu Leu Ala Ser Phe Asp His Xaa Asp
 145 150 155 160
 40 Phe Pro Glu Leu Leu Ser Pro Asn Asn Val Ala Ile Tyr Gly Gly Leu
 165 170 175
 Cys Ala Leu Ala Thr Phe
 180

 45 <210> 1210
 <211> 239
 <212> PRT
 <213> Homo sapiens

 50 <400> 1210
 Lys Lys Ala Leu Leu Lys Leu Glu Lys Leu Asp Thr Asp Leu Lys Asn
 1 5 10 15
 Tyr Lys Gly Asn Ser Ile Lys Glu Ser Ile Arg Arg Gly His Asp Asp
 20 25 30
 55 Leu Gly Asp His Tyr Leu Asp Cys Gly Asp Leu Ser Asn Ala Leu Lys
 35 40 45
 Cys Tyr Ser Arg Ala Arg Asp Tyr Cys Thr Ser Ala Lys His Val Ile
 50 55 60
 Asn Met Cys Leu Asn Val Ile Lys Val Ser Val Tyr Leu Gln Asn Trp
 60 65 70 75 80
 Ser His Val Leu Ser Tyr Val Ser Lys Ala Glu Ser Thr Pro Glu Ile
 85 90 95
 Ala Glu Arg Gly Glu Arg Asp Ser Gln Thr Gln Ala Ile Leu Thr Lys

100 105 110
 Leu Lys Cys Ala Ala Gly Leu Ala Glu Leu Ala Ala Arg Lys Tyr Lys
 115 120 125
 5 Gln Ala Ala Lys Cys Leu Leu Leu Ala Ser Phe Asp His Cys Asp Phe
 130 135 140
 Pro Glu Leu Leu Ser Pro Ser Asn Val Ala Ile Tyr Gly Gly Leu Cys
 145 150 155 160
 Ala Leu Ala Thr Phe Asp Arg Gln Glu Leu Gln Arg Asn Val Ile Phe
 165 170 175
 10 Ser Ser Ser Phe Lys Leu Phe Leu Glu Leu Glu Pro Xaa Val Arg Asp
 180 185 190
 Ile Ile Phe Lys Phe Tyr Glu Xaa Lys Tyr Ala Ser Cys Leu Lys Asn
 195 200 205
 15 Ala Gly Pro Arg Met Lys Gly Gln Pro Cys Ser Leu Asp Ile Val Xaa
 210 215 220
 Trp Ala Pro Ile Val Lys Asp Pro Cys Thr Pro Gln Ile Ser Lys
 225 230 235

 <210> 1211
 20 <211> 245
 <212> PRT
 <213> Homo sapiens

 <400> 1211
 25 Lys Lys Ala Leu Leu Lys Leu Glu Lys Leu Asp Thr Asp Leu Lys Asn
 1 5 10 15
 Tyr Lys Gly Asn Ser Ile Lys Glu Ser Ile Arg Arg Gly His Asp Asp
 20 25 30
 30 Leu Gly Asp His Tyr Leu Asp Cys Gly Asp Leu Ser Asn Ala Leu Lys
 35 40 45
 Cys Tyr Ser Arg Ala Arg Asp Tyr Cys Thr Ser Ala Lys His Val Ile
 50 55 60
 Asn Met Cys Leu Asn Val Ile Lys Val Ser Val Tyr Leu Gln Asn Trp
 65 70 75 80
 35 Ser His Val Leu Ser Tyr Val Ser Lys Ala Glu Ser Thr Pro Glu Ile
 85 90 95
 Ala Glu Arg Gly Glu Arg Asp Ser Gln Thr Gln Ala Ile Leu Thr Lys
 100 105 110
 40 Leu Lys Cys Ala Ala Gly Leu Ala Glu Leu Ala Ala Arg Lys Tyr Lys
 115 120 125
 Gln Ala Ala Lys Cys Leu Leu Leu Ala Ser Phe Asp His Cys Asp Phe
 130 135 140
 Pro Glu Leu Leu Ser Pro Ser Asn Val Ala Ile Tyr Gly Gly Leu Cys
 145 150 155 160
 45 Ala Leu Ala Thr Phe Asp Arg Gln Glu Leu Gln Arg Asn Val Ile Phe
 165 170 175
 Ser Ser Phe Phe Lys Leu Phe Leu Glu Leu Glu Pro Gln Xaa Arg Asp
 180 185 190
 50 Ile Ile Phe Lys Phe Tyr Glu Xaa Gln Val Pro Leu Met Phe Xaa Arg
 195 200 205
 Cys Leu Asp Glu Asn Glu Arg Thr Thr Leu Xaa Leu Asp Asn Val Xaa
 210 215 220
 Trp Pro Pro Leu Leu Xaa Thr Leu Tyr Asn Pro Lys Phe Arg Asn Arg
 225 230 235 240
 55 Xaa Pro Ser Phe Ser
 245

 <210> 1212
 <211> 210
 60 <212> PRT
 <213> Homo sapiens

 <400> 1212

Ser Glu Met Ile Phe Ser Asp Met Asn Thr Val Ser Gly Ser Pro Lys
 1 5 10 15
 Val His Pro Pro Asn Gly Thr Arg Phe Tyr Thr Phe Gln Glu Phe Ala
 20 25 30
 5 Ala Leu Thr Lys Glu Leu Asn Ala Cys Arg Glu Gln Leu Leu Glu Lys
 35 40 45
 Glu Glu Glu Ile Ser Glu Leu Lys Ala Glu Arg Asn Asn Thr Arg Leu
 50 55 60
 10 Leu Leu Glu His Leu Glu Cys Leu Val Ser Arg His Glu Arg Ser Leu
 65 70 75 80
 Arg Met Thr Val Val Lys Arg Gln Ala Gln Ser Pro Ser Gly Val Ser
 85 90 95
 Ser Glu Val Glu Val Leu Lys Ala Leu Lys Ser Leu Phe Glu His His
 100 105 110
 15 Lys Ala Leu Asp Glu Lys Val Arg Glu Arg Leu Arg Val Ser Leu Glu
 115 120 125
 Arg Val Ser Ala Leu Glu Glu Leu Ala Ala Ala Asn Gln Glu Ile
 130 135 140
 20 Val Ala Leu Arg Glu Gln Asn Val His Ile Gln Arg Lys Met Ala Ser
 145 150 155 160
 Ser Glu Gly Ser Thr Glu Ser Glu His Leu Glu Gly Met Glu Pro Gly
 165 170 175
 Gln Lys Val His Glu Lys Arg Leu Ser Asn Gly Ser Ile Asp Ser Thr
 180 185 190
 25 Asp Glu Thr Ser Gln Ile Val Glu Leu Gln Glu Leu Leu Glu Lys Gln
 195 200 205
 Asn Gln
 210

30 <210> 1213
 <211> 97
 <212> PRT
 <213> Homo sapiens

35 <400> 1213
 Ser Glu Met Ile Phe Ser Asp Met Asn Thr Val Ser Gly Ser Pro Lys
 1 5 10 15
 Val His Pro Pro Asn Gly Thr Arg Phe Tyr Thr Phe Gln Glu Phe Ala
 20 25 30
 40 Ala Leu Thr Lys Glu Leu Asn Ala Cys Arg Glu Gln Leu Leu Glu Lys
 35 40 45
 Glu Glu Glu Ile Ser Glu Leu Lys Ala Glu Arg Asn Asn Thr Arg Leu
 50 55 60
 45 Leu Leu Glu His Leu Glu Cys Leu Val Ser Arg His Glu Arg Ser Leu
 65 70 75 80
 Arg Met Thr Val Val Lys Arg Gln Ala Gln Ser Pro Ser Gly Val Ser
 85 90 95
 Lys

50 <210> 1214
 <211> 209
 <212> PRT
 <213> Homo sapiens

55 <400> 1214
 Glu Met Ile Phe Ser Asp Met Asn Thr Val Ser Gly Ser Pro Lys Val
 1 5 10 15
 His Pro Pro Asn Gly Thr Arg Phe Tyr Thr Phe Gln Glu Phe Ala Ala
 20 25 30
 60 Leu Thr Lys Glu Leu Asn Ala Cys Arg Glu Gln Leu Leu Glu Lys Glu
 35 40 45
 Glu Glu Ile Ser Glu Leu Lys Ala Glu Arg Asn Asn Thr Arg Leu Leu

50 55 60
 Leu Glu His Leu Glu Cys Leu Val Ser Arg His Glu Arg Ser Leu Arg
 65 70 75 80
 Met Thr Val Val Lys Arg Gln Ala Gln Ser Pro Ser Gly Val Ser Ser
 5 85 90 95
 Glu Val Glu Val Leu Lys Ala Leu Lys Ser Leu Phe Glu His His Lys
 100 105 110
 Ala Leu Asp Glu Lys Val Arg Glu Arg Leu Arg Val Ser Leu Glu Arg
 115 120 125
 10 Val Ser Ala Leu Glu Glu Glu Leu Ala Ala Ala Asn Gln Glu Ile Val
 130 135 140
 Ala Leu Arg Glu Gln Asn Val His Ile Gln Arg Lys Met Ala Ser Ser
 145 150 155 160
 Glu Gly Ser Thr Glu Ser Glu His Leu Glu Gly Met Glu Pro Gly Gln
 15 165 170 175
 Lys Val His Glu Lys Arg Leu Ser Asn Gly Ser Ile Asp Ser Thr Asp
 180 185 190
 Glu Thr Ser Gln Ile Val Glu Leu Gln Glu Leu Leu Glu Lys Gln Asn
 195 200 205
 20 Gln

25
 <210> 1215
 <211> 98
 <212> PRT
 <213> Homo sapiens

<400> 1215
 30 Gly Gly Met Asn Asp Leu Phe Phe Gln Glu Phe Ala Ala Leu Thr Lys
 1 5 10 15
 Glu Leu Asn Ala Cys Arg Glu Gln Leu Leu Glu Lys Glu Glu Ile
 20 25 30
 Ser Glu Leu Lys Ala Glu Arg Asn Asn Thr Arg Leu Leu Leu Glu His
 35 35 40 45
 Leu Glu Cys Leu Val Ser Arg His Glu Arg Ser Leu Arg Met Thr Val
 50 55 60
 Val Lys Arg Gln Ala Gln Ser Pro Ser Gly Val Ser Ser Glu Val Glu
 65 70 75 80
 Val Leu Lys Ala Leu Lys Ser Leu Phe Glu Pro Thr Arg Pro Trp Met
 40 85 90 95
 Lys Xaa

45
 <210> 1216
 <211> 214
 <212> PRT
 <213> Homo sapiens

<400> 1216
 50 Xaa Gln Arg Thr Asn Phe Xaa Leu Lys Xaa Ile Phe Ser Leu Pro Ser
 1 5 10 15
 Gly His Ser Asp Ala Gln Thr Leu Ala Met Met Leu Gln Glu Gln Leu
 20 25 30
 Asp Ala Ile Asn Lys Glu Ile Arg Leu Ile Gln Glu Glu Lys Glu Ser
 55 35 40 45
 Thr Glu Leu Arg Ala Glu Glu Ile Glu Asn Arg Val Ala Ser Val Ser
 50 55 60
 Leu Glu Gly Leu Asn Leu Ala Arg Val His Pro Gly Thr Ser Ile Thr
 65 70 75 80
 60 Ala Ser Val Thr Ala Ser Ser Leu Ala Ser Ser Pro Pro Ser Gly
 85 90 95
 His Ser Thr Pro Lys Leu Thr Pro Arg Ser Pro Ala Arg Glu Met Asp
 100 105 110

Arg Met Gly Val Met Thr Leu Pro Ser Asp Xaa Arg Lys His Arg Arg
 115 120 125
 Lys Ile Ala Val Val Glu Glu Asp Gly Arg Glu Asp Lys Ala Thr Ile
 130 135 140
 5 Lys Cys Glu Thr Ser Pro Pro Pro Thr Pro Arg Ala Leu Arg Met Thr
 145 150 155 160
 His Thr Leu Pro Ser Ser Tyr His Asn Asp Ala Arg Ser Ser Leu Ser
 165 170 175
 Val Ser Leu Glu Pro Glu Ser Leu Gly Leu Gly Ser Ala Asn Ser Ser
 10 180 185 190
 Gln Asp Ser Xaa His Lys Ala Pro Lys Lys Lys Gly Ile Lys Ser Ser
 195 200 205
 Ile Gly Arg Leu Phe Gly
 210
 15
 <210> 1217
 <211> 63
 <212> PRT
 <213> Homo sapiens
 20
 <400> 1217
 Leu Leu Leu Ile Arg Arg Trp Trp Pro Cys Val Asn Gln Asn Val His
 1 5 10 15
 Xaa Gln Arg Lys Met Ala Ser Ser Arg Gly Ile Xaa Gln Ser Gln Asn
 25 20 25 30
 Xaa Phe Glu Gly Met Glu Pro Gly Thr Glu Ser Pro Xaa Lys Ser Val
 35 40 45
 Xaa Pro Met Gly Phe Leu Asp Leu Thr Arg Xaa Lys Leu Val Gln
 50 55 60
 30
 <210> 1218
 <211> 169
 <212> PRT
 <213> Homo sapiens
 35
 <400> 1218
 Arg Cys Glu Pro Phe Thr Met Lys Met Leu Lys Asp Ile Lys Glu Gly
 1 5 10 15
 Val Lys Gln Tyr Gly Ser Asn Ser Pro Tyr Ile Arg Thr Leu Leu Asp
 40 20 25 30
 Ser Ile Ala His Gly Asn Arg Leu Thr Pro Tyr Asp Trp Glu Ile Leu
 35 40 45
 Ala Lys Ser Ser Leu Ser Ser Ser Gln Tyr Leu Gln Phe Lys Thr Trp
 50 55 60
 45 Trp Ile Asp Gly Val Gln Glu Gln Val Arg Lys Asn Gln Ala Thr Lys
 65 70 75 80
 Pro Thr Val Asn Ile Asp Ala Asp Gln Leu Leu Gly Thr Gly Pro Asn
 85 90 95
 Trp Ser Thr Ile Asn Gln Gln Ser Val Met Gln Asn Glu Ala Ile Glu
 50 100 105 110
 Gln Val Arg Ala Ile Cys Leu Arg Ala Trp Gly Lys Ile Gln Asp Pro
 115 120 125
 Gly Thr Ala Phe Pro Ile Asn Ser Ile Arg Gln Gly Ser Lys Glu Pro
 130 135 140
 55 Tyr Pro Ala Leu Trp Gln Asp Tyr Lys Met Leu Leu Lys Ser Leu Leu
 145 150 155 160
 Gln Met Thr Met Pro Glu Lys Leu Leu
 165
 60
 <210> 1219
 <211> 224
 <212> PRT
 <213> Homo sapiens

<400> 1219

	Trp	Met	Ile	Arg	Leu	Asn	Xaa	Ala	Xaa	Leu	Ile	Trp	Phe	Xaa	Gln	Asn
	1				5					10					15	
5	Val	Arg	Lys	Xaa	Asn	Phe	Pro	Ile	Leu	Tyr	Xaa	Ser	Xaa	Xaa	Glu	Pro
		20							25					30		
	His	Leu	Ile	Tyr	Gln	Gly	Pro	Leu	Xaa	Lys	Ala	Asn	Asp	Gln	Ala	Asp
		35						40					45			
10	Leu	Leu	Val	Ser	Ser	Ala	Phe	Met	Xaa	Ala	Gln	Glu	Leu	His	Ala	Leu
		50					55					60				
	Thr	His	Val	Asn	Ala	Ile	Gly	Leu	Lys	Asn	Lys	Phe	Asp	Ile	Thr	Trp
	65					70					75				80	
	Lys	Gln	Pro	Lys	Asn	Ile	Val	Gln	His	Cys	Thr	Gln	Cys	Gln	Ile	Leu
					85					90					95	
15	His	Leu	Ala	Thr	Gln	Glu	Ala	Arg	Val	Asn	Pro	Arg	Gly	Leu	Cys	Pro
				100					105					110		
	Asn	Val	Leu	Trp	Gln	Met	Asp	Val	Met	His	Val	Pro	Ser	Phe	Gly	Lys
		115						120					125			
20	Leu	Ser	Phe	Val	His	Val	Thr	Val	Asp	Thr	Tyr	Ser	His	Phe	Ile	Trp
		130					135					140				
	Ala	Thr	Cys	Gln	Thr	Gly	Glu	Ser	Thr	Ser	His	Val	Lys	Arg	His	Leu
	145					150					155				160	
	Leu	Ser	Cys	Phe	Pro	Val	Met	Gly	Val	Pro	Glu	Lys	Val	Lys	Thr	Asp
					165					170					175	
25	Asn	Gly	Pro	Gly	Tyr	Cys	Ser	Lys	Ala	Phe	Gln	Lys	Xaa	Leu	Asn	Gln
				180					185					190		
	Trp	Lys	Ile	Thr	His	Thr	Ile	Gly	Ile	Leu	Tyr	Asn	Ser	Gln	Gly	Gln
		195						200					205			
30	Ala	Ile	Ile	Glu	Arg	Thr	Asn	Arg	Thr	Leu	Lys	Ala	Gln	Leu	Val	Lys
		210					215					220				

<210> 1220

<211> 178

<212> PRT

35 <213> Homo sapiens

<400> 1220

	Gln	Pro	Thr	Ala	Met	Ala	Ser	Asn	Ser	Pro	Ala	Thr	Gln	Asp	Ala	Ala
	1				5					10					15	
40	Leu	Tyr	Pro	Gln	Pro	Pro	Thr	Val	Arg	Leu	Asn	Pro	Thr	Ala	Ser	Arg
			20						25					30		
	Ser	Gly	Gln	Gly	Gly	Ala	Leu	His	Ala	Val	Ile	Asp	Glu	Ala	Arg	Lys
		35					40						45			
45	Gln	Gly	Asp	Leu	Glu	Ala	Trp	Arg	Phe	Leu	Val	Ile	Leu	Gln	Leu	Val
		50					55					60				
	Gln	Ala	Gly	Glu	Glu	Thr	Gln	Val	Gly	Ala	Pro	Ala	Arg	Ala	Glu	Thr
	65					70					75				80	
	Arg	Cys	Glu	Pro	Phe	Thr	Met	Lys	Met	Leu	Lys	Asp	Ile	Lys	Glu	Gly
					85					90					95	
50	Val	Lys	Gln	Tyr	Gly	Ser	Asn	Ser	Pro	Tyr	Ile	Arg	Thr	Leu	Leu	Asp
				100					105					110		
	Ser	Ile	Ala	His	Gly	Asn	Arg	Leu	Thr	Pro	Tyr	Asp	Trp	Glu	Ile	Leu
		115					120						125			
55	Ala	Lys	Ser	Ser	Phe	His	Pro	Leu	Ser	Ile	Tyr	Ser	Leu	Lys	Pro	Gly
		130					135					140				
	Gly	Leu	Met	Glu	Tyr	Lys	Glu	Gln	Val	Arg	Lys	Asn	Gln	Ala	Thr	Asn
	145					150					155				160	
	Pro	Cys	Tyr	Ile	Asp	Ala	Asp	Gln	Leu	Leu	Gly	Thr	Gly	Gln	Ile	Gly
					165					170					175	
60	Ala	His														

<210> 1221

<211> 152
 <212> PRT
 <213> Homo sapiens

5 <400> 1221
 Lys Ile Asn Leu Ile Ser His Gly Asn Arg Gln Lys Ile Leu Tyr Asn
 1 5 10 15
 Ile Ala Pro Ser Val Arg Phe Tyr Thr Trp Pro Leu Arg Arg Gln Glu
 20 25 30
 10 Leu Ile Pro Glu Val Tyr Val Leu Met Cys Tyr Gly Lys Trp Met Ser
 35 40 45
 Cys Thr Val Pro Ser Phe Gly Lys Leu Ser Phe Val His Val Thr Val
 50 55 60
 Asp Thr Tyr Ser His Phe Ile Trp Ala Thr Cys Gln Thr Gly Glu Ser
 15 65 70 75 80
 Thr Ser His Val Lys Arg His Leu Leu Ser Cys Phe Pro Val Met Gly
 85 90 95
 Val Pro Glu Lys Val Lys Thr Asp Asn Gly Pro Gly Tyr Cys Ser Lys
 100 105 110
 20 Ala Phe Gln Lys Phe Leu Asn Gln Trp Lys Ile Thr His Thr Ile Gly
 115 120 125
 Ile Leu Tyr Asn Ser Gln Gly Gln Ala Ile Ile Glu Arg Thr Asn Arg
 130 135 140
 Thr Leu Lys Ala Gln Leu Val Lys
 25 145 150

<210> 1222
 <211> 231
 <212> PRT
 30 <213> Homo sapiens

 <400> 1222
 Arg Glu Ser Pro Lys Tyr Val His Gly Gln Pro Cys Gly Lys Leu Val
 1 5 10 15
 35 Cys Leu Glu Glu Pro Arg Val Thr Met Gly Gln Thr Glu Ser Lys Tyr
 20 25 30
 Ala Ser Tyr Leu Ser Phe Ile Lys Ile Leu Leu Arg Arg Gly Gly Val
 35 40 45
 Arg Ala Ser Thr Glu Asn Leu Ile Thr Leu Phe Gln Thr Ile Glu Gln
 40 50 55 60
 Phe Cys Pro Trp Phe Pro Glu Gln Gly Thr Leu Asp Leu Lys Asp Trp
 65 70 75 80
 Glu Lys Ile Gly Lys Glu Leu Lys Gln Ala Asn Arg Glu Gly Lys Ile
 85 90 95
 45 Ile Pro Leu Thr Val Trp Asn Asp Trp Ala Ile Ile Lys Ala Thr Leu
 100 105 110
 Glu Pro Phe Gln Thr Gly Glu Asp Ile Val Ser Val Ser Asp Ala Pro
 115 120 125
 Lys Ser Cys Val Thr Asp Cys Glu Glu Glu Ala Gly Thr Glu Ser Gln
 50 130 135 140
 Gln Gly Thr Glu Ser Ser His Cys Lys Tyr Val Ala Glu Ser Val Met
 145 150 155 160
 Ala Gln Ser Thr Gln Asn Val Asp Tyr Ser Gln Leu Gln Glu Ile Ile
 165 170 175
 55 Tyr Pro Glu Ser Ser Lys Leu Gly Glu Gly Gly Pro Glu Ser Leu Gly
 180 185 190
 Pro Ser Glu Pro Lys Pro Arg Ser Pro Ser Thr Pro Pro Ser Ala Val
 195 200 205
 60 Gln Met Pro Val His Ser Thr Ser Asn Arg Arg Leu Asp Lys Pro Lys
 210 215 220
 Pro Pro Arg Glu Asn Gln Val
 225 230

<210> 1223
 <211> 299
 <212> PRT
 <213> Homo sapiens

5

<400> 1223

Glu Glu Gly Ser Arg Gly Gly Arg Glu Gly Ala Gly Lys Met Val Val
 1 5 10 15
 Thr Arg Ser Ala Arg Ala Lys Ala Ser Ile Gln Ala Ala Ser Ala Glu
 20 25 30
 Ser Ser Gly Gln Lys Ser Phe Ala Ala Asn Gly Ile Gln Ala His Pro
 35 40 45
 Glu Ser Ser Thr Gly Ser Asp Ala Arg Thr Thr Ala Glu Ser Gln Thr
 50 55 60
 Thr Gly Lys Gln Ser Leu Ile Pro Arg Thr Pro Lys Ala Arg Lys Arg
 65 70 75 80
 Lys Ser Arg Thr Thr Gly Ser Leu Pro Lys Gly Thr Glu Pro Ser Thr
 85 90 95
 Asp Gly Glu Thr Ser Glu Ala Glu Ser Asn Tyr Ser Val Ser Glu His
 100 105 110
 His Asp Thr Ile Leu Arg Val Thr Arg Arg Arg Gln Ile Leu Ile Ala
 115 120 125
 Cys Ser Pro Val Ser Ser Val Arg Lys Lys Pro Lys Val Thr Pro Thr
 130 135 140
 Lys Glu Ser Tyr Thr Glu Glu Ile Val Ser Glu Ala Glu Ser His Val
 145 150 155 160
 Ser Gly Ile Ser Arg Ile Val Leu Pro Thr Glu Lys Thr Thr Gly Ala
 165 170 175
 Arg Arg Ser Lys Ala Lys Ser Leu Thr Asp Pro Ser Gln Glu Ser His
 180 185 190
 Thr Glu Ala Ile Ser Asp Ala Glu Thr Ser Ser Ser Asp Ile Ser Phe
 195 200 205
 Ser Gly Ile Ala Thr Arg Arg Thr Arg Ser Met Gln Arg Lys Leu Lys
 210 215 220
 Ala Gln Thr Glu Lys Lys Asp Ser Lys Ile Val Pro Gly Asn Glu Lys
 225 230 235 240
 Gln Ile Val Gly Thr Pro Val Asn Ser Glu Asp Ser Asp Thr Arg Gln
 245 250 255
 Thr Ser His Leu Gln Ala Arg Ser Leu Ser Glu Ile Asn Lys Pro Asn
 260 265 270
 Phe Tyr Asn Asn Asp Phe Asp Asp Asp Phe Ser His Arg Ser Ser Glu
 275 280 285
 Asn Ile Leu Thr Val His Arg Thr Gly Gln Cys
 290 295

45

<210> 1224
 <211> 182
 <212> PRT
 <213> Homo sapiens

50

<400> 1224

Val Thr Arg Ser Ala Arg Ala Lys Ala Ser Ile Gln Ala Ala Ser Ala
 1 5 10 15
 Glu Ser Ser Gly Gln Lys Ser Phe Ala Ala Asn Gly Ile Gln Ala His
 20 25 30
 Pro Glu Ser Ser Thr Gly Ser Asp Ala Arg Thr Thr Ala Glu Ser Gln
 35 40 45
 Thr Thr Gly Lys Gln Ser Leu Ile Pro Arg Thr Pro Lys Ala Arg Lys
 50 55 60
 Arg Lys Ser Arg Thr Thr Gly Ser Leu Pro Lys Gly Thr Glu Pro Ser
 65 70 75 80
 Thr Asp Gly Glu Thr Ser Glu Ala Glu Ser Asn Tyr Ser Val Ser Glu
 85 90 95

His His Asp Thr Ile Leu Arg Val Thr Arg Arg Arg Gln Ile Leu Ile
 100 105 110
 Ala Cys Ser Pro Val Ser Ser Val Arg Lys Lys Pro Lys Val Thr Pro
 115 120 125
 5 Thr Lys Glu Ser Tyr Thr Glu Glu Ile Val Ser Glu Ala Glu Ser His
 130 135 140
 Val Ser Gly Ile Ser Arg Ile Xaa Leu Pro Thr Glu Lys Thr Thr Gly
 145 150 155 160
 Ala Arg Arg Ser Lys Xaa Lys Ser Leu Asp Arg Ser Asn Gln Glu Ser
 165 170 175
 10 His Thr Arg Asn Tyr Ile
 180

15 <210> 1225
 <211> 194
 <212> PRT
 <213> Homo sapiens

<400> 1225
 20 Ser Ile Ala Leu Gly Leu Arg Ile Xaa Gln Leu Gly Gly Leu Tyr Ile
 1 5 10 15
 Asn Phe Xaa Ala Asp Lys Xaa Gln Phe Asn Lys Arg Thr Xaa Xaa Gln
 20 25 30
 Xaa Lys Xaa Lys Lys Lys Asn Glu Phe Xaa Gln Lys Ala Val Ile Thr
 35 40 45
 25 Pro Asp Phe Glu Lys Asn His Cys Val Xaa Pro Tyr Ser Glu Ser Lys
 50 55 60
 Xaa Gln Leu Gln Lys Lys Arg Arg Lys Xaa Arg Gln Lys Pro Xaa Gly
 65 70 75 80
 30 Asp Gly Trp Phe Gly Met Lys Ala Pro Glu Met Thr Asn Glu Leu Lys
 85 90 95
 Asn Asp Xaa Lys Ala Xaa Lys Met Arg Ala Ser Met Asp Pro Lys Arg
 100 105 110
 Phe Xaa Lys Lys Asn Asp Arg Asp Gly Phe Pro Lys Tyr Phe Gln Ile
 115 120 125
 35 Gly Thr Ile Val Asp Asn Pro Ala Asp Xaa Tyr His Ser Xaa Ile Pro
 130 135 140
 Lys Lys Gln Arg Lys Arg Thr Ile Val Glu Glu Leu Leu Ala Asp Xaa
 145 150 155 160
 40 Glu Phe Arg Arg Tyr Asn Arg Arg Lys Xaa Ser Glu Ile Met Ala Glu
 165 170 175
 Lys Ala Ala Asn Ala Ala Gly Lys Lys Phe Arg Lys Lys Lys Lys Phe
 180 185 190
 Arg Asn

45 <210> 1226
 <211> 188
 <212> PRT
 50 <213> Homo sapiens

<400> 1226
 Ser His Asp Thr Ile Leu Arg Val Thr Arg Arg Arg Gln Ile Leu Ile
 1 5 10 15
 55 Ala Cys Ser Pro Val Ser Ser Val Arg Lys Lys Pro Lys Val Thr Pro
 20 25 30
 Thr Lys Glu Ser Tyr Thr Glu Glu Ile Val Ser Glu Ala Glu Ser His
 35 40 45
 Val Ser Gly Ile Ser Arg Ile Val Leu Pro Thr Glu Lys Thr Thr Gly
 50 55 60
 Ala Arg Arg Ser Lys Ala Lys Ser Leu Thr Asp Pro Ser Gln Glu Ser
 65 70 75 80
 His Thr Glu Ala Ile Ser Asp Ala Glu Thr Ser Ser Ser Asp Ile Ser

85 90 95
 Phe Ser Gly Ile Ala Thr Arg Arg Thr Arg Ser Met Gln Arg Lys Leu
 100 105 110
 5 Lys Ala Gln Thr Glu Lys Lys Asp Ser Lys Ile Val Pro Gly Asn Glu
 115 120 125
 Lys Gln Ile Val Gly Thr Pro Val Asn Ser Glu Asp Ser Asp Thr Arg
 130 135 140
 Gln Thr Ser His Leu Gln Ala Arg Ser Leu Ser Glu Ile Asn Lys Pro
 145 150 155 160
 10 Asn Phe Tyr Asn Asn Asp Phe Asp Asp Asp Phe Ser His Arg Ser Ser
 165 170 175
 Glu Asn Ile Leu Thr Val His Arg Thr Gly Gln Cys
 180 185
 15 <210> 1227
 <211> 199
 <212> PRT
 <213> Homo sapiens
 20 <400> 1227
 Glu Glu Gly Ser Arg Gly Gly Arg Glu Gly Ala Gly Lys Met Val Val
 1 5 10 15
 Thr Arg Ser Ala Arg Ala Lys Ala Ser Ile Gln Ala Ala Ser Ala Glu
 20 25 30
 25 Ser Ser Gly Gln Lys Ser Phe Ala Ala Asn Gly Ile Gln Ala His Pro
 35 40 45
 Glu Ser Ser Thr Gly Ser Asp Ala Arg Thr Thr Ala Glu Ser Gln Thr
 50 55 60
 Thr Gly Lys Gln Ser Leu Ile Pro Arg Thr Pro Lys Ala Arg Lys Arg
 65 70 75 80
 30 Lys Ser Arg Thr Thr Gly Ser Leu Pro Lys Gly Thr Glu Pro Ser Thr
 85 90 95
 Asp Gly Glu Thr Ser Glu Ala Glu Ser Asn Tyr Ser Val Ser Glu His
 100 105 110
 35 His Asp Thr Ile Leu Arg Val Thr Arg Arg Arg Gln Ile Leu Ile Ala
 115 120 125
 Cys Ser Pro Val Ser Xaa Val Arg Lys Lys Pro Lys Val Thr Pro Thr
 130 135 140
 Lys Glu Ser Tyr Thr Glu Ile Xaa Ser Glu Ala Lys Xaa His Val
 145 150 155 160
 40 Ser Xaa Ile Ser Arg Ile Xaa Leu Pro Thr Xaa Lys Thr Thr Gly Ala
 165 170 175
 Arg Xaa Ser Lys Ala Lys Ser Leu Thr Xaa Pro Ser Gln Glu Ser His
 180 185 190
 45 Thr Glu Ala Ile Ser Asp Ala
 195
 <210> 1228
 <211> 132
 50 <212> PRT
 <213> Homo sapiens
 <400> 1228
 Ile Lys Asp Gln Leu Gln Lys Lys Arg Arg Lys Glu Arg Gln Lys Thr
 1 5 10 15
 Ala Gly Asp Gly Trp Phe Gly Met Lys Ala Pro Glu Met Thr Asn Glu
 20 25 30
 Leu Lys Asn Asp Leu Lys Ala Leu Lys Met Arg Ala Ser Met Asp Pro
 35 40 45
 60 Lys Arg Phe Xaa Lys Lys Asn Asp Arg Asp Gly Phe Pro Lys Tyr Phe
 50 55 60
 Gln Ile Gly Thr Ile Val Xaa Asn Pro Ala Asp Phe Tyr His Ser Arg
 65 70 75 80

Ile Pro Lys Lys Gln Arg Lys Arg Thr Ile Val Glu Glu Leu Leu Ala
 85 90 95
 Asp Ser Glu Phe Arg Arg Tyr Asn Arg Arg Lys Tyr Ser Glu Ile Met
 100 105 110
 5 Ala Glu Lys Ala Ala Asn Ala Ala Gly Lys Lys Phe Arg Lys Lys Lys
 115 120 125
 Lys Phe Arg Asn
 130

 10 <210> 1229
 <211> 117
 <212> PRT
 <213> Homo sapiens

 15 <400> 1229
 Ser Pro Ser Ile Leu Ser Asp Ser Ser Ser Cys Glu Ile Ala Tyr Gln
 1 5 10 15
 Asp Ala Val Asn Leu Gln Asn Tyr Val Glu Glu Lys Leu Ile Pro Thr
 20 25 30
 20 Trp Asn Trp Met Val Ser Ile Met Asp Ser Thr Glu Ala Gln Leu Arg
 35 40 45
 Tyr Gly Ser Ala Leu Ala Ser Ala Gly Asp Pro Gly His Pro Asn His
 50 55 60
 25 Pro Leu His Ala Ser Gln Asn Ser Ala Arg Arg Glu Arg Met Thr Ala
 65 70 75 80
 Arg Glu Glu Ala Ser Leu Arg Thr Leu Glu Gly Arg Arg Arg Ala Thr
 85 90 95
 Leu Leu Ser Ala Arg Gln Gly Met Met Ser Ala Arg Gly Asp Phe Leu
 100 105 110
 30 Asn Tyr Ala Leu Leu
 115

 <210> 1230
 <211> 143
 35 <212> PRT
 <213> Homo sapiens

 <400> 1230
 40 Asp Asp Ile Glu Gln Glu Thr Phe Met Leu Asp Glu Pro Leu Glu Arg
 1 5 10 15
 Thr Thr Asn Ser Ser His Ala Asn Gly Ala Ala Gln Ala Pro Arg Ser
 20 25 30
 Met Gln Trp Ala Val Arg Asn Thr Gln His Gln Arg Ala Ala Ser Thr
 35 40 45
 45 Ala Pro Ser Ser Thr Ser Thr Pro Ala Ala Ser Ser Ala Gly Leu Ile
 50 55 60
 Tyr Ile Asp Pro Ser Asn Leu Arg Arg Ser Gly Thr Ile Ser Thr Ser
 65 70 75 80
 50 Ala Ala Ala Ala Ala Ala Ala Leu Glu Ala Ser Asn Ala Ser Ser Tyr
 85 90 95
 Leu Thr Ser Ala Ser Ser Leu Ala Arg Ala Tyr Ser Ile Val Ile Arg
 100 105 110
 Gln Ile Ser Asp Leu Met Gly Leu Ile Pro Lys Tyr Asn His Leu Val
 115 120 125
 55 Tyr Ser Gln Ile Pro Ala Ala Val Lys Leu Leu Thr Lys Met Gln
 130 135 140

 <210> 1231
 <211> 140
 60 <212> PRT
 <213> Homo sapiens

 <400> 1231

Leu Ala Arg Ala Tyr Ser Ile Val Ile Arg Gln Ile Ser Asp Leu Met
 1 5 10 15
 Gly Leu Ile Pro Lys Tyr Asn His Leu Val Tyr Ser Gln Ile Pro Ala
 20 25 30
 5 Ala Val Lys Leu Thr Tyr Gln Asp Ala Val Asn Leu Gln Asn Tyr Val
 35 40 45
 Glu Glu Lys Leu Ile Pro Thr Trp Asn Trp Met Val Ser Ile Met Asp
 50 55 60
 10 Ser Thr Glu Ala Gln Leu Arg Tyr Gly Ser Ala Leu Ala Ser Ala Gly
 65 70 75 80
 Asp Pro Gly His Pro Asn His Pro Leu His Ala Ser Gln Asn Ser Ala
 85 90 95
 Arg Arg Glu Arg Met Thr Ala Arg Glu Ala Ser Leu Arg Thr Leu
 100 105 110
 15 Glu Gly Arg Arg Arg Ala Thr Leu Ser Ala Arg Gln Gly Met Met
 115 120 125
 Ser Ala Arg Gly Asp Phe Leu Asn Tyr Ala Leu Leu
 130 135 140
 20 <210> 1232
 <211> 143
 <212> PRT
 <213> Homo sapiens
 25 <400> 1232
 Asp Asp Ile Glu Gln Glu Thr Phe Met Leu Asp Glu Pro Leu Glu Arg
 1 5 10 15
 Thr Thr Asn Ser Ser His Ala Asn Gly Ala Ala Gln Ala Pro Arg Ser
 20 25 30
 30 Met Gln Trp Ala Val Arg Asn Thr Gln His Gln Arg Ala Ala Ser Thr
 35 40 45
 Ala Pro Ser Ser Thr Ser Thr Pro Ala Ala Ser Ser Ala Gly Leu Ile
 50 55 60
 35 Tyr Ile Asp Pro Ser Asn Leu Arg Arg Ser Gly Thr Ile Ser Thr Ser
 65 70 75 80
 Ala Ala Ala Ala Ala Ala Leu Glu Ala Ser Asn Ala Ser Ser Tyr
 85 90 95
 Leu Thr Ser Ala Ser Ser Leu Ala Arg Ala Tyr Ser Ile Val Ile Arg
 100 105 110
 40 Gln Ile Ser Asp Leu Met Gly Leu Ile Pro Lys Tyr Asn His Leu Val
 115 120 125
 Tyr Ser Gln Ile Pro Ala Ala Val Lys Leu Leu Thr Lys Met Gln
 130 135 140
 45 <210> 1233
 <211> 93
 <212> PRT
 <213> Homo sapiens
 50 <400> 1233
 Phe Phe Gln Phe Lys Arg Trp Xaa Trp Ser Ile Val Glu Lys Met Ser
 1 5 10 15
 Met Xaa Asp Xaa Gln Asp Leu Val Tyr Phe Trp Thr Ser Ser Pro Ser
 20 25 30
 55 Leu Pro Ala Ser Glu Glu Gly Phe Gln Pro Met Pro Ser Ile Thr Ile
 35 40 45
 Arg Pro Pro Asp Asp Gln His Leu Pro Thr Ala Asn Thr Cys Ile Ser
 50 55 60
 60 Arg Leu Tyr Val Pro Leu Tyr Ser Ser Lys Gln Ile Leu Lys Gln Lys
 65 70 75 80
 Leu Leu Leu Ala Ile Lys Thr Lys Asn Phe Gly Phe Val
 85 90

<210> 1234
 <211> 196
 <212> PRT
 <213> Homo sapiens

5

<400> 1234

Arg Val Pro Val Val Ile Ala Gly Val Val Tyr Cys Gln Glu Ala Leu
 1 5 10 15
 Arg Asp Trp Gly Arg Val Thr Ala Ser Ser Thr Gly Ala Met Ala Phe
 20 25 30
 Leu Arg Ser Met Trp Gly Val Leu Ser Ala Leu Gly Arg Ser Gly Ala
 35 40 45
 Glu Leu Cys Thr Gly Cys Gly Ser Arg Leu Arg Ser Pro Phe Ser Phe
 50 55 60
 Val Tyr Leu Pro Arg Trp Phe Ser Ser Val Leu Ala Ser Cys Pro Lys
 65 70 75 80
 Lys Pro Val Ser Ser Tyr Leu Arg Phe Ser Lys Glu Gln Leu Pro Ile
 85 90 95
 Phe Lys Ala Gln Asn Pro Asp Ala Lys Thr Thr Glu Leu Ile Arg Arg
 100 105 110
 Ile Ala Gln Arg Trp Arg Glu Leu Pro Asp Ser Lys Lys Lys Ile Tyr
 115 120 125
 Gln Asp Ala Tyr Arg Ala Glu Trp Gln Val Tyr Lys Glu Glu Ile Ser
 130 135 140
 Arg Phe Lys Glu Gln Leu Thr Pro Ser Gln Ile Met Ser Leu Glu Lys
 145 150 155 160
 Glu Ile Met Asp Lys His Leu Lys Arg Lys Ala Met Thr Lys Lys Lys
 165 170 175
 Glu Leu Thr Leu Leu Gly Lys Pro Lys Arg Pro Arg Ser Ala Tyr Asn
 180 185 190
 Arg Leu Cys Ser
 195

<210> 1235
 <211> 58
 <212> PRT
 <213> Homo sapiens

35

<400> 1235

Trp Lys Asn Leu Ser Asp Ser Glu Lys Glu Leu Tyr Ile Gln His Ala
 1 5 10 15
 Lys Glu Asp Glu Thr Arg Tyr His Asn Glu Met Lys Ser Trp Glu Glu
 20 25 30
 Gln Met Ile Glu Val Gly Arg Lys Asp Leu Leu Arg Arg Thr Ile Lys
 35 40 45
 Lys Gln Arg Lys Tyr Gly Ala Glu Glu Cys
 50 55

<210> 1236
 <211> 196
 <212> PRT
 <213> Homo sapiens

50

<400> 1236

Arg Val Pro Val Val Ile Ala Gly Val Val Tyr Cys Gln Glu Ala Leu
 1 5 10 15
 Arg Asp Trp Gly Arg Val Thr Ala Ser Ser Thr Gly Ala Met Ala Phe
 20 25 30
 Leu Arg Ser Met Trp Gly Val Leu Ser Ala Leu Gly Arg Ser Gly Ala
 35 40 45
 Glu Leu Cys Thr Gly Cys Gly Ser Arg Leu Arg Ser Pro Phe Ser Phe
 50 55 60
 Val Tyr Leu Pro Arg Trp Phe Ser Ser Val Leu Ala Ser Cys Pro Lys

487

Asp Tyr Lys Lys Arg Asn Ser Ala Leu Gly Lys Lys Ala Leu Pro Gly
 20 25 30
 Leu Thr Val Gln His Ser Leu Ala Ser Gly Ile Leu Ser Leu Leu Thr
 35 40 45
 5 Val Tyr Ile Thr Thr Leu Val His Ser Gly His Phe Ser Phe Leu Glu
 50 55 60
 Ser Pro Val Asp Leu Thr Pro Met Pro Met Ile Phe Phe Ser Trp Leu
 65 70 75 80
 10 Ile Lys Asn Ser Leu Phe Leu Leu Arg His Pro Cys His Tyr Lys
 85 90 95

<210> 1239

<211> 113

<212> PRT

15 <213> Homo sapiens

<400> 1239

Thr Glu Val Arg Ala Ser Gln Val Val Phe Xaa Thr Ser Val Ser Pro
 1 5 10 15
 20 Lys Xaa Ser Ser Leu Gln Xaa Asp Met Arg Xaa Xaa Arg Gly Lys Lys
 20 25 30
 Val Phe Xaa Val Leu His Leu Gln Lys Xaa Val Xaa Ser Gln Asp Pro
 35 40 45
 25 Leu Gly Ala Thr Arg Gly Pro Ala Gln Cys Gln Gln Trp Thr Pro Pro
 50 55 60
 Ala Gly Thr Pro Pro Gly Ala Arg Ala Gly Pro Pro Gly Val Val Ala
 65 70 75 80
 Cys Thr Glu Gly Thr Thr Tyr Val Cys Ser Val Cys Pro Ala Lys Phe
 85 90 95
 30 Asp Gln Ile Glu Gln Phe Asn Asp His Met Arg Met His Val Ser Asp
 100 105 110
 Gly

<210> 1240

<211> 177

<212> PRT

<213> Homo sapiens

<400> 1240

Ala Ala Cys Cys Gly Thr Ala Ala Ala Phe Leu Leu Gly Arg Arg Gly
 1 5 10 15
 Gln Val Ala Gly Pro Arg Gln Gln Ser Pro Pro Gly Pro Gly Gly Ala
 20 25 30
 45 Ala Glu Arg Ala Ala Gly His Ala Arg Pro His Leu Arg Tyr Glu Val
 35 40 45
 Gln Arg Leu Pro Glu Gln Ala Gly Lys Ala Ala Gln Lys Gly Asn Cys
 50 55 60
 Pro Ser Pro Lys Gln Ala Glu Pro Ala Ala Gln Pro Ala Pro Ala His
 65 70 75 80
 Gly Ala Arg Leu Gly Arg Leu Arg Arg Gly Arg Ser Cys Ala Gly Ala
 85 90 95
 Arg Arg Arg Ala Lys Lys Ser Phe Arg Gly Trp Arg Leu Phe Cys Ser
 100 105 110
 55 Gln Gly Lys Gly Arg Gly Ala His Ala Glu Thr Xaa Xaa Val Glu Glu
 115 120 125
 Glu Xaa Pro Xaa Lys Ala Pro Gly Arg Arg Ser Ser Pro Xaa Ala Phe
 130 135 140
 Gly Val Xaa Arg Ala Asn Xaa Glu Pro Gly Arg Gly Pro Trp Gly Arg
 145 150 155 160
 60 Lys Ala Thr Pro Arg Arg Pro Trp Ala Phe Glu Phe Lys Ile Phe Phe
 165 170 175
 Gln

5 <210> 1241
 <211> 270
 <212> PRT
 <213> Homo sapiens

<400> 1241
 10 Leu Lys Glu Val Pro Asp Tyr Leu Asp His Ile Lys His Pro Met Asp
 1 5 10 15
 Phe Ala Thr Met Arg Lys Arg Leu Glu Ala Gln Gly Tyr Lys Asn Leu
 20 25 30
 His Glu Phe Glu Glu Asp Phe Asp Leu Ile Ile Asp Asn Cys Met Lys
 35 40 45
 15 Tyr Asn Ala Arg Asp Thr Val Phe Tyr Arg Ala Ala Val Arg Leu Arg
 50 55 60
 Asp Gln Gly Gly Val Val Leu Arg Gln Ala Arg Arg Glu Val Asp Ser
 65 70 75 80
 20 Ile Gly Leu Glu Glu Ala Ser Gly Met His Leu Pro Glu Arg Pro Ala
 85 90 95
 Ala Ala Pro Arg Arg Pro Phe Ser Trp Glu Asp Val Asp Arg Leu Leu
 100 105 110
 Asp Pro Ala Asn Arg Ala His Leu Gly Leu Glu Glu Gln Leu Arg Glu
 115 120 125
 25 Leu Leu Asp Met Leu Asp Leu Thr Cys Ala Met Lys Ser Ser Gly Ser
 130 135 140
 Arg Ser Lys Arg Ala Lys Leu Leu Lys Lys Glu Ile Ala Leu Leu Arg
 145 150 155 160
 30 Asn Lys Leu Ser Gln Gln His Ser Gln Pro Leu Pro Thr Gly Pro Gly
 165 170 175
 Leu Glu Gly Phe Glu Glu Asp Gly Ala Ala Leu Gly Pro Gly Gly Gly
 180 185 190
 Arg Arg Ser Pro Ser Glu Val Gly Asp Ser Ser Ala Ala Lys Glu Lys
 195 200 205
 35 Val Ala Glu His Met Arg Arg Leu Xaa Xaa Trp Arg Arg Ser Xaa Xaa
 210 215 220
 Glu Lys Arg Leu Asp Ala Gly Leu His Gln Xaa Leu Leu Gly Cys Xaa
 225 230 235 240
 40 Glu Pro Thr Xaa Asn Pro Ala Gly Gly Leu Gly Gly Gly Arg Pro His
 245 250 255
 Pro Asp Asp Leu Gly Pro Ser Ser Ser Arg Phe Ser Phe Lys
 260 265 270

45 <210> 1242
 <211> 66
 <212> PRT
 <213> Homo sapiens

<400> 1242
 50 Met Phe Asn Asn Phe Val Asn His Ala Leu Tyr Xaa Glu Tyr His Leu
 1 5 10 15
 Phe Asn Lys Thr Gly Cys Lys Phe Thr Met Thr Asn Val Tyr Phe Lys
 20 25 30
 55 Lys Glu Asn Xaa Ile Ile Leu Asn Gly Thr Leu Trp Lys Glu Gly Arg
 35 40 45
 Ile Lys Leu Cys Cys Asp Ile Thr Cys Arg Ser Pro Lys Thr Leu Arg
 50 55 60
 Cys Pro
 65

60 <210> 1243
 <211> 85
 <212> PRT

<213> Homo sapiens

<400> 1243

5 Ser Tyr Ala Val Thr Ser Leu Ala Asp His Gln Lys His Ser Ala Ala
 1 5 10 15
 Arg Asp Arg Arg Trp Val Cys Pro Arg Ser Arg Arg Pro Ala His Leu
 20 25 30
 Lys Pro Arg Arg Cys Ala Ser Gln Arg Ile Ile Tyr Cys Arg Lys Cys
 35 40 45
 10 Ile His Leu Leu Tyr Asn Glu Lys Tyr Ile Cys Lys Gly Ile Leu Ile
 50 55 60
 Cys Ile Phe Ile Gln Ala His Lys Asn Ser Thr Trp Leu Gly Ser Arg
 65 70 75 80
 15 Met His Cys Ile Val
 85

<210> 1244

<211> 56

<212> PRT

20 <213> Homo sapiens

<400> 1244

Val Val Leu Xaa Val Lys Ser Met Ile Tyr Lys Ile Ile Lys His Ser
 1 5 10 15
 25 Lys Val Phe Lys Lys Lys Leu His Ile Lys Xaa Ser Asp Ala Xaa Thr
 20 25 30
 Pro Xaa Leu Gly Asp Val Arg Xaa Xaa Xaa Leu Gly Leu Pro Gly Arg
 35 40 45
 30 Ala Pro Pro Leu Tyr Arg Ala Lys
 50 55

<210> 1245

<211> 227

<212> PRT

35 <213> Homo sapiens

<400> 1245

Gly Asp Pro Val Gly Arg Glu Glu Gly Gly Lys Met Val Leu Glu Ser
 1 5 10 15
 40 Thr Met Val Cys Val Asp Asn Ser Glu Tyr Met Arg Asn Gly Asp Phe
 20 25 30
 Leu Pro Thr Arg Leu Gln Ala Gln Gln Asp Ala Val Asn Ile Val Cys
 35 40 45
 His Ser Lys Thr Arg Ser Asn Pro Glu Asn Asn Val Gly Leu Ile Thr
 50 55 60
 Leu Ala Asn Asp Cys Glu Val Leu Thr Thr Leu Thr Pro Asp Thr Gly
 65 70 75 80
 Arg Ile Leu Ser Lys Leu His Thr Val Gln Pro Lys Gly Lys Ile Thr
 85 90 95
 50 Phe Cys Thr Gly Ile Arg Val Ala His Leu Ala Leu Lys His Arg Gln
 100 105 110
 Gly Lys Asn His Lys Met Arg Ile Ile Ala Phe Val Gly Ser Pro Val
 115 120 125
 Glu Asp Asn Glu Lys Asp Leu Val Lys Leu Ala Lys Arg Leu Lys Lys
 55 130 135 140
 Glu Lys Val Asn Val Asp Ile Ile Asn Phe Gly Glu Glu Val Asn
 145 150 155 160
 Thr Glu Lys Leu Thr Ala Phe Val Asn Thr Leu Asn Gly Lys Asp Gly
 165 170 175
 60 Thr Gly Ser Tyr Leu Val Thr Val Pro Ser Gly Pro Ser Leu Ala Asp
 180 185 190
 Ala Leu Ile Ser Ser Xaa Ile Leu Ala Gly Glu Xaa Gly Ala Leu Ala
 195 200 205

Gly Ser Trp Val Pro Val Thr Phe Glu Phe Trp Ser Xaa Il Pro Xaa
 210 215 220
 Leu Asp Pro
 225

5

<210> 1246
 <211> 141
 <212> PRT
 <213> Homo sapiens

10

<400> 1246
 Gln Asn Thr Ala Lys Val Asn Cys Val Gly Glu Pro His Leu His Arg
 1 5 10 15
 Asn Gln Ile Asn Glu Phe Arg Gly Tyr Asp Tyr Ser Asn Leu Arg Ala
 20 25 30
 His Gln Lys Gln Ala Ser Arg Ser Gln Phe Ala Ser Val Cys Leu Ser
 35 40 45
 Gly Asp Lys Trp Glu Asn Met Val Pro Pro Val Arg Asp Pro Leu Ser
 50 55 60
 Cys Ala Ala His Ser Thr Thr Ser Leu Cys Cys Phe His Gln Ala Glu
 65 70 75 80
 Thr Leu Pro Tyr Gly Val Tyr Gly Leu Leu Pro Val His Gln Cys Asp
 85 90 95
 Arg Lys Asp Ser Cys His Tyr Cys Pro Trp Leu Gln Phe Lys Gly Ile
 100 105 110
 Gln Cys Arg Cys Lys Phe Tyr Gly Thr Ile Phe Ile Gly Gly Phe Gly
 115 120 125
 Gln Asn Ala Val Val Val Gln Leu Ile Asn Thr Asn Cys
 130 135 140

20

<210> 1247
 <211> 106
 <212> PRT
 <213> Homo sapiens

30

<400> 1247
 Gly Pro Thr Arg Ser Arg Pro Arg Gly Val Asn Leu Pro Leu Cys Ala
 1 5 10 15
 Ser Val Glu Thr Ser Gly Lys Thr Trp Ser His Leu Cys Glu Thr Pro
 20 25 30
 Cys Pro Val Leu Leu Thr Gln Gln His Leu Cys Val Ala Phe Thr Arg
 35 40 45
 Leu Arg Pro Tyr Pro Met Gly Tyr Met Gly Phe Tyr Leu Cys Thr Ser
 50 55 60
 Val Thr Gly Lys Ile His Val Thr Thr Val Arg Gly Tyr Asn Ser Lys
 65 70 75 80
 Val Ser Asn Val Ala Val Asn Phe Met Ala Leu Phe Leu Leu Glu Asp
 85 90 95
 Leu Val Arg Met Gln Leu Leu Tyr Asn Ser
 100 105

40

<210> 1248
 <211> 194
 <212> PRT
 <213> Homo sapiens

50

<400> 1248
 Pro Lys Glu Glu Asp Met Glu Val Asp Ile Pro Ala Val Lys Val Lys
 1 5 10 15
 Glu Glu Pro Arg Asp Glu Glu Glu Glu Ala Lys Met Lys Ala Pro Pro
 20 25 30
 Lys Ala Ala Arg Lys Thr Pro Gly Leu Pro Lys Asp Val Ser Val Ala
 35 40 45

Glu Leu Leu Arg Glu Leu Ser Leu Thr Lys Glu Glu Glu Leu Leu Phe
 50 55 60
 Leu Gln Leu Pro Asp Thr Leu Pro Gly Gln Pro Pro Thr Gln Asp Ile
 65 70 75 80
 5 Lys Pro Ile Lys Thr Glu Val Gln Gly Glu Asp Gly Gln Val Val Leu
 85 90 95
 Ile Lys Gln Glu Lys Asp Arg Glu Ala Lys Leu Ala Glu Asn Ala Cys
 100 105 110
 10 Thr Leu Ala Asp Leu Thr Glu Gly Gln Val Gly Lys Leu Leu Ile Arg
 115 120 125
 Lys Ser Gly Arg Val Gln Leu Leu Leu Gly Lys Val Thr Leu Asp Val
 130 135 140
 Thr Met Gly Thr Ala Cys Ser Phe Leu Gln Glu Leu Val Ser Val Gly
 145 150 155 160
 15 Leu Gly Asp Ser Arg Thr Gly Glu Met Thr Val Leu Gly His Val Lys
 165 170 175
 His Lys Leu Val Cys Ser Pro Asp Phe Glu Ser Leu Leu Asp His Lys
 180 185 190
 His Arg

20

<210> 1249

<211> 106

<212> PRT

25

<213> Homo sapiens

<400> 1249

Gln Gly Gln Val Pro Ser Ser Lys Asp Val Pro Ser Pro Arg Cys Arg
 1 5 10 15
 30 Lys Val Thr Val Pro Phe Thr Ala Ala Val Gly Gly Asn Pro Gly Gly
 20 25 30
 Pro Gly Thr Met Val Ala Lys Gly Trp Asn Glu Trp Ala Gln Met Gly
 35 35 40 45
 35 Pro Leu Leu Gly Xaa Gln Asn Ser Arg Thr Lys Cys Xaa Gly Gln Gly
 50 55 60
 Xaa Asn Pro Gly Ala Gln Gly Ala Xaa Leu Pro Ser Pro Xaa Tyr Phe
 65 70 75 80
 Tyr Arg Xaa Phe Gly Ile Pro Xaa Gly Ile Xaa Lys Ser Arg Gly Xaa
 85 90 95
 40 Tyr Xaa Phe Val Ala Tyr Val Phe Pro Arg
 100 105

<210> 1250

<211> 113

45

<212> PRT

<213> Homo sapiens

<400> 1250

Asp Ile Asn Thr Lys Ile Asn Ser Arg Ala Lys Ser Pro Ala Ala Arg
 1 5 10 15
 Met Cys His Leu His Ala Ala Gly Arg Ser Leu Cys His Ser Gln Leu
 20 25 30
 Leu Trp Glu Thr Leu Gly Asp Leu Glu Gln Trp Leu Pro Lys Ala
 35 40 45
 55 Gly Met Ser Gly Leu Lys Trp Gly Pro Phe Trp Gly Xaa Lys Ile Gln
 50 55 60
 Glu Gln Asn Xaa Leu Asp Lys Ala Xaa Thr Arg Gly Pro Lys Ala Pro
 65 70 75 80
 Xaa Phe Leu His Leu Xaa Ile Phe Thr Xaa Gly Leu Gly Ser Gln Xaa
 85 90 95
 60 Gly Xaa Lys Asn Gln Gly Glu Xaa Thr Xaa Leu Trp Leu Thr Phe Ser
 100 105 110
 Gln

5 <210> 1251
 <211> 114
 <212> PRT
 <213> Homo sapiens

<400> 1251
 10 Ala His Ser Phe Gln Pro Leu Ala Thr Ile Val Pro Gly Pro Pro Gly
 1 5 10 15
 Phe Pro Pro Thr Ala Ala Val Asn Gly Thr Val Thr Phe Leu Gln Arg
 20 25 30
 Gly Asp Gly Thr Ser Leu Leu Leu Gly Thr Trp Pro Cys Tyr Leu Phe
 35 40 45
 15 Leu Tyr Leu Cys Leu Asn Leu Phe His Leu Met His Pro Pro Arg Val
 50 55 60
 Asp Gly Glu Gly Leu Cys Glu Gly Ala Gly Phe Ser Trp Cys Leu Leu
 65 70 75 80
 Gly Cys Arg Gly Arg Lys Arg Val Asp Cys Ser Phe Cys Trp Cys Ser
 85 90 95
 20 Pro Arg Pro Pro Gly Gly Ser Ile Gly Glu Arg Ala Arg Ile Glu Ser
 100 105 110
 Glu Thr

25 <210> 1252
 <211> 126
 <212> PRT
 <213> Homo sapiens

30 <400> 1252
 Ser Glu Arg Ser Ser Met Ser Val Gly Leu Gly Arg Ser Gln Leu Asp
 1 5 10 15
 Ser Lys Gly Gly Val Val Gly Gly Thr Ile Asp Val Asn Ala Leu Glu
 20 25 30
 Met Xaa Ala His Ile Ser Glu His Pro Asn Gln Gln Pro Xaa His Lys
 35 40 45
 Ile Gln Ile Thr Met Gly Ser Thr Glu Ala Arg Val Asp Tyr Met Gly
 50 55 60
 40 Ser Ser Ile Leu Met Gly Ile Phe Ser Asn Ala Asp Leu Lys Leu Gln
 65 70 75 80
 Asp Glu Trp Lys Val Asn Leu Tyr Asn Thr Leu Asp Ser Ser Ile Thr
 85 90 95
 Asp Lys Ser Glu Ile Phe Val Xaa Trp Arg Phe Glu Xaa Gly Ile Phe
 100 105 110
 45 Phe Gln Xaa Asn Xaa Xaa Xaa Xaa Gln Pro His Xaa Ile Trp
 115 120 125

50 <210> 1253
 <211> 87
 <212> PRT
 <213> Homo sapiens

<400> 1253
 55 Lys Ser Leu Phe Phe Gly Gly Arg Leu Arg Asn Trp Ser Pro Arg Lys
 1 5 10 15
 Thr Glu Xaa Val Cys Trp Ile Lys Leu Leu Cys Glu Lys Ile Xaa Xaa
 20 25 30
 Ala Ser Phe Leu Phe Phe Thr Arg Xaa Gly Val Val Xaa Leu Xaa Xaa
 35 40 45
 60 Xaa Xaa Xaa Gly Lys Ile Ser His Xaa Gln Ile Ser Xaa Gly Arg Lys
 50 55 60
 Ser His Phe Tyr Gln Leu Cys Leu Asn Pro Met Tyr Tyr Thr Ser Leu

	65					70						75					80
	Leu	Ser	Ile	His	Pro	Glu	Ala										
						85											
5	<210>	1254															
	<211>	50															
	<212>	PRT															
	<213>	Homo sapiens															
10	<400>	1254															
	Lys	Gln	Leu	Asn	Val	Gln	Met	Asn	Met	Ser	Asn	Val	Met	Gly	Asn	Thr	
	1				5					10					15		
	Thr	Trp	Thr	Thr	Ser	Gly	Leu	Lys	Ser	Gln	Gly	Arg	Leu	Ser	Val	Gly	
				20				25						30			
15	Ser	Asn	Arg	Asp	Pro	Arg	Asp	Gln	Ala	Cys	Leu	Leu	Val	Trp	Glu	Asp	
		35					40						45				
	His	Asn															
	50																
20	<210>	1255															
	<211>	220															
	<212>	PRT															
	<213>	Homo sapiens															
25	<400>	1255															
	Glu	Ala	Gly	Thr	Thr	Pro	Ala	Lys	Asp	Trp	Thr	Leu	Val	Glu	Thr	Pro	
	1				5					10					15		
	Pro	Gly	Glu	Glu	Gln	Ala	Lys	Gln	Asn	Ala	Asn	Ser	Gln	Leu	Ser	Ile	
			20					25						30			
30	Leu	Phe	Ile	Glu	Lys	Pro	Gln	Gly	Gly	Thr	Val	Lys	Val	Gly	Glu	Asp	
		35					40						45				
	Ile	Thr	Phe	Ile	Ala	Lys	Val	Lys	Ala	Glu	Asp	Leu	Leu	Arg	Lys	Pro	
	50					55					60						
35	Thr	Ile	Lys	Trp	Phe	Lys	Gly	Lys	Trp	Met	Asp	Leu	Ala	Ser	Lys	Ala	
	65					70					75					80	
	Gly	Lys	His	Leu	Gln	Leu	Lys	Glu	Thr	Phe	Glu	Arg	His	Ser	Arg	Val	
				85						90					95		
	Tyr	Thr	Phe	Glu	Met	Gln	Ile	Ile	Lys	Ala	Lys	Asp	Asn	Phe	Ala	Gly	
			100						105					110			
40	Asn	Tyr	Arg	Cys	Glu	Val	Thr	Tyr	Lys	Asp	Lys	Phe	Asp	Ser	Cys	Ser	
			115					120					125				
	Phe	Asp	Leu	Glu	Val	His	Glu	Ser	Thr	Gly	Thr	Thr	Pro	Asn	Ile	Asp	
	130					135						140					
45	Ile	Arg	Ser	Ala	Phe	Lys	Arg	Arg	Glu	Val	Lys	Gln	Gln	Glu	Glu	Glu	
	145					150					155					160	
	Pro	Gln	Val	Asp	Val	Trp	Glu	Leu	Leu	Lys	Asn	Ala	Lys	Pro	Ser	Glu	</

20 25 30
 Ala Thr Leu Asn Cys Ser Val Arg Gly Asn Pro Lys Pro Lys Ile Thr
 35 40 45
 Trp Met Lys Asn Lys Val Ala Ile Val Asp Asp Pro Arg Tyr Arg Met
 5 50 55 60
 Phe Ser Asn Gln Gly Val Cys Thr Leu Glu Ile Arg Lys Pro Ser Pro
 65 70 75 80
 Tyr Asp Gly Gly Thr Tyr Cys Cys Lys Ala Val Asn Asp Leu Gly Thr
 85 90 95
 10 Val Glu Ile Glu Cys Lys Leu Glu Val Lys Gly Gly Leu Ser Xaa Cys
 100 105 110
 Arg Leu Leu Leu Gln Xaa Val Pro Pro Asn Ile Ile Asp Ser Tyr Xaa
 115 120 125
 Arg Asp Leu His Ser Ser Asn Pro Glu Glu Tyr
 15 130 135

<210> 1257

<211> 210

<212> PRT

20 <213> Homo sapiens

<400> 1257

Cys Leu Ser Leu Pro Ser Ser Trp Asp His Arg Gln Leu Tyr Leu Ser
 1 5 10 15
 25 Met Asn Ile Asp Asp Lys Leu Glu Gly Leu Phe Leu Lys Cys Gly Gly
 20 25 30
 Ile Asp Glu Met Gln Ser Ser Arg Thr Met Val Val Met Gly Gly Val
 35 40 45
 Ser Gly Gln Ser Thr Val Ser Gly Glu Leu Gln Asp Ser Val Leu Gln
 50 55 60
 30 Asp Arg Ser Met Pro His Gln Glu Ile Leu Ala Ala Asp Glu Val Leu
 65 70 75 80
 Gln Glu Ser Glu Met Arg Gln Gln Asp Met Ile Ser His Asp Glu Leu
 85 90 95
 35 Met Val His Glu Glu Thr Val Lys Asn Asp Glu Glu Gln Met Glu Thr
 100 105 110
 His Glu Arg Leu Pro Gln Gly Leu Gln Tyr Ala Leu Asn Val Pro Ile
 115 120 125
 Ser Val Lys Gln Glu Ile Thr Phe Thr Asp Val Ser Glu Gln Leu Met
 130 135 140
 40 Arg Asp Lys Lys Gln Ile Arg Glu Pro Val Asp Leu Gln Lys Lys Lys
 145 150 155 160
 Lys Arg Lys Gln Arg Ser Pro Ala Lys Ile Leu Thr Ile Asn Glu Asp
 165 170 175
 45 Gly Ser Leu Gly Leu Lys Thr Pro Lys Ser His Val Cys Glu His Cys
 180 185 190
 Asn Ala Ala Phe Arg Thr Asn Tyr Pro Tyr Arg Asp Met Ser Ser Ser
 195 200 205
 Tyr Arg
 50 210

<210> 1258

<211> 198

<212> PRT

55 <213> Homo sapiens

<400> 1258

Ser Phe Ser Asp Ser Asp Asp Ser Cys Leu Trp Lys Arg Lys Arg
 1 5 10 15
 60 Gln Lys Cys Phe Asn Pro Pro Pro Lys Pro Glu Pro Phe Gln Phe Gly
 20 25 30
 Gln Ser Ser Gln Lys Pro Pro Val Ala Gly Gly Lys Lys Ile Asn Asn
 35 40 45

Ile Trp Gly Ala Val Leu Gln Glu Gln Asn Gln Asp Ala Val Ala Thr
 50 55 60
 Glu Leu Gly Ile Leu Gly Met Glu Gly Thr Ile Asp Arg Ser Arg Gln
 65 70 75 80
 5 Ser Glu Thr Tyr Asn Tyr Leu Leu Ala Lys Lys Leu Arg Lys Glu Ser
 85 90 95
 Gln Glu His Thr Lys Asp Leu Asp Lys Glu Leu Asp Glu Tyr Met His
 100 105 110
 Gly Gly Lys Lys Met Gly Ser Lys Glu Glu Glu Asn Gly Gln Gly His
 115 120 125
 10 Leu Lys Arg Lys Arg Pro Val Lys Asp Arg Leu Gly Asn Arg Pro Glu
 130 135 140
 Met Asn Tyr Lys Gly Arg Tyr Gln Ile Thr Ala Glu Asp Ser Gln Glu
 145 150 155 160
 15 Lys Val Ala Asp Glu Ile Ser Phe Arg Leu Gln Glu Pro Lys Lys Asp
 165 170 175
 Leu Ile Ala Pro Ser Ser Glu Asp Tyr Trp Tyr Lys Lys Ala Ile Glu
 180 185 190
 Leu Leu Met Glu Thr Arg
 195

<210> 1259

<211> 103

<212> PRT

25 <213> Homo sapiens

<400> 1259

Arg Gln Ser Leu Ala Leu Ser Pro Arg Leu Glu Tyr Ser Gly Thr Ile
 1 5 10 15
 30 Ser Ala His Cys Asn Leu Cys Leu Pro Gly Ser Gly Asp Ser Pro Ala
 20 25 30
 Ser Ala Ser Arg Val Ala Gly Ile Ile Gly Met Glu Asn His Thr Trp
 35 40 45
 Leu Xaa Phe Val Phe Leu Val Xaa Met Lys Phe His His Val Gly Leu
 50 55 60
 35 Ala Gly Leu Lys Leu Leu Thr Ser Ser Asp Leu Pro Ala Leu Val Ser
 65 70 75 80
 Gln Ser Val Gly Ile Thr Gly Val Ser His Arg Ala Trp Pro Met Leu
 85 90 95
 40 Val Phe Ile Leu Lys Ile Ala
 100

<210> 1260

<211> 98

<212> PRT

45 <213> Homo sapiens

<400> 1260

Phe Thr Ala Lys Ile Asn Leu Lys Lys Gln Thr Asn Leu Gln Met Val
 1 5 10 15
 Cys Tyr Asp Leu Asp Lys Thr Asp Tyr Gln Leu Val Ile Leu Ile Ile
 20 25 30
 Ser Thr Cys Asn Lys Ile Glu Lys Leu Asn Pro Val Leu Tyr Thr Leu
 35 40 45
 55 Lys Val Phe Leu Xaa Lys Tyr Ile Phe Lys Met Phe Tyr Gln Leu His
 50 55 60
 Phe Phe Pro His Ile Phe Leu Asn Gln Glu Lys Gln Xaa Gly Leu Phe
 65 70 75 80
 Leu Gln Glu Phe Ser Trp Phe Ile Gln Val Ala Lys Thr Leu Ala Ile
 85 90 95
 60 Ser Ser

<210> 1261
 <211> 266
 <212> PRT
 <213> Homo sapiens

5

<400> 1261

Glu Leu Ala Arg Leu Gln Val Asp Thr Ser Gly Ser Lys Ala Ala Phe
 1 5 10 15
 Glu Pro Ala Ile Asp Met Gln Lys Ser Val Pro Asn Lys Ala Leu Glu
 10 20 25 30
 Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Glu Ile Leu Pro Ser Glu
 35 40 45
 Ser Lys Gln Lys Asp Tyr Glu Glu Ser Ser Trp Asp Ser Glu Ser Leu
 50 55 60
 Cys Glu Thr Val Ser Gln Lys Asp Val Cys Leu Pro Lys Ala Ala His
 15 65 70 75 80
 Gln Lys Glu Ile Asp Lys Ile Asn Gly Lys Leu Glu Gly Ser Pro Val
 85 90 95
 Lys Asp Gly Leu Leu Lys Ala Asn Cys Gly Met Lys Val Ser Ile Pro
 100 105 110
 Thr Lys Ala Leu Glu Leu Met Asp Met Gln Thr Phe Lys Ala Glu Pro
 115 120 125
 Pro Glu Lys Pro Ser Ala Phe Glu Pro Ala Ile Glu Met Gln Lys Ser
 130 135 140
 Val Pro Asn Lys Ala Leu Glu Leu Lys Asn Glu Gln Thr Leu Arg Ala
 145 150 155 160
 Asp Glu Ile Leu Pro Ser Glu Ser Lys Gln Lys Asp Tyr Glu Glu Ser
 165 170 175
 Ser Trp Asp Ser Glu Ser Leu Cys Glu Thr Val Ser Gln Lys Asp Val
 180 185 190
 Cys Leu Pro Lys Ala Ala His Gln Lys Glu Ile Asp Lys Ile Asn Gly
 195 200 205
 Lys Leu Glu Gly Ser Pro Val Lys Asp Gly Leu Leu Lys Ala Asn Cys
 210 215 220
 Gly Met Lys Val Ser Ile Pro Thr Lys Ala Leu Glu Leu Met Asp Met
 225 230 235 240
 Gln Thr Phe Lys Ala Glu Pro Pro Glu Lys Pro Ser Ala Phe Glu Pro
 245 250 255
 Ala Ile Glu Met Gln Lys Val Cys Ser Lys
 260 265

<210> 1262
 <211> 335
 <212> PRT
 <213> Homo sapiens

45

<400> 1262

Lys Glu Leu Glu Val Lys Gln Gln Leu Glu Gln Ala Leu Arg Ile Gln
 1 5 10 15
 Asp Ile Glu Leu Lys Ser Val Glu Ser Asn Leu Asn Gln Val Ser His
 20 25 30
 Thr His Glu Asn Glu Asn Tyr Leu Leu His Glu Asn Cys Met Leu Lys
 35 40 45
 Lys Glu Ile Ala Met Leu Lys Leu Glu Ile Ala Thr Leu Lys His Gln
 50 55 60
 Tyr Gln Glu Lys Glu Asn Lys Tyr Phe Glu Asp Ile Lys Ile Leu Lys
 65 70 75 80
 Glu Lys Asn Ala Glu Leu Gln Met Thr Leu Lys Leu Lys Glu Glu Ser
 85 90 95
 Leu Thr Lys Arg Ala Ser Gln Tyr Ser Gly Gln Leu Lys Val Leu Ile
 100 105 110
 Ala Glu Asn Thr Met Leu Thr Ser Lys Leu Lys Glu Lys Gln Asp Lys
 115 120 125

Glu Ile Leu Glu Ala Glu Ile Glu Ser His His Pro Arg Leu Ala Ser
 130 135 140
 Ala Val Gln Asp His Asp Gln Ile Val Thr Ser Arg Lys Ser Gln Glu
 145 150 155 160
 5 Pro Ala Phe His Ile Ala Gly Asp Ala Cys Leu Gln Arg Lys Met Asn
 165 170 175
 Val Asp Val Ser Ser Thr Ile Tyr Asn Asn Glu Val Leu His Gln Pro
 180 185 190
 10 Leu Phe Glu Ala Gln Arg Lys Ser Lys Ser Leu Lys Ile Asn Xaa Asn
 195 200 205
 Tyr Ala Gly Asp Ala Xaa Arg Glu Asn Thr Leu Val Ser Glu His Ala
 210 215 220
 Gln Arg Asp Gln Arg Glu Thr Gln Cys Gln Met Lys Glu Ala Glu His
 225 230 235 240
 15 Met Tyr Gln Asn Glu Gln Asp Asn Val Asn Lys His Thr Glu Gln Gln
 245 250 255
 Glu Ser Xaa Asp Gln Lys Leu Phe Gln Leu Gln Ser Lys Asn Met Trp
 260 265 270
 20 Leu Gln Gln Gln Leu Val His Ala His Lys Lys Ala Asp Asn Lys Ser
 275 280 285
 Lys Ile Thr Ile Asp Ile His Phe Leu Glu Arg Lys Met Gln His His
 290 295 300
 Leu Leu Lys Glu Lys Asn Glu Glu Ile Phe Asn Tyr Asn Asn His Leu
 305 310 315 320
 25 Lys Asn Arg Ile Tyr Gln Tyr Glu Lys Arg Lys Gln Lys Gln Lys
 325 330 335

<210> 1263

<211> 225

30 <212> PRT

<213> Homo sapiens

<400> 1263

35 Ala Glu Pro Pro Glu Lys Pro Ser Ala Phe Glu Pro Ala Ile Glu Met
 1 5 10 15
 Gln Lys Ser Val Pro Asn Lys Ala Leu Glu Leu Lys Asn Glu Gln Thr
 20 25 30
 Leu Arg Ala Asp Glu Ile Leu Pro Ser Glu Ser Lys Gln Lys Asp Tyr
 35 40 45
 40 Glu Glu Ser Ser Trp Asp Ser Glu Ser Leu Cys Glu Thr Val Ser Gln
 50 55 60
 Lys Asp Val Cys Leu Pro Lys Ala Ala His Gln Lys Glu Ile Asp Lys
 65 70 75 80
 45 Ile Asn Gly Lys Leu Glu Gly Ser Pro Val Lys Asp Gly Leu Leu Lys
 85 90 95
 Ala Asn Cys Gly Met Lys Val Ser Ile Pro Thr Lys Ala Leu Glu Leu
 100 105 110
 Met Asp Met Gln Thr Phe Lys Ala Glu Pro Pro Glu Lys Pro Ile Cys
 115 120 125
 50 Phe Glu Pro Ala Ile Glu Met Gln Lys Ser Val Pro Asn Lys Ala Leu
 130 135 140
 Glu Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Glu Ile Leu Pro Ser
 145 150 155 160
 Glu Ser Lys Gln Lys Asp Tyr Glu Glu Ser Ser Trp Asp Ser Glu Ser
 165 170 175
 55 Leu Cys Glu Thr Val Ser Xaa Arg Met Cys Val Ser Gln Gly Cys Ala
 180 185 190
 Ser Lys Arg Asn Arg Leu Asn Asn Gly Lys Leu Glu Xaa Leu Leu Leu
 195 200 205
 60 Arg Xaa Leu Leu Lys Leu Thr Ala Asp Glu Ser Ser Xaa Pro Leu Lys
 210 215 220
 Pro
 225

<210> 1264
 <211> 153
 <212> PRT
 5 <213> Homo sapiens

<400> 1264
 Arg Gln Ser Leu Thr Leu Ser Leu Arg Leu Glu Cys Ser Ser Gly Ile
 1 5 10 15
 10 Ser Ala His Leu Pro Leu Gly Phe Lys Pro Phe Ser Cys Leu Ser Leu
 20 25 30
 Pro Ser Ser Trp Asp Tyr Arg Gly Val His His His Asp His Leu Ile
 35 40 45
 15 Phe Ser Cys Leu Phe Cys Phe Phe Gly Phe Cys Phe Phe Leu Xaa Trp
 50 55 60
 Ser Leu Ser Leu Ser Pro Arg Leu Glu Cys Ser Ser Gly Ile Ser Ala
 65 70 75 80
 His Leu Pro Pro Gly Phe Lys Pro Phe Ser Cys Leu Ser Leu Pro Ser
 85 90 95
 20 Ser Trp Asp Tyr Arg Gly Val His His His Ala His Leu Ile Phe Ser
 100 105 110
 Cys Phe Xaa Phe Leu Val Leu Phe Xaa Thr Xaa Ser Cys Ser Val Ala
 115 120 125
 25 Gln Ala Gly Val Xaa Trp Arg Asp Leu Ser Ser Leu Gln Ala Pro Pro
 130 135 140
 Pro Arg Phe Thr Pro Phe Cys Tyr Glu
 145 150

<210> 1265
 30 <211> 223
 <212> PRT
 <213> Homo sapiens

<400> 1265
 35 Ile Leu Pro Ser Glu Ser Lys Gln Lys Asp Tyr Glu Glu Ser Ser Trp
 1 5 10 15
 Asp Ser Glu Ser Leu Cys Glu Thr Val Ser Gln Lys Asp Val Cys Leu
 20 25 30
 40 Pro Lys Ala Ala His Gln Lys Glu Ile Asp Lys Ile Asn Gly Lys Leu
 35 40 45
 Glu Gly Ser Pro Val Lys Asp Gly Leu Leu Lys Ala Asn Cys Gly Met
 50 55 60
 Lys Val Ser Ile Pro Thr Lys Ala Leu Glu Leu Met Asp Met Gln Thr
 65 70 75 80
 45 Phe Lys Ala Glu Pro Pro Glu Lys Pro Ser Ala Phe Glu Pro Ala Ile
 85 90 95
 Glu Met Gln Lys Ser Val Pro Asn Lys Ala Leu Glu Leu Lys Asn Glu
 100 105 110
 50 Gln Thr Leu Arg Ala Asp Glu Ile Leu Pro Ser Glu Ser Lys Gln Lys
 115 120 125
 Asp Tyr Glu Glu Ser Ser Trp Asp Ser Glu Ser Leu Cys Glu Thr Val
 130 135 140
 Ser Gln Lys Asp Val Cys Leu Pro Lys Ala Ala His Gln Lys Glu Ile
 145 150 155 160
 55 Asp Lys Ile Asn Gly Lys Leu Glu Gly Ser Pro Val Lys Asp Gly Leu
 165 170 175
 Leu Lys Ala Asn Cys Gly Met Lys Val Ser Ile Pro Thr Lys Ala Leu
 180 185 190
 60 Glu Leu Met Asp Met Gln Thr Phe Lys Ala Glu Pro Pro Glu Lys Pro
 195 200 205
 Ser Ala Phe Glu Pro Ala Ile Glu Met Gln Lys Val Cys Xaa Lys
 210 215 220

<210> 1266
 <211> 91
 <212> PRT
 <213> Homo sapiens

5

<400> 1266

Ser Phe Cys Leu Asp Ser Asp Gly Ser Ile Ser Ser Ala Leu Asn Val
 1 5 10 15
 Cys Ser Phe Phe Asn Ser Lys Ala Leu Phe Gly Thr Asp Phe Cys Ile
 10 20 25 30
 Ser Met Ala Gly Ser Lys Ala Asp Gly Phe Ser Gly Gly Ser Ala Leu
 35 40 45
 Lys Val Cys Met Ser Ile Asn Ser Lys Ala Leu Val Gly Ile Glu Thr
 50 55 60
 Phe Ile Pro Gln Leu Ala Phe Arg Arg Pro Ser Leu Thr Gly Asp Pro
 15 65 70 75 80
 Ser Asn Phe Pro Phe Ile Leu Ser Ile Ser Phe
 85 90

20

<210> 1267
 <211> 171
 <212> PRT
 <213> Homo sapiens

25

<400> 1267

Asn Glu Gln Thr Leu Arg Ala Asp Glu Ile Leu Pro Ser Glu Ser Lys
 1 5 10 15
 Gln Lys Asp Tyr Glu Glu Ser Ser Trp Asp Ser Glu Ser Leu Cys Glu
 20 25 30
 Thr Val Ser Gln Lys Asp Val Cys Leu Pro Lys Ala Thr His Gln Lys
 35 40 45
 Glu Ile Asp Lys Ile Asn Gly Lys Leu Glu Glu Ser Pro Asp Asn Asp
 50 55 60
 Gly Phe Leu Lys Ala Pro Cys Arg Met Lys Val Ser Ile Pro Thr Lys
 35 65 70 75 80
 Ala Leu Glu Leu Met Asp Met Gln Thr Phe Lys Ala Glu Pro Pro Glu
 85 90 95
 Lys Pro Ser Ala Phe Glu Pro Ala Ile Glu Met Gln Lys Ser Val Pro
 100 105 110
 Asn Lys Ala Leu Glu Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Gln
 40 115 120 125
 Met Phe Pro Ser Glu Ser Lys Gln Lys Lys Val Glu Glu Asn Ser Trp
 130 135 140
 Asp Ser Glu Ser Leu Arg Glu Thr Val Ser Gln Lys Asp Val Cys Val
 45 145 150 155 160
 Pro Arg Leu His Ile Lys Lys Lys Trp Ile Lys
 165 170

50

<210> 1268
 <211> 169
 <212> PRT
 <213> Homo sapiens

<400> 1268

Gln Lys Asp Tyr Glu Glu Ser Ser Trp Asp Ser Glu Ser Leu Cys Glu
 1 5 10 15
 Thr Val Ser Gln Lys Asp Val Cys Leu Pro Lys Ala Ala His Gln Lys
 20 25 30
 Glu Ile Asp Lys Ile Asn Gly Lys Leu Glu Gly Ser Pro Val Lys Asp
 35 40 45
 Gly Leu Leu Lys Ala Asn Cys Gly Met Lys Val Ser Ile Pro Thr Lys
 50 55 60
 Ala Leu Glu Leu Met Asp Met Gln Thr Phe Lys Ala Glu Pro Pro Glu

501

Asp Thr Val Phe His Val Gly Leu Phe Val His Val Leu Lys Pro Met
 85 90 95
 Tyr Phe Leu Leu Xaa His Leu Arg His Asn
 100 105

5

<210> 1271
 <211> 168
 <212> PRT
 <213> Homo sapiens

10

<400> 1271
 Asn Glu Gln Thr Leu Arg Ala Asp Glu Ile Leu Pro Ser Glu Ser Lys
 1 5 10 15
 Gln Lys Asp Tyr Glu Glu Ser Ser Trp Asp Ser Glu Ser Leu Cys Glu
 15 20 25 30
 Thr Val Ser Gln Lys Asp Val Cys Leu Pro Lys Ala Ala His Gln Lys
 35 40 45
 Glu Ile Asp Lys Ile Asn Gly Lys Leu Glu Gly Ser Pro Val Lys Asp
 50 55 60
 20 Gly Leu Leu Lys Ala Asn Cys Gly Met Lys Val Ser Ile Pro Thr Lys
 65 70 75 80
 Ala Leu Glu Leu Met Asp Met Gln Thr Phe Lys Ala Glu Pro Pro Glu
 85 90 95
 Lys Pro Ser Ala Phe Glu Pro Ala Ile Glu Met Gln Lys Ser Val Pro
 25 100 105 110
 Asn Lys Ala Leu Glu Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Glu
 115 120 125
 Ile Leu Pro Ser Glu Ser Lys Gln Lys Asp Tyr Glu Glu Ser Ser Trp
 130 135 140
 30 Asp Ser Glu Ser Leu Cys Glu Thr Val Ser Xaa Lys Asp Val Cys Phe
 145 150 155 160
 Pro Arg Leu Arg Ile Lys Lys Lys
 165

35

<210> 1272
 <211> 91
 <212> PRT
 <213> Homo sapiens

40

<400> 1272
 Ser Phe Cys Leu Asp Ser Asp Gly Ser Ile Ser Ser Ala Leu Asn Val
 1 5 10 15
 Cys Ser Phe Phe Asn Ser Lys Ala Leu Phe Gly Thr Asp Phe Cys Ile
 20 25 30
 45 Ser Met Ala Gly Ser Lys Ala Asp Gly Phe Ser Gly Gly Ser Ala Leu
 35 40 45
 Lys Val Cys Met Ser Ile Asn Ser Lys Ala Leu Val Gly Ile Glu Thr
 50 55 60
 Phe Ile Pro Gln Leu Ala Phe Arg Arg Pro Ser Leu Thr Gly Asp Pro
 50 65 70 75 80
 Ser Asn Phe Pro Phe Ile Leu Ser Ile Ser Phe
 85 90

55

<210> 1273
 <211> 177
 <212> PRT
 <213> Homo sapiens

60

<400> 1273
 Ser Asn Trp Thr Ser Arg Lys Ser Gln Glu Pro Ala Phe His Xaa Ala
 1 5 10 15
 Gly Asp Ala Cys Leu Gln Arg Lys Met Asn Val Asp Val Ser Ser Thr
 20 25 30

Ile Tyr Asn Asn Glu Val Leu His Gln Pro Leu Xaa Xaa Ala Gln Arg
 35 40 45
 Lys Ser Lys Ser Leu Lys Ile Asn Leu Asn Tyr Ala Gly Asp Ala Xaa
 50 55 60
 5 Arg Glu Asn Thr Leu Val Ser Glu His Ala Gln Arg Asp Gln Arg Glu
 65 70 75 80
 Xaa Gln Cys Gln Met Lys Glu Ala Glu Xaa Met Tyr Gln Asn Glu Gln
 85 90 95
 Asp Asn Val Asn Lys His Thr Glu Gln Gln Glu Ser Xaa Asp Gln Lys
 10 100 105 110
 Leu Phe Gln Leu Gln Ser Lys Asn Met Trp Leu Gln Gln Gln Leu Val
 115 120 125
 His Ala His Lys Lys Ala Asp Asn Lys Ser Lys Ile Thr Ile Asp Ile
 130 135 140
 15 His Phe Leu Glu Arg Lys Met Gln His His Xaa Leu Lys Glu Lys Asn
 145 150 155 160
 Glu Glu Ile Phe Asn Tyr Asn Asn His Leu Lys Asn Arg Ile Tyr Gln
 165 170 175
 Tyr
 20

<210> 1274

<211> 106

<212> PRT

25 <213> Homo sapiens

<400> 1274

Ile Ser Pro His Phe Ser Leu Leu Gly Xaa Asp Val Ala Phe Ser Ser
 1 5 10 15
 30 Gln Glu Asn Glu Tyr Gln Leu Leu Ser Cys Phe Cys Cys Gln Leu Ser
 20 25 30
 Tyr Val His Glu Leu Ile Ala Val Glu Ala Thr Tyr Phe Cys Phe Val
 35 40 45
 Val Glu Ile Ile Ser Asp Leu Xaa Thr Pro Ala Val Gln Cys Val Cys
 35 50 55 60
 Ser His Tyr Leu Val Arg Phe Asp Thr Xaa Val Gln Leu Pro Ser Phe
 65 70 75 80
 Asp Thr Xaa Phe His Val Gly Leu Phe Val His Val Leu Lys Pro Met
 85 90 95
 40 Tyr Phe Leu Leu Xaa His Leu Arg His Asn
 100 105

<210> 1275

<211> 181

45 <212> PRT

<213> Homo sapiens

<400> 1275

Glu Ile Leu Glu Ala Glu Ile Glu Ser His His Pro Arg Leu Ala Ser
 1 5 10 15
 50 Ala Val Gln Asp His Asp Gln Ile Val Thr Ser Arg Lys Ser Gln Glu
 20 25 30
 Pro Ala Phe His Ile Ala Gly Asp Ala Cys Leu Gln Arg Lys Met Asn
 35 40 45
 55 Val Asp Val Ser Ser Thr Ile Tyr Asn Asn Glu Val Leu His Gln Pro
 50 55 60
 Leu Ser Glu Ala Gln Arg Lys Ser Lys Ser Leu Lys Ile Asn Leu Asn
 65 70 75 80
 Tyr Ala Gly Asp Ala Leu Arg Glu Asn Thr Leu Val Ser Glu His Ala
 85 90 95
 60 Gln Arg Asp Gln Arg Glu Thr Gln Cys Gln Met Lys Glu Ala Glu His
 100 105 110
 Met Tyr Gln Asn Glu Gln Asp Asn Val Asn Lys His Thr Glu Gln Gln

115 120 125
 Glu Ser Leu Asp Gln Lys Leu Phe Gln Leu Gln Ser Lys Asn Met Trp
 130 135 140
 Leu Gln Gln Gln Leu Val His Ala His Lys Lys Ala Asp Asn Lys Ser
 5 145 150 155 160
 Lys Ile Gln Leu Ile Phe Ile Phe Leu Arg Gly Lys Cys Asn Ile Ser
 165 170 175
 Pro Lys Arg Glu Lys
 180
 10
 <210> 1276
 <211> 57
 <212> PRT
 <213> Homo sapiens
 15
 <400> 1276
 Ser Phe Cys Xaa Pro Gln Ala Val Xaa Pro Phe Ser Val Phe Val His
 1 5 10 15
 Leu Ser Xaa Ile His Ser Asp Leu Val Xaa Thr Phe Ser Ile Phe Ile
 20 20 25 30
 Lys Leu Ser Leu Thr Val Leu Thr Leu Ile Ala Leu Met Leu Gln Asp
 35 40 45
 Val Phe Ser Ser Trp Cys Arg Thr Ile
 50 55
 25
 <210> 1277
 <211> 146
 <212> PRT
 <213> Homo sapiens
 30
 <400> 1277
 Phe Phe Glu Ala Gln Lys Xaa Ile Pro Lys Ser Leu Lys Ile Ile Phe
 1 5 10 15
 Asn Tyr Ala Gly Asp Gly Phe Lys Arg Lys Xaa Met Gly Phe Arg Thr
 35 20 25 30
 Cys Thr Lys Ser Gln Arg Glu Thr Gln Cys Gln Met Lys Glu Xaa Glu
 35 40 45
 His Met Phe Gln Asn Glu Gln Asp Asn Val Asn Lys His Ile Glu Gln
 50 55 60
 40 Gln Glu Ser Xaa Asp Gln Lys Leu Phe Gln Leu Gln Ser Lys Asn Met
 65 70 75 80
 Trp Leu Gln Gln Gln Leu Val His Ala His Lys Lys Ala Xaa Asn Lys
 85 90 95
 Ser Lys Ile Thr Ile Asp Ile His Phe Leu Glu Arg Lys Met Gln His
 45 100 105 110
 His Leu Leu Lys Glu Lys Asn Glu Glu Ile Phe Asn Tyr Asn Asn His
 115 120 125
 Leu Lys Asn Arg Ile Tyr Gln Tyr Glu Lys Glu Lys Ala Glu Thr Glu
 130 135 140
 50 Asn Ser
 145
 <210> 1278
 <211> 184
 55 <212> PRT
 <213> Homo sapiens
 <400> 1278
 Lys Glu Leu Glu Val Lys Gln Gln Leu Glu Gln Ala Leu Arg Ile Gln
 60 1 5 10 15
 Asp Ile Glu Leu Lys Ser Val Glu Ser Asn Leu Asn Gln Val Ser His
 20 25 30
 Thr His Glu Asn Glu Asn Tyr Leu Leu His Glu Asn Cys Met Leu Lys

35 40 45
 Lys Glu Ile Ala Met Leu Lys Leu Glu Ile Ala Thr Leu Lys His Gln
 50 55 60
 Tyr Gln Glu Lys Glu Asn Lys Tyr Phe Glu Asp Ile Lys Ile Leu Lys
 5 65 70 75 80
 Glu Lys Asn Ala Glu Leu Gln Met Thr Leu Lys Leu Lys Glu Glu Ser
 85 90 95
 Leu Thr Lys Arg Ala Ser Gln Tyr Ser Gly Gln Leu Lys Val Leu Ile
 100 105 110
 10 Ala Glu Asn Thr Met Leu Thr Ser Lys Leu Lys Glu Lys Gln Asp Lys
 115 120 125
 Glu Ile Leu Glu Ala Glu Ile Glu Ser His His Pro Arg Leu Ala Ser
 130 135 140
 15 Ala Val Gln Asp His Asp Gln Ile Val Thr Ser Arg Lys Ser Gln Glu
 145 150 155 160
 Pro Ala Phe His Ile Ala Gly Asp Ala Cys Leu Gln Arg Lys Met Asn
 165 170 175
 Val Asp Val Ser Ser Thr Asp Ile
 180
 20
 <210> 1279
 <211> 220
 <212> PRT
 <213> Homo sapiens
 25
 <400> 1279
 Ala Phe Glu Pro Ala Ile Asp Met Gln Lys Ser Val Pro Asn Lys Ala
 1 5 10 15
 Leu Glu Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Glu Ile Leu Pro
 20 25 30
 Ser Glu Ser Lys Gln Lys Asp Tyr Glu Glu Ser Ser Trp Asp Ser Glu
 35 40 45
 Ser Leu Cys Glu Thr Val Ser Gln Lys Asp Val Cys Leu Pro Lys Ala
 50 55 60
 35 Ala His Gln Lys Glu Ile Asp Lys Ile Asn Gly Lys Leu Glu Gly Ser
 65 70 75 80
 Pro Val Lys Asp Gly Leu Leu Lys Ala Asn Cys Gly Met Lys Val Ser
 85 90 95
 Ile Pro Thr Lys Ala Leu Glu Leu Met Asp Met Gln Thr Phe Lys Ala
 100 105 110
 40 Glu Pro Pro Glu Lys Pro Ser Ala Phe Glu Pro Ala Ile Glu Met Gln
 115 120 125
 Lys Ser Val Pro Asn Lys Ala Leu Glu Leu Lys Asn Glu Gln Thr Leu
 130 135 140
 45 Arg Ala Asp Glu Ile Leu Pro Ser Glu Ser Lys Gln Lys Asp Tyr Glu
 145 150 155 160
 Glu Ser Ser Trp Asp Ser Glu Ser Leu Cys Glu Thr Val Ser Arg Arg
 165 170 175
 Met Cys Val Tyr Pro Xaa Leu Ala Xaa Gln Lys Glu Ile Asp Lys Ile
 180 185 190
 50 Asn Gly Lys Leu Glu Xaa Arg Tyr Ala Ala Glu Phe Lys Thr Phe Phe
 195 200 205
 Ala Met Ile Arg Ala Ser Val Lys Glu Gly Leu Leu
 210 215 220
 55
 <210> 1280
 <211> 195
 <212> PRT
 <213> Homo sapiens
 60
 <400> 1280
 Leu Cys Glu Thr Val Ser Gln Lys Asp Val Cys Leu Pro Lys Ala Ala
 1 5 10 15

His Gln Lys Glu Ile Asp Lys Ile Asn Gly Lys Leu Glu Gly Ser Pro
 20 25 30
 Val Lys Asp Gly Leu Leu Lys Ala Asn Cys Gly Met Lys Val Ser Ile
 35 40 45
 5 Pro Thr Lys Ala Leu Glu Leu Met Asp Met Gln Thr Phe Lys Ala Glu
 50 55 60
 Pro Pro Glu Lys Pro Ser Ala Phe Glu Pro Ala Ile Glu Met Gln Lys
 65 70 75 80
 Ser Val Pro Asn Lys Ala Leu Glu Leu Lys Asn Glu Gln Thr Leu Arg
 10 85 90 95
 Ala Asp Glu Ile Leu Pro Ser Glu Ser Lys Gln Lys Asp Tyr Glu Glu
 100 105 110
 Ser Ser Trp Asp Ser Glu Ser Leu Cys Glu Thr Val Ser Gln Lys Asp
 115 120 125
 15 Val Cys Leu Pro Lys Ala Ala His Gln Lys Glu Ile Asp Xaa Ile Xaa
 130 135 140
 Gly Lys Leu Glu Gly Ser Pro Val Lys Asp Gly Leu Leu Lys Ala Asn
 145 150 155 160
 Cys Gly Met Lys Val Ser Ile Ser Thr Lys Ala Leu Arg Ile Asp Gly
 20 165 170 175
 His Ala Asn Phe Gln Ser Arg Ala Xaa Arg Glu Ala Ile Cys Leu Arg
 180 185 190
 Ala Cys His
 195
 25
 <210> 1281
 <211> 209
 <212> PRT
 <213> Homo sapiens
 30
 <400> 1281
 Asn Leu Asn Gln Val Ser His Thr His Glu Asn Glu Asn Tyr Leu Leu
 1 5 10 15
 His Glu Asn Cys Met Leu Lys Lys Glu Ile Ala Met Leu Lys Leu Glu
 35 20 25 30
 Ile Ala Thr Leu Lys His Gln Tyr Gln Glu Lys Glu Asn Lys Tyr Phe
 35 40 45
 Glu Asp Ile Lys Ile Leu Lys Glu Lys Asn Ala Glu Leu Gln Met Thr
 50 55 60
 40 Leu Lys Leu Lys Glu Glu Ser Leu Thr Lys Arg Ala Ser Gln Tyr Ser
 65 70 75 80
 Gly Gln Leu Lys Val Leu Ile Ala Glu Asn Thr Met Leu Thr Ser Lys
 85 90 95
 Leu Lys Glu Lys Gln Asp Lys Glu Ile Leu Glu Ala Glu Ile Glu Ser
 45 100 105 110
 His His Pro Arg Leu Ala Ser Ala Val Gln Asp His Asp Gln Ile Val
 115 120 125
 Thr Ser Arg Lys Ser Gln Glu Pro Ala Phe His Ile Ala Gly Asp Ala
 130 135 140
 50 Cys Leu Gln Arg Lys Met Asn Val Asp Val Ser Ser Thr Ile Tyr Asn
 145 150 155 160
 Asn Glu Val Leu His Gln Pro Leu Ser Glu Ala Gln Arg Lys Ser Lys
 165 170 175
 Ser Leu Lys Ile Asn Leu Asn Tyr Ala Gly Asp Ala Leu Arg Glu Asn
 55 180 185 190
 His Trp Phe Gln Asn Met Xaa Lys Glu Thr Asn Val Lys His Ser Val
 195 200 205
 Lys

60

<210> 1282
 <211> 120
 <212> PRT

<213> Homo sapiens

<400> 1282

5 Ser Tyr Asn Phe Ala Ala Lys Asn Ser Ala Val Val Pro Gln Gly Phe
 1 5 10 15
 Met Ile Lys Ser Lys Leu Leu Gly Val Val Tyr Arg Val Leu Arg Ile
 20 25 30
 Trp Thr Phe Leu Leu Leu His Val Phe Thr Gly Leu Phe Phe Gly Leu
 35 40 45
 10 Glu His Phe Ser Gln Val Leu Gly Leu Leu Pro Gln Phe Leu Ser Leu
 50 55 60
 Ser Pro Phe Cys Pro Thr Pro Trp Leu Gly Leu Ser Leu Pro Leu Thr
 65 70 75 80
 15 Pro Pro Cys Arg Tyr Leu Ser Gln Ser Leu Ser His Arg Ile Ile Cys
 85 90 95
 Phe Phe Thr Cys Leu Phe Leu Pro Leu Asn His Glu Val Phe Glu Gly
 100 105 110
 Arg Val Arg Gly Leu Val Ile Phe
 115 120

<210> 1283

<211> 81

<212> PRT

<213> Homo sapiens

<400> 1283

25 Lys Ile Thr Lys Pro Leu Thr Arg Pro Ser Lys Thr Ser Trp Phe Lys
 1 5 10 15
 Gly Arg Asn Arg Gln Val Lys Lys Gln Ile Ile Leu Cys Asp Arg Asp
 20 25 30
 Cys Asp Lys Tyr Leu Gln Gly Gly Val Ser Gly Arg Leu Asn Pro Ser
 35 40 45
 Gln Gly Val Gly Gln Lys Gly Glu Arg Glu Arg Asn Trp Gly Arg Ser
 50 55 60
 35 Pro Asn Thr Trp Glu Lys Cys Ser Lys Pro Lys Asn Ser Pro Val Asn
 65 70 75 80
 Thr

<210> 1284

<211> 181

<212> PRT

<213> Homo sapiens

<400> 1284

45 Gln Asp His Asp Gln Ile Val Thr Ser Arg Lys Ser Gln Glu Pro Ala
 1 5 10 15
 Phe His Ile Ala Gly Asp Ala Cys Leu Gln Arg Lys Met Asn Val Asp
 20 25 30
 50 Val Ser Ser Thr Ile Tyr Asn Asn Glu Val Leu His Gln Pro Leu Phe
 35 40 45
 Glu Ala Gln Arg Lys Ser Lys Ser Leu Lys Ile Asn Xaa Asn Tyr Ala
 50 55 60
 Gly Asp Ala Xaa Arg Glu Asn Thr Leu Val Ser Glu His Ala Gln Arg
 65 70 75 80
 55 Asp Gln Arg Glu Thr Gln Cys Gln Met Lys Glu Ala Glu His Met Tyr
 85 90 95
 Gln Asn Glu Gln Asp Asn Val Asn Lys His Thr Glu Gln Gln Glu Ser
 100 105 110
 60 Xaa Asp Gln Lys Leu Phe Gln Leu Gln Ser Lys Asn Met Trp Leu Gln
 115 120 125
 Gln Gln Leu Val His Ala His Lys Lys Ala Asp Asn Lys Ser Lys Ile
 130 135 140

Thr Ile Asp Ile His Phe Leu Glu Arg Lys Met Gln His His Leu Leu
 145 150 155 160
 Lys Glu Lys Asn Glu Glu Ile Phe Asn Tyr Asn Asn His Leu Lys Asn
 165 170 175
 5 Arg Ile Tyr Gln Tyr
 180
 <210> 1285
 <211> 106
 10 <212> PRT
 <213> Homo sapiens
 <400> 1285
 15 Ile Ser Pro His Phe Ser Leu Leu Gly Asp Asp Val Ala Phe Ser Ser
 1 5 10 15
 Gln Glu Asn Glu Tyr Gln Leu Leu Ser Cys Phe Cys Cys Gln Leu Ser
 20 25 30
 Tyr Val His Glu Leu Ile Ala Val Glu Ala Thr Tyr Phe Cys Phe Val
 35 40 45
 20 Val Glu Ile Ile Ser Asp Leu Xaa Thr Pro Ala Val Gln Cys Val Cys
 50 55 60
 Ser His Tyr Leu Val Arg Phe Asp Thr Cys Val Gln Leu Pro Ser Phe
 65 70 75 80
 Asp Thr Val Phe His Val Gly Leu Phe Val His Val Leu Lys Pro Met
 25 85 90 95
 Tyr Phe Leu Leu Xaa His Leu Arg His Asn
 100 105
 <210> 1286
 30 <211> 105
 <212> PRT
 <213> Homo sapiens
 <400> 1286
 35 Ser Phe Cys Leu Asp Ser Asp Gly Ser Ile Ser Ser Ala Leu Asn Val
 1 5 10 15
 Cys Ser Phe Phe Asn Ser Lys Ala Leu Phe Gly Thr Asp Phe Cys Ile
 20 25 30
 Ser Met Ala Gly Ser Lys Ala Asp Gly Phe Ser Gly Gly Ser Ala Leu
 40 35 40 45
 Lys Val Cys Met Ser Ile Asn Ser Lys Ala Leu Val Gly Ile Glu Thr
 50 55 60
 Phe Ile Pro Gln Leu Ala Phe Arg Arg Pro Ser Leu Thr Gly Asp Leu
 65 70 75 80
 45 Ile Ile Ala Glu Asn Val Leu Asn Ser Ala Ala Tyr Leu Pro Ser Asn
 85 90 95
 Phe Pro Phe Ile Leu Ser Ile Ser Phe
 100 105
 50 <210> 1287
 <211> 229
 <212> PRT
 <213> Homo sapiens
 55 <400> 1287
 Cys Val Ser Leu Lys Pro Pro Glu Lys Pro Ser Ala Phe Glu Pro Ala
 1 5 10 15
 Ile Glu Met Gln Lys Ser Val Pro Asn Lys Ala Leu Glu Leu Lys Asn
 20 25 30
 60 Glu Gln Thr Leu Arg Ala Asp Glu Ile Leu Pro Ser Glu Ser Lys Gln
 35 40 45
 Lys Asp Tyr Glu Glu Ser Ser Trp Asp Ser Glu Ser Leu Cys Glu Thr
 50 55 60

Val Ser Gln Lys Asp Val Cys Leu Pro Lys Ala Ala His Gln Lys Glu
 65 70 75 80
 Ile Asp Lys Ile Asn Gly Lys Leu Glu Gly Arg Tyr Ala Ala Glu Phe
 85 90 95
 5 Arg Thr Phe Ser Ala Met Ile Arg Ser Pro Val Lys Asp Gly Leu Leu
 100 105 110
 Lys Ala Asn Cys Gly Met Lys Val Ser Ile Pro Thr Lys Ala Leu Glu
 115 120 125
 10 Leu Met Asp Met Gln Thr Phe Lys Ala Glu Pro Pro Glu Lys Pro Ser
 130 135 140
 Ala Phe Glu Pro Ala Ile Glu Met Gln Lys Ser Val Pro Asn Lys Ala
 145 150 155 160
 Leu Glu Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Glu Ile Leu Pro
 165 170 175
 15 Ser Glu Ser Lys Gln Lys Asp Tyr Glu Glu Ser Ser Trp Asp Ser Glu
 180 185 190
 Ser Leu Cys Glu Thr Val Ser Gln Lys Asp Val Cys Leu Pro Lys Ala
 195 200 205
 20 Ala His Gln Lys Glu Ile Asp Lys Ile Asn Gly Lys Leu Glu Ala Ile
 210 215 220
 Arg Asp Gly Ser Thr
 225

25 <210> 1288
 <211> 174
 <212> PRT
 <213> Homo sapiens

<400> 1288
 30 Cys Val Ser Leu Lys Pro Pro Glu Lys Pro Ser Ala Phe Glu Pro Ala
 1 5 10 15
 Ile Glu Met Gln Lys Ser Val Pro Asn Lys Ala Leu Glu Leu Lys Asn
 20 25 30
 35 Glu Gln Thr Leu Arg Ala Asp Glu Ile Leu Pro Ser Glu Ser Lys Gln
 35 40 45
 Lys Asp Tyr Glu Glu Ser Ser Trp Asp Ser Glu Ser Leu Cys Glu Thr
 50 55 60
 Val Ser Gln Lys Asp Val Cys Leu Pro Lys Ala Ala His Gln Lys Glu
 65 70 75 80
 40 Ile Asp Lys Ile Asn Gly Lys Leu Glu Gly Arg Tyr Ala Ala Glu Phe
 85 90 95
 Arg Thr Phe Ser Ala Met Ile Arg Ser Pro Val Lys Asp Gly Leu Leu
 100 105 110
 Lys Ala Asn Cys Gly Met Lys Val Ser Ile Pro Thr Lys Ala Leu Glu
 115 120 125
 45 Leu Met Asp Met Gln Thr Phe Lys Ala Glu Pro Pro Glu Lys Pro Ser
 130 135 140
 Ala Phe Glu Pro Xaa Ile Gly Lys Pro Lys Val Cys Xaa Gln Ile Lys
 145 150 155 160
 50 Ala Phe Gly Ile Gly Arg Met Asp Gln Xaa Leu Gly Ala Arg
 165 170

55 <210> 1289
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 1289
 60 Pro Phe Gly Trp Xaa Ser Glu Gly Xaa Tyr Ser His Arg Ala Pro Xaa
 1 5 10 15
 Gly Trp Ser Ile Leu Pro Ile Pro Lys Ala Phe Ile Trp Xaa Gln Thr
 20 25 30
 Phe Gly Phe Pro Met Xaa Gly Ser Lys Ala Asp Gly Phe Ser Gly Gly

35 40 45
 Ser Ala Leu Lys Val Cys Met Ser Ile Asn Ser Lys Ala Leu Val Gly
 50 55 60
 Ile Glu Thr Phe Ile Pro Gln Leu Ala Phe Arg Arg Pro Ser Leu Thr
 5 65 70 75 80
 Gly Asp Leu Ile Ile Ala Glu Asn Val Leu Asn Ser Ala Ala Tyr Leu
 85 90 95
 Pro Ser Asn Phe Pro Phe Ile Leu Ser Ile Ser Phe
 100 105
 10
 <210> 1290
 <211> 117
 <212> PRT
 <213> Homo sapiens
 15
 <400> 1290
 Ile Gln Gln His Ile Tyr Leu Leu Ile Phe His Leu Phe Tyr Leu Phe
 1 5 10 15
 Leu Phe Asp Ala Gln Pro Trp Val Asn Thr His Pro Ser Val Lys Gln
 20 20 25 30
 Ser His Arg Asp Ser Gln Asn Pro Lys Asn Phe Leu His Ser Pro Phe
 35 40 45
 Val Trp Ile Leu Met Gly Val Ser His Leu Leu Ser Met Phe Val His
 50 55 60
 25 Ser Ser Ile Pro Arg Leu Tyr Leu Glu Gln Thr Phe Ala Phe Gln Trp
 65 70 75 80
 Gln Ala Arg Arg Gln Met Ala Ser Arg Glu Ala Leu Met Lys His Ile
 85 90 95
 Arg Ile Thr Tyr Ile Ile Pro Phe Ile Leu Phe Phe Asn Ile Ala Tyr
 30 100 105 110
 Leu Trp Lys Gly Thr
 115
 35
 <210> 1291
 <211> 189
 <212> PRT
 <213> Homo sapiens
 40
 <400> 1291
 Ile Leu Pro Ser Glu Ser Lys Gln Lys Asp Tyr Glu Glu Ser Ser Trp
 1 5 10 15
 Asp Ser Glu Ser Leu Cys Glu Thr Val Ser Gln Lys Asp Val Cys Leu
 20 25 30
 Pro Lys Ala Ala His Gln Lys Glu Ile Asp Lys Ile Asn Gly Lys Leu
 45 35 40 45
 Glu Gly Arg Tyr Ala Ala Glu Phe Arg Thr Phe Ser Ala Met Ile Arg
 50 55 60
 Ser Pro Val Lys Asp Gly Leu Leu Lys Ala Asn Cys Gly Met Lys Val
 65 70 75 80
 50 Ser Ile Pro Thr Lys Ala Leu Glu Leu Met Asp Met Gln Thr Phe Lys
 85 90 95
 Ala Glu Pro Pro Glu Lys Pro Ser Ala Phe Glu Pro Ala Ile Glu Met
 100 105 110
 Gln Lys Ser Val Pro Asn Lys Ala Leu Glu Leu Lys Asn Glu Gln Thr
 55 115 120 125
 Leu Arg Ala Asp Glu Ile Leu Pro Ser Glu Ser Lys Gln Lys Asp Tyr
 130 135 140
 Glu Glu Ser Ser Trp Asp Ser Glu Ser Leu Cys Glu Thr Val Ser Gln
 145 150 155 160
 60 Lys Asp Val Cys Leu Pro Lys Ala Ala His Gln Lys Glu Ile Asp Lys
 165 170 175
 Ile Asn Gly Lys Leu Glu Ala Ile Arg Asp Gly Ser Thr
 180 185

<210> 1292
 <211> 105
 <212> PRT
 5 <213> Homo sapiens

<400> 1292
 Ser Phe Cys Leu Asp Ser Asp Gly Ser Ile Ser Ser Ala Leu Asn Val
 1 5 10 15
 10 Cys Ser Phe Phe Asn Ser Lys Ala Leu Phe Gly Thr Asp Phe Cys Ile
 20 25 30
 Ser Met Ala Gly Ser Lys Ala Asp Gly Phe Ser Gly Gly Ser Ala Leu
 35 40 45
 15 Lys Val Cys Met Ser Ile Asn Ser Lys Ala Leu Val Gly Ile Glu Thr
 50 55 60
 Phe Ile Pro Gln Leu Ala Phe Arg Arg Pro Ser Leu Thr Gly Asp Leu
 65 70 75 80
 Ile Ile Ala Glu Asn Val Leu Asn Ser Ala Ala Tyr Leu Pro Ser Asn
 85 90 95
 20 Phe Pro Phe Ile Leu Ser Ile Ser Phe
 100 105

<210> 1293
 <211> 181
 25 <212> PRT
 <213> Homo sapiens

<400> 1293
 Gln Xaa His Asp Gln Ile Val Thr Ser Arg Lys Ser Gln Glu Pro Ala
 1 5 10 15
 Phe His Ile Ala Gly Asp Ala Cys Leu Gln Arg Lys Met Asn Val Asp
 20 25 30
 Val Ser Ser Thr Ile Tyr Asn Asn Glu Val Leu His Gln Pro Leu Ser
 35 35 40 45
 35 Glu Ala Gln Arg Lys Ser Lys Ser Leu Lys Ile Asn Xaa Asn Tyr Ala
 50 55 60
 Gly Asp Ala Leu Arg Glu Asn Thr Leu Val Ser Glu His Ala Gln Arg
 65 70 75 80
 Asp Gln Arg Glu Xaa Gln Cys Gln Met Lys Glu Ala Glu His Met Tyr
 85 90 95
 40 Gln Asn Glu Gln Asp Asn Val Asn Lys His Thr Glu Gln Gln Glu Ser
 100 105 110
 Leu Asp Gln Lys Leu Phe Gln Leu Gln Ser Lys Asn Met Trp Leu Gln
 115 120 125
 45 Gln Gln Leu Val His Ala His Lys Lys Ala Asp Asn Lys Ser Lys Ile
 130 135 140
 Thr Ile Asp Ile His Phe Leu Glu Arg Lys Met Gln His His Leu Leu
 145 150 155 160
 Lys Glu Lys Asn Glu Glu Ile Phe Asn Tyr Asn Asn His Leu Lys Asn
 165 170 175
 50 Arg Ile Tyr Gln Tyr
 180

<210> 1294
 55 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 1294
 Ile Ser Pro His Phe Ser Leu Leu Gly Asp Asp Val Ala Phe Ser Ser
 1 5 10 15
 Gln Glu Asn Glu Tyr Gln Leu Leu Ser Cys Phe Cys Cys Gln Leu Ser
 20 25 30

Tyr Val His Glu Leu Ile Ala Val Glu Ala Thr Tyr Phe Cys Phe Val
 35 40 45
 Val Glu Ile Ile Ser Asp Leu Glu Thr Pro Ala Val Gln Cys Val Cys
 50 55 60
 5 Ser His Tyr Leu Val Arg Phe Asp Thr Cys Val Gln Leu Pro Ser Phe
 65 70 75 80
 Asp Thr Xaa Phe His Val Gly Leu Phe Val His Val Leu Lys Pro Met
 85 90 95
 10 Tyr Phe Leu Leu Glu His Leu Arg His Asn
 100 105

<210> 1295

<211> 185

<212> PRT

15 <213> Homo sapiens

<400> 1295

Tyr Gly Arg Phe Leu Leu Leu Ile Val Gly Tyr Phe Cys Phe Ser Tyr
 1 5 10 15
 20 Cys His Leu Lys Tyr Ile Phe Asn Val Glu Ile Leu Thr Ala Cys Leu
 20 25 30
 Met Lys Ser Ser Phe Gln Ile Phe Leu Gly Ser Pro Val Lys Asp Gly
 35 40 45
 25 Leu Leu Lys Ala Asn Cys Gly Met Lys Val Ser Ile Pro Thr Lys Ala
 50 55 60
 Leu Glu Leu Met Asp Met Gln Thr Phe Lys Ala Glu Pro Pro Glu Lys
 65 70 75 80
 Pro Ser Ala Phe Glu Pro Ala Ile Glu Met Gln Lys Ser Val Pro Asn
 85 90 95
 30 Lys Ala Leu Glu Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Glu Ile
 100 105 110
 Leu Pro Ser Glu Ser Lys Gln Lys Asp Tyr Glu Glu Ser Ser Trp Asp
 115 120 125
 35 Ser Glu Ser Leu Cys Glu Thr Val Ser Gln Lys Asp Val Cys Leu Pro
 130 135 140
 Lys Ala Ala His Gln Lys Glu Ile Asp Lys Ile Asn Gly Lys Leu Glu
 145 150 155 160
 Gly Arg Tyr Ala Ala Glu Phe Arg Thr Phe Ser Ala Met Ile Arg Xaa
 165 170 175
 40 Pro Val Lys Arg Trp Ser Ser Glu Gly
 180 185

<210> 1296

<211> 130

45 <212> PRT

<213> Homo sapiens

<400> 1296

Xaa Ile Ile Phe Ile Phe Met Ser Xaa Arg Asn Leu Thr Leu Xaa Ser
 1 5 10 15
 50 Ser Cys Ser His Leu Thr Phe Trp Phe Ser Asn Trp Asp Phe Ile Ser
 20 25 30
 Phe Ala Ser Asp Ser Phe Phe Phe Ser Thr Gln Asn Phe Phe Phe Ile
 35 40 45
 55 Cys Ser Ile Phe Pro Xaa Val Val His Xaa Asp Leu Phe Glu Val Pro
 50 55 60
 Leu Leu Phe His Lys Asn Glu Xaa Tyr Pro Lys Phe Leu Ile Gly Xaa
 65 70 75 80
 60 Leu Asn Leu Xaa Ile Phe His Leu Phe Tyr Pro Phe Leu Phe Asp Xaa
 85 90 95
 Asn Leu Gly Xaa Thr Xaa His Pro Ser Xaa Glu Gln Val Xaa Thr Glu
 100 105 110
 Asp Leu Ser Xaa Asn Pro Lys Asn Phe Leu Gln Pro Phe Phe Cys Phe

	115	120	125
	Asp Ser 130		
5	<210> 1297 <211> 103 <212> PRT <213> Homo sapiens		
10	<400> 1297		
	Met Gly Thr Arg Ala Xaa Gln Cys Glu Val Ser Xaa Thr His Glu Asn 1 5 10 15		
	Glu Asn Tyr Xaa Leu His Glu Asn Cys Met Leu Lys Lys Glu Ile Ala 20 25 30		
15	Met Leu Lys Leu Glu Ile Ala Xaa Leu Lys Xaa Gln Tyr Gln Glu Lys 35 40 45		
	Glu Asn Lys Tyr Phe Glu Asp Ile Lys Ile Leu Lys Glu Lys Asn Ala 50 55 60		
	Glu Leu Gln Met Thr Leu Lys Leu Lys Glu Glu Ser Leu Thr Lys Arg 65 70 75 80		
20	Ala Ser Gln Tyr Ser Gly Gln Leu Lys Val Xaa Ile Ala Glu Asn Xaa 85 90 95		
	Met Leu Thr Xaa Lys Leu Lys 100		
25	<210> 1298 <211> 98 <212> PRT <213> Homo sapiens		
30	<400> 1298		
	Xaa Xaa Xaa Xaa Thr Ile Xaa Xaa Arg Phe Xaa Xaa Phe Xaa Phe Lys 1 5 10 15		
	Asn Gln Asn Lys Arg Arg Val Glu Glu Asn Phe Trp Gly Xaa Xaa Lys 20 25 30		
35	Gly Pro Arg Xaa Arg Leu Val Xaa Lys Lys Asp Xaa Gly Xaa Pro Gln 35 40 45		
	Gly Xaa His Gln Lys Glu Met Asp Lys Ile Ser Gly Lys Xaa Glu Asp 50 55 60		
40	Ser Xaa Ser Leu Ser Lys Ile Leu Asp Xaa Val His Ser Cys Glu Arg 65 70 75 80		
	Ala Arg Glu Leu Gln Lys Asp Xaa Cys Glu Gln Xaa Gln Glu Lys Trp 85 90 95		
	Asn Lys		
45	<210> 1299 <211> 207 <212> PRT <213> Homo sapiens		
50	<400> 1299		
	Lys Pro Ser Ala Phe Glu Pro Ala Ile Glu Met Gln Lys Ser Val Pro 1 5 10 15		
55	Asn Lys Ala Leu Glu Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Glu 20 25 30		
	Ile Leu Pro Ser Glu Ser Lys Gln Lys Asp Tyr Glu Glu Ser Ser Trp 35 40 45		
	Asp Ser Glu Ser Leu Cys Glu Thr Val Ser Gln Lys Asp Val Cys Leu 50 55 60		
60	Pro Lys Ala Ala His Gln Lys Glu Ile Asp Lys Ile Asn Gly Lys Leu 65 70 75 80		
	Glu Gly Arg Tyr Ala Ala Glu Phe Gly Thr Phe Ser Ala Met Ile Arg		

85 90 95
 Ser Pro Val Lys Asp Gly Leu Leu Lys Ala Asn Cys Gly Met Lys Val
 100 105 110
 5 Ser Ile Pro Thr Lys Ala Leu Glu Leu Met Asp Met Gln Thr Phe Lys
 115 120 125
 Ala Glu Pro Pro Glu Lys Pro Ser Ala Phe Glu Pro Ala Ile Glu Met
 130 135 140
 Gln Lys Ser Val Pro Asn Lys Ala Leu Glu Leu Lys Asn Glu Gln Thr
 145 150 155 160
 10 Leu Arg Ala Asp Glu Ile Ser His Gln Asn Pro Asn Lys Arg Thr Met
 165 170 175
 Lys Lys Val Leu Gly Ile Leu Arg Val Ser Val Arg Leu Phe His Arg
 180 185 190
 Lys Asp Val Cys Leu Pro Gln Xaa Ala Xaa Gln Lys Glu Ile Asp
 15 195 200 205

<210> 1300

<211> 187

<212> PRT

20 <213> Homo sapiens

<400> 1300

Thr Gly Phe Cys Trp Xaa Lys Ala His Asp Gln Ile Val Thr Ser Arg
 1 5 10 15
 25 Lys Ser Gln Glu Pro Ala Phe His Ile Ala Gly Asp Ala Cys Leu Gln
 20 25 30
 Arg Lys Met Asn Val Asp Val Ser Ser Pro Ile Tyr Asn Asn Glu Val
 35 40 45
 30 Leu His Gln Pro Leu Ser Glu Ala Gln Arg Lys Ser Lys Ser Leu Lys
 50 55 60
 Ile Asn Leu Asn Tyr Ala Gly Asp Ala Leu Arg Glu Asn Thr Leu Val
 65 70 75 80
 Ser Glu His Ala Gln Arg Asp Gln Arg Glu Thr Gln Cys Gln Met Lys
 85 90 95
 35 Glu Ala Glu His Met Tyr Gln Asn Glu Gln Asp Asn Val Asn Lys His
 100 105 110
 Thr Glu Gln Gln Glu Ser Xaa Asp Gln Lys Leu Phe Gln Leu Gln Ser
 115 120 125
 Lys Asn Met Trp Leu Gln Gln Gln Leu Val His Ala His Lys Lys Ala
 130 135 140
 40 Asp Asn Lys Ser Lys Ile Thr Ile Asp Ile His Phe Leu Glu Arg Lys
 145 150 155 160
 Met Gln His His Leu Leu Lys Glu Lys Asn Glu Glu Ile Phe Asn Tyr
 165 170 175
 45 Asn Asn His Leu Lys Asn Arg Ile Tyr Gln Tyr
 180 185

<210> 1301

<211> 164

50 <212> PRT

<213> Homo sapiens

<400> 1301

Pro Ala Ile Glu Met Gln Lys Ser Val Pro Asn Lys Ala Leu Glu Leu
 1 5 10 15
 Lys Asn Glu Gln Thr Leu Arg Ala Asp Gln Met Phe Pro Ser Glu Ser
 20 25 30
 Lys Gln Lys Lys Val Glu Glu Asn Ser Trp Asp Ser Glu Ser Leu Arg
 35 40 45
 60 Glu Thr Val Ser Gln Lys Asp Val Cys Val Pro Lys Ala Thr His Gln
 50 55 60
 Lys Glu Met Asp Lys Ile Ser Gly Lys Leu Glu Asp Ser Thr Ser Leu
 65 70 75 80

Ser Lys Ile Leu Asp Thr Val His Ser Cys Glu Arg Ala Arg Glu Leu
 85 90 95
 Gln Lys Asp His Cys Glu Gln Arg Thr Gly Lys Met Glu Gln Met Lys
 100 105 110
 5 Lys Lys Phe Cys Val Leu Lys Lys Lys Leu S r Glu Ala Lys Glu Ile
 115 120 125
 Lys Ser Gln Leu Glu Asn Gln Lys Val Lys Trp Glu Gln Glu Leu Cys
 130 135 140
 10 Ser Val Arg Val Leu Thr Leu Met Lys Met Lys Ile Ile Ser Tyr Met
 145 150 155 160
 Lys Ile Ala Cys

15 <210> 1302
 <211> 196
 <212> PRT
 <213> Homo sapiens

20 <400> 1303
 Asp Leu Lys Thr Val Lys Glu Lys Asp Asp Ile Leu Phe Glu Asp Leu
 1 5 10 15
 Gln Asp Asn Xaa Asn Glu Asn Gly Glu Gly Glu Ile Glu Asp Glu Glu
 20 25 30
 25 Glu Glu Gly Tyr Asp Asp Asp Asp Asp Trp Asp Trp Asp Glu Gly
 35 40 45
 Val Gly Lys Leu Ala Lys Gly Tyr Val Trp Asn Gly Gly Ser Asn Pro
 50 55 60
 Gln Ala Asn Arg Gln Thr Ser Asp Ser Ser Ser Ala Lys Met Ser Thr
 65 70 75 80
 30 Pro Ala Asp Lys Val Leu Arg Lys Phe Glu Asn Lys Ile Asn Leu Asp
 85 90 95
 Lys Leu Asn Val Thr Asp Ser Val Ile Asn Lys Val Thr Glu Lys Ser
 100 105 110
 Arg Gln Lys Glu Ala Asp Met Tyr Arg Ile Lys Asp Lys Ala Asp Arg
 115 120 125
 35 Ala Thr Val Glu Gln Val Leu Asp Pro Arg Thr Arg Met Ile Leu Phe
 130 135 140
 Lys Met Leu Thr Arg Gly Ile Ile Thr Glu Ile Asn Gly Cys Ile Ser
 145 150 155 160
 40 Thr Gly Lys Glu Ala Asn Val Ser Met Leu Ala Gln Gln Met Glu Arg
 165 170 175
 Ala Glu Gln Ser Lys Phe Ile Lys Leu Leu Phe Trp Cys Ser Lys Ile
 180 185 190
 Gly Ile Asn Met
 45 195

 <210> 1303
 <211> 205
 <212> PRT
 50 <213> Homo sapiens

 <400> 1303
 Phe Phe Ser Pro Asn Glu Asn Phe Met Ala Lys Glu His Asp Phe Leu
 1 5 10 15
 55 Ser Ile Ile Gly Phe Trp Asn Asn Gly Ile Phe Cys Leu Trp Leu Ser
 20 25 30
 Leu Ile Lys Ser Phe Ile Phe Phe Phe Gly Pro Ser Phe Pro His Phe
 35 40 45
 60 Leu Arg Val Ser Phe Thr Ile Ala Met Thr Lys Ser Glu Phe Ser Thr
 50 55 60
 Tyr Ile Phe Ile Pro Ile Phe Glu His Gln Asn Arg Ser Phe Ile Asn
 65 70 75 80
 Phe Asp Cys Ser Ala Leu Ser Ile Cys Cys Ala Ser Met Asp Thr Leu

85 90 95
 Ala Ser Phe Pro Val Leu Met Gln Pro Phe Ile Ser Val Met Ile Pro
 100 105 110
 5 Leu Val Asn Ile Leu Asn Lys Ile Ile Leu Val Leu Gly Ser Asn Thr
 115 120 125
 Cys Ser Thr Val Ala Leu Ser Ala Leu Ser Leu Met Arg Tyr Ile Ser
 130 135 140
 Ala Ser Phe Cys Leu Asp Phe Ser Val Thr Leu Phe Met Thr Glu Ser
 145 150 155 160
 10 Val Thr Phe Ser Leu Ser Lys Leu Ile Leu Phe Ser Asn Phe Arg Lys
 165 170 175
 Thr Leu Ser Ala Gly Val Asp Ile Leu Ala Glu Leu Leu Ser Glu Val
 180 185 190
 15 Cys Arg Phe Ala Cys Gly Leu Leu Pro Pro Phe Gln Thr
 195 200 205

<210> 1304

<211> 164

<212> PRT

20 <213> Homo sapiens

<400> 1304

Pro Ala Ile Glu Met Gln Lys Ser Val Pro Asn Lys Ala Leu Glu Leu
 1 5 10 15
 25 Lys Asn Glu Gln Thr Leu Arg Ala Asp Gln Met Phe Pro Ser Glu Ser
 20 25 30
 Lys Gln Lys Lys Val Glu Glu Asn Ser Trp Asp Ser Glu Ser Leu Arg
 35 40 45
 30 Glu Thr Val Ser Gln Lys Asp Val Cys Val Pro Lys Ala Thr His Gln
 50 55 60
 Lys Glu Met Asp Lys Ile Ser Gly Lys Leu Glu Asp Ser Thr Ser Leu
 65 70 75 80
 Ser Lys Ile Leu Asp Thr Val His Ser Cys Glu Arg Ala Arg Glu Leu
 85 90 95
 35 Gln Lys Asp His Cys Glu Gln Arg Thr Gly Lys Met Glu Gln Met Lys
 100 105 110
 Lys Lys Phe Cys Val Leu Lys Lys Leu Ser Glu Ala Lys Glu Ile
 115 120 125
 Lys Ser Gln Leu Glu Asn Gln Lys Val Lys Trp Glu Gln Glu Leu Cys
 130 135 140
 40 Ser Val Arg Val Leu Thr Leu Met Lys Met Lys Ile Ile Ser Tyr Met
 145 150 155 160
 Lys Ile Ala Cys

<210> 1305

<211> 133

<212> PRT

50 <213> Homo sapiens

<400> 1305

Glu Thr Val Ser Gln Lys Asp Val Cys Val Pro Lys Ala Thr His Gln
 1 5 10 15
 55 Lys Glu Met Asp Lys Ile Ser Gly Lys Leu Glu Asp Ser Thr Ser Leu
 20 25 30
 Ser Lys Ile Leu Asp Thr Val His Ser Cys Glu Arg Ala Arg Glu Leu
 35 40 45
 Gln Lys Asp His Cys Glu Gln Arg Thr Gly Lys Met Glu Gln Met Lys
 50 55 60
 60 Lys Lys Phe Cys Val Leu Lys Lys Lys Leu Ser Glu Ala Lys Glu Ile
 65 70 75 80
 Lys Ser Gln Leu Glu Asn Gln Lys Val Lys Trp Glu Gln Glu Leu Cys
 85 90 95

Ser Val Arg L u Thr Leu Asn Pro Glu Glu Glu Lys Arg Arg Asn Ala
 100 105 110
 Asp Ile Leu Asn Glu Lys Ile Arg Glu Glu Leu Gly Arg Ile Glu Glu
 115 120 125
 5 His Ile Gly Lys Ser
 130
 <210> 1306
 <211> 83
 10 <212> PRT
 <213> Homo sapiens
 <400> 1306
 15 Gln Arg Phe Ile Ser Leu Phe Xaa Asp Gly Xaa Ser Xaa Xaa Xaa Ile
 1 5 10 15
 Ser Ser Leu Ser Xaa Gln Phe Pro Phe Ser Thr Cys Asn Phe Xaa Glu
 20 25 30
 Glu Ile Ile Phe Ile Phe Met Ser Val Arg Thr Leu Ile Gln Xaa Thr
 35 40 45
 20 Phe Tyr Thr Leu Gln Xaa Tyr Ile Leu Tyr Ser Glu Ser Leu Phe Lys
 50 55 60
 Cys Cys Phe Thr Ser Asn Ser Phe Leu Cys Ala Leu Arg Phe Phe Leu
 65 70 75 80
 Ile Leu Pro
 25
 <210> 1307
 <211> 231
 <212> PRT
 30 <213> Homo sapiens
 <400> 1307
 35 Leu Lys Arg Gly Ile Ser Asn Lys Val Gly Gln Leu Lys Val Xaa Xaa
 1 5 10 15
 Ser Leu Arg Thr Gln Cys Ser Leu Phe Lys Leu Lys Glu Xaa Gln Ala
 20 25 30
 Xaa Glu Ile Xaa Glu Ala Glu Ile Glu Ser His His Pro Arg Leu Ala
 35 40 45
 40 Ser Ala Val Gln Asp His Asp Gln Ile Val Thr Ser Arg Lys Ser Gln
 50 55 60
 Glu Pro Ala Phe His Ile Ala Gly Asp Ala Cys Leu Gln Arg Lys Met
 65 70 75 80
 Asn Val Asp Val Ser Ser Thr Ile Tyr Asn Asn Glu Val Leu His Gln
 85 90 95
 45 Pro Leu Ser Glu Ala Gln Arg Lys Ser Lys Ser Leu Lys Ile Asn Leu
 100 105 110
 Asn Tyr Ala Gly Asp Ala Leu Arg Glu Asn Thr Leu Val Ser Glu His
 115 120 125
 50 Ala Gln Arg Asp Gln Arg Glu Xaa Gln Cys Gln Met Lys Glu Ala Glu
 130 135 140
 His Met Tyr Gln Asn Glu Gln Asp Asn Val Asn Lys His Thr Glu Gln
 145 150 155 160
 Gln Glu Ser Xaa Asp Gln Lys Leu Phe Gln Leu Gln Ser Lys Asn Met
 165 170 175
 55 Trp Leu Gln Gln Gln Leu Val His Ala His Lys Lys Ala Asp Asn Lys
 180 185 190
 Ser Lys Ile Thr Ile Asp Ile His Phe Leu Glu Arg Lys Met Gln His
 195 200 205
 60 His Leu Leu Lys Glu Lys Asn Glu Glu Ile Phe Asn Tyr Asn Asn His
 210 215 220
 Leu Lys Xaa Arg Ile Tyr Gln
 225 230

<210> 1308
 <211> 183
 <212> PRT
 <213> Homo sapiens

5

<400> 1308

Asp Leu Lys Thr Val Lys Glu Lys Asp Asp Ile Leu Phe Glu Asp Leu
 1 5 10 15
 Gln Asp Asn Xaa Asn Glu Asn Gly Glu Gly Glu Ile Glu Asp Glu Glu
 10 20 25 30
 Glu Glu Gly Tyr Asp Asp Asp Asp Asp Asp Trp Asp Trp Asp Glu Gly
 35 40 45
 Val Gly Lys Leu Ala Lys Gly Tyr Val Trp Asn Gly Gly Ser Asn Pro
 50 55 60
 Gln Ala Asn Arg Gln Thr Ser Asp Ser Ser Ser Ala Lys Met Ser Thr
 15 65 70 75 80
 Pro Ala Asp Lys Val Leu Arg Lys Phe Glu Asn Lys Ile Asn Leu Asp
 85 90 95
 Lys Leu Asn Val Thr Asp Ser Val Ile Asn Lys Val Thr Glu Lys Ser
 100 105 110
 Arg Gln Lys Glu Ala Asp Met Tyr Arg Ile Lys Asp Lys Ala Asp Arg
 115 120 125
 Ala Thr Val Glu Gln Val Leu Asp Pro Arg Thr Arg Met Ile Leu Phe
 130 135 140
 Lys Met Leu Thr Arg Gly Ile Ile Thr Glu Ile Asn Gly Cys Ile Ser
 145 150 155 160
 Thr Gly Lys Glu Ala Asn Val Ser Met Leu Xaa Thr Ala Asn Gly Glu
 165 170 175
 Ser Arg Ala Ile Lys Ile Tyr
 180

<210> 1309
 <211> 219
 <212> PRT
 <213> Homo sapiens

35

<400> 1309

Glu Glu Cys Ile Arg Met Pro Asp Phe Val His Ala Asp Leu Ser Glu
 1 5 10 15
 Phe Asn Met Leu Tyr His Gly Gly Gly Val Tyr Ile Ile Asp Val Ser
 20 25 30
 Gln Ser Val Glu His Asp His Pro His Ala Leu Glu Phe Leu Arg Lys
 35 40 45
 Asp Cys Ala Asn Val Asn Asp Phe Phe Met Arg His Ser Val Ala Val
 50 55 60
 Met Thr Val Arg Glu Leu Phe Glu Phe Val Thr Asp Pro Ser Ile Thr
 65 70 75 80
 His Glu Asn Met Asp Ala Tyr Leu Ser Lys Ala Met Glu Ile Ala Ser
 85 90 95
 Gln Arg Thr Lys Glu Glu Arg Ser Ser Gln Asp His Val Asp Glu Glu
 100 105 110
 Val Phe Lys Arg Ala Tyr Ile Pro Arg Thr Leu Asn Glu Val Lys Asn
 115 120 125
 Tyr Glu Arg Asp Met Asp Ile Ile Met Lys Leu Lys Glu Glu Asp Met
 130 135 140
 Ala Met Asn Ala Gln Gln Asp Asn Ile Leu Tyr Gln Thr Val Thr Gly
 145 150 155 160
 Leu Lys Lys Asp Leu Ser Gly Val Gln Lys Val Pro Ala Leu Leu Glu
 165 170 175
 Asn Gln Val Glu Glu Arg Thr Cys Ser Asp Ser Glu Asp Ile Gly Ser
 180 185 190
 Ser Glu Cys Ser Asp Thr Asp Ser Glu Glu Gln Gly Asp His Ala Arg
 195 200 205

Pro Lys Lys His Thr Thr Asp Pro Asp Ile Asp
210 215

5 <210> 1310
<211> 191
<212> PRT
<213> Homo sapiens

10 <400> 1310
Glu Pro Asp Gln Lys Pro Glu Pro Val Asp Lys Val Ala Ala Met Arg
1 5 10 15
Glu Phe Arg Val Leu His Thr Ala Leu His Ser Ser Ser Ser Tyr Arg
20 25 30
15 Glu Ala Val Phe Lys Met Leu Ser Asn Lys Glu Ser Leu Asp Gln Ile
35 40 45
Ile Val Ala Thr Pro Gly Leu Ser Ser Asp Pro Ile Ala Leu Gly Val
50 55 60
Leu Gln Asp Lys Asp Leu Phe Ser Val Phe Ala Asp Pro Asn Met Leu
65 70 75 80
20 Asp Thr Leu Val Pro Ala His Pro Ala Leu Val Asn Ala Ile Val Leu
85 90 95
Val Leu His Ser Val Ala Gly Ser Ala Pro Met Pro Gly Thr Asp Ser
100 105 110
Ser Ser Arg Ser Met Pro Ser Ser Ser Tyr Arg Asp Met Pro Gly Gly
115 120 125
25 Phe Leu Phe Glu Gly Leu Ser Xaa Asp Glu Asp Asp Phe His Pro Asn
130 135 140
Thr Arg Ser Thr Pro Ser Ser Ser Thr Pro Ser Ser Arg Gln Pro Pro
145 150 155 160
30 Gly Val Gln Val Glu Leu Leu Gly Pro Gly Pro Ser Pro Lys Val Ser
165 170 175
Trp Pro Pro Pro Trp Pro Trp Pro Ala Xaa Arg Arg Ala Ser Phe
180 185 190

35 <210> 1311
<211> 164
<212> PRT
<213> Homo sapiens

40 <400> 1311
Tyr Arg Asp Met Pro Gly Ala Ser Cys Leu Lys Gly Ser Gln Met Met
1 5 10 15
Arg Met Thr Phe Thr Gln Thr Pro Gly Pro His Pro Xaa Ser Ser Thr
20 25 30
45 Pro Ser Ser Arg Pro Ala Ser Leu Gly Tyr Ser Gly Ala Xaa Gly Pro
35 40 45
Arg Pro Ile Thr Gln Ser Glu Leu Ala Thr Ala Leu Ala Leu Ala Ser
50 55 60
Thr Pro Glu Ser Ser Ser His Thr Pro Thr Pro Gly Thr Gln Gly His
65 70 75 80
50 Ser Ser Gly Thr Ser Pro Met Ser Xaa Gly Val Gln Ser Gly Thr Pro
85 90 95
Ile Thr Asn Asp Leu Phe Ser Gln Ala Leu Gln His Ala Leu Gln Ala
100 105 110
55 Xaa Gly Gln Pro Ser Leu Gln Ser Gln Trp Gln Pro Gln Leu Gln Gln
115 120 125
Leu Arg Asp Met Gly Ile Gln Asp Asp Glu Leu Ser Leu Arg Ala Leu
130 135 140
Gln Ala Thr Gly Gly Asp Ile Gln Ala Ala Leu Glu Leu Ile Phe Ala
145 150 155 160
60 Gly Gly Ala Pro

<210> 1312
 <211> 120
 <212> PRT
 <213> Homo sapiens

5

<400> 1312
 Leu Ser Pro Lys His Gln Val His Thr Xaa Leu Ala Val Leu Pro Ala
 1 5 10 15
 Pro Ala Gln Pro Pro Trp Gly Thr Val Glu Leu Xaa Gly Pro Gly Pro
 10 20 25 30
 Ser Pro Arg Val Ser Trp Pro Pro Pro Trp Pro Trp Pro Ala Leu Arg
 35 40 45
 Arg Ala Ala Leu Thr His Arg Leu Leu Ala Pro Arg Val Ile Pro Gln
 50 55 60
 Gly Pro His Gln Cys Pro Xaa Val Ser Ser Gln Gly Arg Pro Ser Pro
 15 65 70 75 80
 Met Ile Ser Ser Ala Lys Pro Tyr Ser Met Pro Phe Arg Pro Xaa Gly
 85 90 95
 Ser Pro Ala Phe Arg Ala Ser Gly Ser Pro Ser Cys Ser Ser Tyr Val
 20 100 105 110
 Thr Trp Ala Ser Arg Thr Met Ser
 115 120

<210> 1313
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 1313
 Gly Met Thr Leu Gly Ala Arg Ser Arg Cys Val Arg Ala Ala Leu Arg
 1 5 10 15
 Ser Ala Gly Gln Gly Gln Gly Gly Gly Gln Leu Thr Leu Gly Asp Gly
 20 25 30
 Pro Gly Pro Xaa Ser Ser Thr Val Pro Gln Gly Gly Trp Ala Gly Ala
 35 40 45
 Gly Ser Thr Ala Xaa Arg Val Trp Thr Trp Cys Leu Gly Glu Ser His
 50 55 60
 Pro His His Leu Arg Thr Leu Gln Thr Gly Ser Pro Trp His Ile Pro
 65 70 75 80
 Val Leu Ala Gly Xaa His Ala Xaa Gly Xaa Gly Ile Asn Pro Arg His
 85 90 95
 Trp Gly Pro Ala Cys Phe Arg Val Xaa Asn Gln Glu Gln Trp
 100 105 110

<210> 1314
 <211> 225
 <212> PRT
 <213> Homo sapiens

<400> 1314
 Phe Gln Glu Arg Ala Arg Ile Glu Lys Ala Tyr Ala Gln Gln Leu Ala
 1 5 10 15
 Asp Trp Ala Arg Lys Trp Arg Gly Thr Val Glu Lys Gly Pro Gln Tyr
 20 25 30
 Gly Thr Leu Glu Lys Ala Trp His Ala Phe Phe Thr Ala Ala Glu Arg
 35 40 45
 Leu Ser Ala Leu His Leu Glu Val Arg Glu Lys Pro Gln Gly Gln Asp
 50 55 60
 Ser Glu Arg Val Arg Ala Trp Gln Arg Gly Ala Phe His Arg Pro Val
 65 70 75 80
 Leu Gly Gly Phe Arg Glu Ser Arg Ala Ala Glu Asp Gly Phe Arg Lys
 85 90 95
 Ala Gln Lys Pro Trp Leu Lys Arg Leu Lys Glu Val Glu Ala Ser Lys

100 105 110
 Lys Ser Tyr His Ala Ala Arg Lys Asp Glu Lys Thr Ala Gln Thr Arg
 115 120 125
 5 Glu Ser His Ala Lys Ala Asp Ser Ala Val Xaa Gln Glu Gln Leu Arg
 130 135 140
 Lys Leu Gln Glu Arg Val Glu Arg Cys Ala Lys Glu Ala Glu Lys Thr
 145 150 155 160
 Lys Ala Gln Tyr Glu Gln Thr Leu Ala Glu Leu His Arg Tyr Thr Pro
 165 170 175
 10 Arg Tyr Met Glu Asp Met Glu Gln Ala Phe Glu Thr Leu Gln Ala Arg
 180 185 190
 Arg Ala Pro Xaa Ala Ser Phe Leu Xaa Gly Tyr Ala Xaa His Leu Thr
 195 200 205
 15 Pro Thr Pro Gly Pro Phe Ser Ala Val Arg Ser Xaa Met Lys Leu His
 210 215 220
 Pro
 225

20 <210> 1315
 <211> 214
 <212> PRT
 <213> Homo sapiens

<400> 1315
 25 Lys Arg Ser Arg Cys Trp Cys Lys Val Xaa Ser Ile Ser Xaa Lys Lys
 1 5 10 15
 Arg Ser Xaa Trp Arg Ser Ala Gly Leu Gln Gly Leu Lys Gly Leu Phe
 20 25 30
 30 His Val Leu His Val Ala Trp Ser Val Ala Met Gln Leu Cys Gln Arg
 35 40 45
 Leu Leu Ile Leu Ser Phe Cys Leu Leu Gly Leu Leu Gly Thr Ala Phe
 50 55 60
 His Pro Phe Leu Gln Phe Ala Gln Leu Leu Leu Xaa Asp Gly Ala Val
 65 70 75 80
 35 Cys Leu Cys Val Ala Leu Pro Arg Leu Gly Gly Leu Leu Ile Leu Pro
 85 90 95
 Gly Cys Val Val Ala Phe Leu Gly Ser Leu Asn Leu Leu Gln Pro Leu
 100 105 110
 40 Gln Pro Gly Leu Leu Gly Leu Ala Glu Ala Val Leu Gly Arg Pro Ala
 115 120 125
 Leu Ala Glu Ala Ala Gln His Arg Pro Val Glu Ser Pro Pro Leu Pro
 130 135 140
 Gly Ala His Pro Leu Thr Val Leu Pro Leu Arg Leu Leu Pro His Leu
 145 150 155 160
 45 Gln Val Gln Arg Ala Gln Pro Leu Ser Arg Arg Glu Lys Gly Met Pro
 165 170 175
 Gly Leu Leu Gln Cys Ala Ile Leu Gly Ala Leu Leu His Gly Pro Pro
 180 185 190
 50 Pro Leu Ser Gly Pro Val Ser Gln Leu Leu Gly Ile Ser Leu Leu Asp
 195 200 205
 Ala Gly Ala Leu Leu Glu
 210

55 <210> 1316
 <211> 163
 <212> PRT
 <213> Homo sapiens

<400> 1316
 60 Gly Xaa Gln His Ile Leu Xaa Glu Lys Lys Pro Xaa Ala Leu Gly Gly
 1 5 10 15
 Pro Ala Arg Ser Gln Arg Leu Val Pro Cys Pro Pro Cys Ser Val Glu
 20 25 30

Cys Ser Asp Ala Ala Leu Pro Ala Ser Ala His Thr Glu Leu Leu Ser
 35 40 45
 Ser Arg Pro Pro Trp His Ser Val Pro Pro Val Pro Ala Val Cys Ala
 50 55 60
 5 Ala Ala Pro Xaa Arg Arg Arg Cys Leu Pro Leu Arg Gly Ser Pro Ser
 65 70 75 80
 Ser Gly Arg Ser Ser His Pro Ser Gly Leu Arg Gly Ser Phe Ser Trp
 85 90 95
 Lys Pro Gln Pro Pro Ser Ala Ser Ser Ala Arg Ala Ser Gly Pro Cys
 100 105 110
 10 Gly Ser Arg Pro Arg Pro Pro Gly Ser Arg Gly Ser Arg Pro Ala Gln
 115 120 125
 Ala Gly Gly Lys Pro Pro Ala Ala Arg Arg Ala Pro Ala His Cys Pro
 130 135 140
 15 Ala Leu Ala Ala Ser Pro Ala Pro Pro Gly Ala Ala Arg Ser Ala Ala
 145 150 155 160
 Gln Pro Pro

20 <210> 1317
 <211> 162
 <212> PRT
 <213> Homo sapiens

25 <400> 1317
 Thr Arg Pro Phe Pro Thr Ser Pro Phe Pro Arg Gln Arg Pro Leu Pro
 1 5 10 15
 Ser Leu Gly Pro Arg Thr Ser Ser Leu Lys Gly Gln Arg Ser Ser Gln
 20 25 30
 30 Arg Ala Thr Val Gln Gly Pro Glu Gly Pro Ala Leu Gln Glu Lys Leu
 35 40 45
 Gly Ser Glu Pro Gly Trp Val Asn Val Ala Glu Gly Leu Ser Gly His
 50 55 60
 35 Ser Gly Ala His Thr Leu His Val Val Gly Arg Val Gln Ala Asn Ala
 65 70 75 80
 Ala Thr Leu Gln Leu Ala Leu Ala Pro Ala Leu Leu Val Leu Leu Thr
 85 90 95
 His Leu Gln Gln Leu Leu Pro Cys Ser Glu Ala Gln Leu Ile Ser Phe
 100 105 110
 40 Leu Ala Ser Val Val Ile Glu Cys Pro Xaa Arg Thr Pro Val Gly Ala
 115 120 125
 Phe Xaa Gly Leu Ser Ser Ser Asp His Ser Ser Ser Cys Pro Val Pro
 130 135 140
 45 Gly Asp Pro Gly Thr Gly Val Gly Gly Xaa Gly Ile Xaa Val Gly Gln
 145 150 155 160
 Xaa Leu

50 <210> 1318
 <211> 126
 <212> PRT
 <213> Homo sapiens

55 <400> 1318
 Val Phe Leu Phe Leu Cys Val Gly Val Cys Gln Val Leu Ile His Ala
 1 5 10 15
 Arg Thr Ser His Lys Arg Val Leu Leu Gly Gln Asn Tyr Thr His Pro
 20 25 30
 60 Lys Pro Thr Pro Gly Thr Pro Lys Gln Arg Ser Gly Thr Glu Ser Thr
 35 40 45
 Ala Pro Gly Glu Ala Gln Ala Pro Leu Asn Ala Ser Val Thr Ser Asp
 50 55 60
 Leu Pro Ser Cys Pro Gln Pro Arg Leu Val Pro Ser Leu Pro Val Pro

	65	Ser	Leu	Asp	Lys	Gly	Pro	Ser	Pro	Pro	Trp	Val	Pro	Gly	Leu	Pro	Pro	80
					85						90					95		
5		Ser	Arg	Asp	Arg	Gly	Ala	Ala	Arg	Glu	Arg	Arg	Phe	Arg	Ala	Leu	Arg	
				100						105					110			
		Val	Arg	Leu	Ser	Arg	Arg	Ser	Trp	Ala	Leu	Asn	Gln	Gly	Gly			
				115					120					125				
		<210>	1319															
10		<211>	215															
		<212>	PRT															
		<213>	Homo sapiens															
		<400>	1319															
15		Ala	Pro	Pro	Asp	Phe	Leu	Arg	Ala	Thr	Gly	Asp	Arg	Ala	Glu	Pro	Ser	
		1				5					10				15			
		Val	Tyr	Trp	Ala	Ala	Val	Thr	Leu	Arg	Phe	Gln	Met	Lys	Met	Phe	Glu	
				20					25					30				
20		Ser	Ala	Asp	Ser	Thr	Ala	Thr	Arg	Ser	Gly	Gln	Asp	Leu	Trp	Ala	Glu	
				35					40					45				
		Ile	Cys	Ser	Cys	Leu	Pro	Asn	Pro	Glu	Gln	Glu	Asp	Gly	Ala	Asn	Asn	
				50				55					60					
		Ala	Phe	Ser	Asp	Ser	Phe	Val	Asp	Ser	Cys	Pro	Glu	Gly	Glu	Gly	Gln	
							70					75					80	
25		Arg	Glu	Val	Ala	Asp	Phe	Ala	Val	Gln	Pro	Ala	Val	Lys	Pro	Trp	Ala	
						85					90					95		
		Pro	Leu	Gln	Asp	Ser	Glu	Val	Tyr	Leu	Ala	Ser	Leu	Glu	Lys	Lys	Leu	
					100					105					110			
30		Arg	Arg	Ile	Lys	Gly	Leu	Asn	Gln	Glu	Val	Thr	Ser	Lys	Asp	Met	Leu	
				115					120					125				
		Arg	Thr	Leu	Ala	Gln	Ala	Lys	Lys	Glu	Cys	Trp	Asp	Arg	Phe	Leu	Gln	
				130				135					140					
		Glu	Lys	Leu	Ala	Ser	Glu	Phe	Phe	Val	Asp	Gly	Leu	Asp	Ser	Asp	Glu	
							150					155					160	
35		Ser	Thr	Leu	Glu	His	Phe	Lys	Arg	Trp	Leu	Gln	Pro	Asp	Lys	Val	Ala	
						165					170					175		
		Val	Ser	Thr	Glu	Glu	Val	Gln	Tyr	Leu	Ile	Pro	Pro	Glu	Ser	Gln	Val	
					180					185					190			
40		Glu	Lys	Pro	Val	Ala	Arg	Gly	Arg	Thr	Thr	Xaa	Arg	Gly	Thr	Ser	Gln	
				195					200					205				
		Gln	Xaa	Gln	Lys	Gln	Leu	Ile										
				210				215										
		<210>	1320															
45		<211>	185															
		<212>	PRT				</											

Ser Gly Gly Ile Arg Tyr Trp Thr Ser Ser Val Leu Thr Xaa Thr Leu
 115 120 125
 Ser Gly Trp Ser His Leu Leu Lys Cys Ser Lys Xaa Leu Ser Ser Glu
 130 135 140
 5 Ser Ser Pro Ser Thr Lys Asn Ser Glu Ala Asn Phe Ser Trp Arg Asn
 145 150 155 160
 Arg Ser Gln His Phe Xaa Leu Ala Trp Ala Lys Val Arg Ser Met Ser
 165 170 175
 10 Xaa Glu Val Thr Ser Asp Xaa Asn Leu
 180 185

 <210> 1321
 <211> 127
 <212> PRT
 15 <213> Homo sapiens

 <400> 1321
 Asn Phe Xaa Val Xaa Pro Ala Val Xaa Pro Trp Val Pro Phe Gln Xaa
 1 5 10 15
 20 Ser Lys Val Ile Xaa Leu Xaa Arg Glu Glu Xaa Lys Lys Asn Gln Arg
 20 25 30
 Phe Xaa Ser Glu Val Thr Xaa Lys Asp Met Leu Arg Thr Leu Ala Gln
 35 40 45
 25 Ala Xaa Lys Lys Cys Trp Asp Arg Phe Leu Gln Glu Lys Leu Ala Ser
 50 55 60
 Glu Phe Phe Val Asp Gly Leu Asp Ser Asp Glu Ser Xaa Leu Glu His
 65 70 75 80
 Phe Lys Arg Trp Leu Gln Pro Asp Lys Val Xaa Val Ser Thr Glu Glu
 85 90 95
 30 Val Gln Tyr Leu Ile Pro Pro Glu Ser Gln Val Glu Lys Pro Val Ala
 100 105 110
 Glu Asp Glu Pro Ala Ala Gly Asp Lys Pro Ala Ala Ala Glu Gln
 115 120 125

 35 <210> 1322
 <211> 204
 <212> PRT
 <213> Homo sapiens

 40 <400> 1322
 Leu Phe Tyr Lys Gly Asn Glu Lys Lys Tyr Thr Met Ser Asp Glu Val
 1 5 10 15
 Phe Ser Thr Thr Leu Ala Tyr Thr Lys Ser Pro Lys Val Thr Lys Arg
 20 25 30
 45 Thr Thr Phe Gln Asp Glu Leu Ile Arg Ala Ile Thr Ala Arg Ser Ala
 35 40 45
 Arg Gln Arg Ser Ser Glu Tyr Ser Asp Asp Phe Asp Ser Asp Glu Ile
 50 55 60
 Val Ser Leu Gly Asp Phe Ser Asp Thr Ser Ala Asp Glu Asn Ser Val
 65 70 75 80
 50 Asn Lys Lys Met Asn Asp Phe His Ile Ser Asp Asp Glu Glu Lys Asn
 85 90 95
 Pro Ser Lys Leu Leu Phe Leu Lys Thr Asn Lys Ser Asn Gly Asn Ile
 100 105 110
 55 Thr Lys Asp Glu Pro Val Cys Ala Ile Lys Asn Glu Glu Glu Met Ala
 115 120 125
 Pro Asp Gly Cys Glu Asp Ile Val Val Lys Ser Phe Ser Glu Ser Gln
 130 135 140
 60 Asn Lys Asp Glu Glu Phe Glu Lys Asp Lys Ile Lys Met Lys Pro Lys
 145 150 155 160
 Pro Arg Ile Leu Ser Ile Lys Ser Thr Ser Ser Glu Asn Asn Ser Leu
 165 170 175
 Asp Thr Asp Asp His Phe Lys Pro Ser Pro Arg Pro Arg Glu Tyr Val

180 185 190
 Glu Lys Glu Lys Ser His Gly Gly Arg Arg Met Asp
 195 200

5 <210> 1323
 <211> 142
 <212> PRT
 <213> Homo sapiens

10 <400> 1323
 Leu Lys Lys Ala Ser Phe Phe Ser Phe His Phe Ser Thr Ala Val Lys
 1 5 10 15
 Leu Ser Phe Phe Phe Ser Ala Thr Val Ser Ser Ser Phe Cys Phe Phe
 20 25 30
 15 Ala Leu Ser Tyr Ser Leu Ser Phe Leu Phe Phe Ser Leu Arg Tyr Ser
 35 40 45
 Ile Phe Phe Ser Phe His Phe Ser Lys Ala Cys Ser Ala Ser Pro Phe
 50 55 60
 20 Leu Ala Ala Phe Ser Ser Ser Val Phe Leu Leu Phe Phe Ser Ser Ser
 65 70 75 80
 Leu Phe Leu Ala Ala Ile Phe Phe Ala Ser Phe Ser Phe Ile Ala Phe
 85 90 95
 Gln Ala Ser Asn Asp Ala Asn Ala Ser Ser Leu Leu Ala Ala Phe Phe
 100 105 110
 25 Cys Ser Phe Trp Ile Leu Lys Phe Ser Leu Ser Ile Leu Phe Ile Leu
 115 120 125
 Xaa Ile Ser Cys Lys Tyr Thr Phe Phe Phe Ser Asn His Ser
 130 135 140

30 <210> 1324
 <211> 193
 <212> PRT
 <213> Homo sapiens

35 <400> 1324
 Val Phe Glu Glu Ile Leu Val Leu Lys Gly Asp Ser Thr Asp Asn Tyr
 1 5 10 15
 Leu Phe Ser Leu Phe Arg Asp Phe Lys Ser Leu Gly Gln Lys Pro Xaa
 20 25 30
 40 Gln Lys Gln Ser Ile Glu Pro Asp Arg Ala Asp Asn Ile Arg Ala Ala
 35 40 45
 Val Tyr Gln Glu Trp Leu Glu Lys Lys Asn Val Tyr Leu His Glu Met
 50 55 60
 45 Xaa Arg Ile Lys Arg Ile Glu Ser Glu Asn Leu Arg Ile Gln Asn Glu
 65 70 75 80
 Gln Lys Lys Ala Ala Lys Arg Glu Glu Ala Leu Ala Ser Phe Glu Ala
 85 90 95
 Trp Lys Ala Met Lys Glu Lys Glu Ala Lys Lys Ile Ala Ala Lys Lys
 100 105 110
 50 Arg Leu Glu Glu Lys Asn Lys Arg Lys Thr Glu Glu Glu Asn Ala Ala
 115 120 125
 Arg Lys Gly Glu Ala Leu Gln Ala Phe Glu Lys Trp Lys Glu Lys Lys
 130 135 140
 55 Met Glu Tyr Leu Lys Glu Lys Asn Arg Lys Glu Arg Glu Tyr Glu Arg
 145 150 155 160
 Ala Lys Lys Gln Lys Glu Glu Glu Thr Val Ala Glu Lys Lys Lys Asp
 165 170 175
 Asn Leu Thr Ala Val Glu Lys Trp Asn Glu Lys Lys Glu Ala Phe Phe
 180 185 190

60 Lys

<210> 1325

<211> 214
 <212> PRT
 <213> Homo sapiens

5 <400> 1325
 Lys Met Asn Leu Pro Thr Pro Phe Xaa Pro Ile Thr Ala Arg Pro Pro
 1 5 10 15
 Met Tyr Glu Asp Tyr Met Pro Leu His Ala Pro Leu Pro Pro Thr Ser
 20 25 30
 10 Pro Gln Pro Pro Glu Glu Pro Pro Leu Pro Asp Glu Asp Glu Glu Leu
 35 40 45
 Ser Ser Glu Glu Ser Glu Tyr Glu Ser Thr Asp Asp Glu Asp Arg Gln
 50 55 60
 Arg Met Asn Lys Leu Met Glu Leu Ala Asn Leu Gln Pro Lys Arg Pro
 15 65 70 75 80
 Lys Thr Ile Lys Gln Arg His Val Arg Lys Lys Arg Lys Ile Lys Asp
 85 90 95
 Met Leu Asn Thr Pro Leu Cys Pro Ser His Ser Leu His Pro Val Leu
 100 105 110
 20 Leu Pro Ser Asp Val Phe Asp Gln Pro Gln Pro Val Gly Asn Lys Arg
 115 120 125
 Ile Glu Phe His Ile Ser Thr Asp Met Pro Ala Ala Phe Lys Lys Asp
 130 135 140
 Leu Glu Lys Glu Gln Asn Cys Glu Glu Lys Asn His Asp Leu Pro Ala
 145 150 155 160
 25 Thr Glu Val Asp Ala Ser Asn Ile Gly Phe Gly Lys Ile Phe Pro Lys
 165 170 175
 Pro Asn Leu Asp Ile Thr Glu Glu Ile Lys Glu Asp Ser Asp Glu Met
 180 185 190
 30 Pro Ser Glu Cys Ile Ser Arg Xaa Glu Leu Gly Lys Gly Arg Ile Ser
 195 200 205
 Arg Lys Arg Asn Gly Asn
 210

35 <210> 1326
 <211> 140
 <212> PRT
 <213> Homo sapiens

40 <400> 1326
 Arg Ser Phe Xaa Met Lys Gly Xaa Gln Asn Val Phe Xaa Lys Xaa Asn
 1 5 10 15
 Trp Lys Arg Ala Glu Phe Xaa Arg Xaa Glu Met Glu Xaa Leu Ser Val
 20 25 30
 45 Phe Xaa Ser Tyr Xaa Pro Xaa Glu Pro Asn Cys Arg Ile Xaa Val Lys
 35 40 45
 Asn Leu Ala Lys Xaa Val Gln Xaa Lys Xaa Leu Lys Xaa Ile Phe Gly
 50 50 55 60
 Xaa Xaa Val Xaa Phe Ser Ser Xaa Xaa Gln Xaa Ile Met Phe Xaa Lys
 65 70 75 80
 50 Arg Xaa Xaa Lys Lys Gly Xaa Met Lys Xaa Gln Ala Phe Ile Gly Leu
 85 90 95
 Pro Asn Glu Lys Ala Xaa Ala Lys Xaa Leu Lys Glu Xaa Asn Gly Xaa
 100 105 110
 55 Xaa Leu Phe Gly Lys Pro Met Xaa Val Gln Phe Ala Arg Xaa Xaa Xaa
 115 120 125
 Pro Xaa Gln Asp Pro Lys Glu Gly Lys Xaa Lys Xaa
 130 135 140

60 <210> 1327
 <211> 214
 <212> PRT
 <213> Homo sapiens

<400> 1327

1 Gln Lys Asp Tyr Glu Glu Ser Ser Trp Asp S r Glu Ser Leu Cys Glu
 5 Thr Val Ser Gln Lys Asp Val Cys Leu Pro Lys Ala Thr His Gln Lys
 Glu Ile Asp Lys Ile Asn Gly Lys Leu Xaa Glu Ser Pro Asp Asn Asp
 Gly Phe Leu Lys Ala Pro Cys Xaa Met Lys Val Ser Ile Pro Thr Lys
 10 Ala Leu Xaa Leu Met Asp Met Gln Thr Phe Lys Ala Glu Pro Pro Glu
 Lys Xaa Ser Ala Phe Glu Pro Ala Ile Glu Met Gln Lys Ser Val Pro
 15 Asn Lys Ala Leu Glu Leu Lys Asn Glu Xaa Thr Leu Arg Ala Asp Gln
 Met Phe Pro Ser Xaa Ser Lys Gln Lys Lys Xaa Glu Glu Asn Ser Trp
 Asp Ser Xaa Ser Leu Xaa Glu Thr Val Ser Gln Lys Asp Val Cys Val
 20 Pro Lys Ala Thr His Gln Lys Glu Met Asp Lys Ile Ser Gly Lys Leu
 Glu Asp Ser Thr Ser Leu Ser Lys Ile Leu Asp Thr Val His Ser Cys
 25 Glu Arg Xaa Xaa Glu Leu Xaa Lys Asp Pro Val Asn Asn Arg Xaa Xaa
 Lys Met Glu Gln Met Lys Lys Lys Phe Trp Cys Xaa Glu Lys Glu Thr
 Val Arg Ser Gln Arg Ser
 30 210

<210> 1328

<211> 86

<212> PRT

35 <213> Homo sapiens

<400> 1328

1 Leu Phe Xaa Asn Cys Lys Xaa Cys Xaa Gly Phe Pro Ser Xaa Leu Met
 40 Ser Ser Arg Leu His Ser Ile His Pro Asp Leu Val Xaa Ser Leu Arg
 Trp Ser Ala Val Ala Gln Xaa Ser Ala His Cys Lys Leu Cys Leu Pro
 Gly Ser Arg His Ser Pro Ala Thr Ala Ser Arg Val Val Gly Leu Gln
 45 Ala Pro Ala Thr Thr Pro Thr Tyr Phe Phe Phe Cys Ile Phe Ser Arg
 Asp Gly Phe Xaa Pro Cys
 50 85

<210> 1329

<211> 77

<212> PRT

55 <213> Homo sapiens

<400> 1329

1 Val Pro Xaa Leu Gln Lys Xaa Xaa Arg Ile Pro Ile Xaa Pro Asp Glu
 60 Gln Gln Thr Ser Phe Asn Pro Pro Arg Ser Arg Xaa Val Thr Gln Val
 Glu Cys Ser Gly Ala Xaa Phe Gly Ser Leu Gln Thr Leu Pro Pro Arg
 Phe Thr Pro Phe Ser Cys His Ser Leu Pro Ser Ser Gly Thr Thr Gly

50 55 60
Ala Cys His His Ala His Leu Phe Phe Phe Leu Tyr Phe
65 70 75

5 <210> 1330
<211> 189
<212> PRT
<213> Homo sapiens

10 <400> 1330
Tyr Asp Asp Asp Asp Asp Asp Trp Asp Trp Asp Glu Gly Val Gly Lys
1 5 10
Leu Ala Lys Gly Tyr Val Trp Asn Gly Ser Asn Pro Gln Ala Asn
20 25 30
15 Arg Gln Thr Ser Asp Ser Ser Ser Ala Lys Met Ser Thr Pro Ala Asp
35 40 45
Lys Val Leu Arg Lys Phe Glu Asn Lys Ile Asn Leu Asp Lys Leu Asn
50 55 60
Val Thr Asp Ser Val Ile Asn Lys Val Thr Glu Lys Ser Arg Gln Lys
65 70 75 80
20 Glu Ala Asp Met Tyr Arg Ile Lys Asp Lys Ala Asp Arg Ala Thr Val
85 90 95
Glu Gln Val Leu Asp Pro Arg Thr Arg Met Ile Leu Phe Lys Met Leu
100 105 110
25 Thr Arg Gly Ile Ile Thr Glu Ile Asn Gly Cys Ile Ser Thr Gly Lys
115 120 125
Glu Ala Asn Val Xaa His Ala Ser Thr Ala Asn Gly Glu Ser Arg Ala
130 135 140
Ile Lys Ile Tyr Lys Thr Ser Ile Leu Val Phe Lys Asp Arg Asp Lys
145 150 155 160
30 Tyr Xaa Ser Gly Glu Phe Xaa Phe Arg His Gly Tyr Cys Lys Gly Asn
165 170 175
Pro Xaa Lys Met Xaa Lys Thr Trp Ala Xaa Lys Arg Lys
180 185

35 <210> 1331
<211> 126
<212> PRT
<213> Homo sapiens

40 <400> 1331
Ile Leu Ile Ala Leu Leu Ser Pro Phe Ala Val Leu Ala Trp Xaa Thr
1 5 10
Leu Ala Ser Phe Pro Val Leu Met Gln Pro Phe Ile Ser Val Met Ile
20 25 30
45 Pro Leu Val Asn Ile Leu Asn Lys Ile Ile Leu Val Leu Gly Ser Asn
35 40 45
Thr Cys Ser Thr Val Ala Leu Ser Ala Leu Ser Leu Met Arg Tyr Ile
50 55 60
Ser Ala Ser Phe Cys Leu Asp Phe Ser Val Thr Leu Phe Met Thr Glu
65 70 75 80
Ser Val Thr Phe Ser Leu Ser Lys Leu Ile Leu Phe Ser Asn Phe Arg
85 90 95
55 Lys Thr Leu Ser Ala Gly Val Asp Ile Leu Ala Glu Leu Leu Ser Glu
100 105 110
Val Cys Arg Phe Ala Cys Gly Leu Leu Pro Pro Phe Gln Thr
115 120 125

60 <210> 1332
<211> 241
<212> PRT
<213> Homo sapiens

<400> 1332

	Ser	Gly	Cys	Gln	Thr	Trp	Pro	Met	Gln	Ile	Xaa	Ser	Asp	Phe	Asn	Met
	1				5					10					15	
5	Leu	Xaa	Pro	Gly	Xaa	Xaa	Val	Xaa	Ile	Ile	Asp	Val	Ser	Pro	Val	Arg
				20					25					30		
	Gly	Gly	Arg	Xaa	Thr	Pro	His	Ala	Leu	Glu	Phe	Leu	Arg	Lys	Asp	Cys
			35					40					45			
	Ala	Asn	Val	Asn	Asp	Phe	Phe	Met	Arg	His	Ser	Val	Ala	Val	Met	Thr
		50					55					60				
10	Val	Arg	Glu	Leu	Phe	Glu	Phe	Val	Thr	Asp	Pro	Ser	Ile	Thr	His	Glu
	65					70				75					80	
	Asn	Met	Asp	Ala	Tyr	Leu	Ser	Lys	Ala	Met	Glu	Ile	Ala	Ser	Gln	Arg
				85					90						95	
	Thr	Lys	Glu	Glu	Arg	Ser	Ser	Gln	Asp	His	Val	Asp	Glu	Glu	Val	Phe
15				100					105					110		
	Lys	Arg	Ala	Tyr	Ile	Pro	Arg	Thr	Leu	Asn	Glu	Val	Lys	Asn	Tyr	Glu
			115					120					125			
	Arg	Asp	Met	Asp	Ile	Ile	Met	Lys	Leu	Lys	Glu	Glu	Asp	Met	Ala	Met
		130					135					140				
20	Asn	Ala	Gln	Gln	Asp	Asn	Ile	Xaa	Tyr	Gln	Thr	Val	Thr	Gly	Leu	Lys
	145					150					155				160	
	Lys	Asp	Leu	Ser	Gly	Val	Gln	Lys	Val	Pro	Ala	Leu	Leu	Glu	Asn	Gln
				165					170					175		
	Val	Glu	Glu	Arg	Thr	Cys	Xaa	Asp	Ser	Glu	Asp	Ile	Gly	Ser	Xaa	Glu
25				180					185					190		
	Cys	Xaa	Asp	Thr	Asp	Xaa	Glu	Glu	Gln	Gly	Asp	His	Ala	Arg	Pro	Lys
			195					200					205			
	Lys	His	Thr	Thr	Asp	Pro	Asp	Ile	Asp	Lys	Lys	Glu	Arg	Lys	Lys	Met
		210					215					220				
30	Val	Lys	Glu	Ala	Gln	Arg	Glu	Lys	Arg	Lys	Asn	Lys	Ile	Pro	Lys	His
	225					230					235					240
	Val															